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1. Ticks of public health importance in Continental Europe

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About forty species of hard ticks and twenty species of soft ticks have been reported in Continental Europe (Arthur 1963, Hillyard 1996, Morel 2003), with minor variations due to remaining ambiguities concerning tick taxonomy and progressive fluctuating European boundaries. For hard ticks, the genus *Ixodes* is majorly represented with more than twenty species. For soft ones, the genus *Argas* is predominant with about ten species. Among this whole tick community, seventeen species are clearly identified as vectors of bacteria and/or viruses (Parola & Raoult 2001, Hubalek 1996).

Although the global list of European ticks of health importance is well established, their detailed geographical distribution as well as their vectorial competence and/or capacity for pathogens, for which the tick species are considered to be occasional vectors, remain poorly known. This results in our deficient ability to assess temporal and spatial risks of (re)-emergence, and also spread, of many tick-borne diseases in Europe. Such gaps are further worsen by the dysfunction or the absence of entomological surveillance systems for ticks and tick-borne diseases in many Europe countries. Tick surveillance initiatives remained punctual, individual and are not well coordinated. However, some networks have recently emerged, that are not all centred on Europe, like the “Integrated Consortium on Ticks and Tick-borne Diseases” (ICTTD) (http://www.icttd.nl/) or the “European network for surveillance of tick borne diseases” (http://www.ist-world.org/ProjectDetails.aspx?ProjectId=31d3130892f64a56a209399738236fd7).

When available, surveillance or research data on tick distribution has long been mainly originating from Western Europe whereas little information was apparently accessible from Eastern countries. This was probably due to the lack of scientific exchange between the two blocks during the cold war and to the use of the Russian language in scientific publications from the East. Mainly tick samplings to assess species distribution were conducted before the 1960s during the glorious period of medical and veterinary entomology. Such historical data may not or partially reflect the current status of ticks in Europe and might present some biases or failings (Vial 2009): (i) the information is not homogeneous because it came from distinct collectors that have used different protocols and techniques; (ii) samplings may have been conducted in accessible areas only, for example along the main roads, which is not representative of realized distribution; (iii) data generally correspond to presence data only because scientists did not document absences or because records come from museum collections where only specimens that were found are stored, which is not sufficient to assess abundance of ticks and seasonal dynamics of populations; and (iv) misidentification may have occurred depending on the expertise and the sense of responsibility of the collectors and because of the complexity and the ambiguity of the morphological keys used at this period for tick identification.

Tick species	Geographical range	Transmitted pathogens
Ixodes ricinus	Western Europe to Central Asia, North Africa	Lyme borreliosis (*B. burgdorferi ss, B. garinii, B. afzelii*) Human granulocytic ehrlichiosis Tularaemia Rickettsiosis (*R. helvetica, R. monacensis*) Babesiosis (*B. divergens, B. microti*) Tick-borne encephalitis Louping ill Tribec virus
Ixodes persulcatus	Eastern Europe, Russia, Asia, Northern Japan	Lyme borreliosis (*B. garinii, B. afzelii*) Tick-borne encephalitis
Ixodes uriae	Circumpolar in both hemispheres, Europe, Asia	Lyme borreliosis (*B. garinii*) Many seabird viruses
Ixodes trianguliceps	Europe, Russia, Asia	Lyme borreliosis (*B. garinii*) Coxiellosis Babesiosis (*B. microti*)
Ixodes hexagonus	Europe, Russia, North Africa, Southern Asia	Lyme borreliosis (*B. garinii*)
Rhipicephalus sanguineus	Mediterranean littoral, Africa, USA, India, Israel, Black sea	Rickettsiosis (*R. conorii, R. massiliae*) Coxiella burnetti Thogoto virus
Rhipicephalus bursa	Southern Europe, North Africa, Russia, Central Asia	Thogoto virus Bhanja virus (occasionally)
Dermacentor reticulatus	Europe to Central Asia	Tularaemia Rickettsiosis (*R. slovaca, R. raoulti*)
Dermacentor marginatus	From Morocco through Spain and France, Central Europe, Central Asia	Rickettsiosis (*R. slovaca, R. raoulti*) Tularaemia Coxiella burnetti Bhanja virus Dhori virus
Haemaphysalis punctata	Europe from Britain to Spain, North Africa, Turkey to Caucasus and China	Tribec virus (occasionally) Bhanja virus
Hyalomma marginatum	Southern Europe, North Africa, Russia, Middle East, Central Asia to China	*R. aeschlimannii* Crimean-Congo Haemorrhagic Fever (main vector) Dhori virus Bhanja virus (occasionally)
Hyalomma scupense	South-Eastern Europe, North Africa, Central Asia to China, Russia	Dhori virus
Boophilus annulatus	Worldwide	Thogoto virus Bhanja virus (occasionally)
Ornithodoros erraticus	Iberian Peninsula, North Africa, Greece, Cyprus, Syria	Tick-borne relapsing fever (*B. hispanica*)
Ornithodoros tholozani	Eastern Europe, former USSR, Egypt to China	Tick-borne relapsing fever (*B. persica*)
Ornithodoros asperus	Eastern Europe, Caucasia	Tick-borne relapsing fever (*B. caucasica*)
Ornithodoros maritimus	Coasts of Great Britain, Ireland, France, Sardinia and Tunisia	Seabird viruses

Similarly, most of the available knowledge concerning vectorial competence and/or capacity of ticks comes from past studies and may be not or partially representative of the current situation in Europe. Those surveys were essentially conducted through experimental infections in laboratory and do not reflect the natural conditions of transmission, including the tick-host contacts defining the vectorial capacity and thus the risk of transmission. Finally, technical difficulties remain unresolved to rapidly and totally screen ticks from the field for diverse infections although improvements have been recently done (Halos et al. 2006).

An exception is observed for the “famous” *I. ricinus* tick transmitting Lyme borreliosis, which is the most prevalent arthropod-transmitted human infection in northern Europe. Many records are available concerning the tick presence (Estrada-Pena 1999, Gern & Humair 2002) and prediction models of suitable habitat have been established for Europe (Estrada-Pena 1999, Beugnet et al. 2009). Data are also available, at least at the national level, on the Lyme borreliosis distribution based on clinical case report and seroprevalence studies although comparisons between countries may be impaired by the disparate surveillance systems among European countries (Cimmino 1998). All these studies allowed establishing that the incidence of Lyme borreliosis in human depends on the acarological risk (the density of infected nymphs) and the human exposure (degree of human contact with infection and susceptibility to infection). Because *Borrelia burgdorferi* sl infected ticks are found almost everywhere in the distribution of the vector, on a large scale, the distribution of the Lyme borreliosis closely matches the distribution of the vectors. At a finer scale, the distribution of Lyme borreliosis is linked to deciduous moist forest, as well as recreational, leisure and occupational activities (Jaenson et al. 2009). Specific surveys focusing on the ecology of *I. ricinus* showed that an increase in distribution and abundance could be linked to climate changes, such as modifications of temperature and summer rainfall (Estrada-Pena & Venzal 2006, Lindgren & Jaenson 2006, Daniel et al. 2009, Gray et al. 2009). However, the emergence of Lyme borreliosis in Europe cannot exclusively be attributed to climatic factors but also to changes in human behaviour, as well as increased awareness of ticks as vectors and increasing interest in the disease (Randolph 2001).

Conversely, some groups of ticks remain completely neglected regarding human and animal health, for example the soft ticks. These ticks are endophilous (living in underground microhabitats like mammal burrows, caves and deep cracks or fissures in human and animal buildings) and are generally undetectable (Sonenshine 1993). They engorge rapidly on their hosts (30 minutes to 1 hour for most instars) and can be collected only in their microhabitat, not on their hosts (Morel 2003, Vial 2009). However, the soft ticks of the genus *Ornithodoros* can transmit to humans tick-borne relapsing fever (TBRF) that is caused by spirochetes of the genus *Borrelia* and is historically known in Europe (Rebaudet & Parola 2006) and to domestic and wild suids African swine fever virus that has been recently introduced in Caucasus and may spread in the next decades into Europe (Rowlands et al. 2008). Nevertheless, TBRF is still considered a negligible disease because it rarely causes the death of patients and it can be treated with antibiotics although many complications may occur. Its reporting is not systematic neither obligatory in European countries and its incidence is probably underestimated because of misdiagnosis (Vial in press).

Key words: Ticks, tick-borne diseases, Europe.

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2. Invasive ticks in the associated European territories: the example of the tropical bont tick in the Caribbean Region - current situation and output of the CaribVET working group

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Tropical Bont Tick (TBT), *Amblyomma variegatum*, is a major constraint to ruminants breeding in Africa and the Caribbean: first, bites induce attachment lesions and direct losses by blood spoliation. Second, TBT favors the development of the acute form of dermatophilosis, a skin disease caused by the bacteria *Dermatophilus congolensis* (Martinez et al., 1992). Finally, TBT is the vector of *Ehrlichia ruminantium*, an intracellular bacteria, causal agent of the ruminant's fatal disease heartwater. In the Caribbean, dermatophilosis has been responsible of direct and indirect losses in livestock population (e.g., a loss of 75 % of the cattle population in Nevis has been recorded in the 1990s, Hadrill et al., 1990). Heartwater is currently present in the islands of Guadeloupe, Marie-Galante and Antigua, and apparently absent from the other islands, and was estimated to cause annual losses of 10% to 20% for national livestock herds (Barré et al., 1996). TBT may also transmit *Coxiella burnetti*, the agent of Q-fever, to humans.
It is believed that TBT was first imported into the Caribbean by livestock coming from West Africa to the island of Guadeloupe around the 19th century (Uilenberg et al., 1984). Spatial distribution of TBT was confined to three to four islands until the late 1960's when it began to spread rapidly. By the end of the 1980's, 18 Caribbean islands had become infested (Barré et al., 1987). The recent increased of TBT is believed to be partly associated with the establishment of cattle egrets (*Bubulcus ibis*) and ground feeding birds that live in close contact with livestock (Uilenberg, 1990; Corn et al, 1993; Barré et al, 1987). Costs of TBT introduction for American animal industry have been estimated to be worth than US$760 millions (Gersabeck, 1994).

A programme aiming to eradicate the TBT from the English Lesser Antilles was launched in 1994: the Caribbean *Amblyomma* Programme (CAP). Nine islands participated to the eradication activities: Anguilla, Antigua and Barbuda, Barbados, Dominica, Montserrat, Nevis, St Kitts, St Lucia and Saint Maarten (Pegram et al., 1998). To reach the objective of TBT eradication, CAP was organised in two overlapping stages. First, a treatment phase of all domestic ruminants was implemented during two to three years to control all adult TBT. Second, active surveillance programme was implemented to inform participants during treatments and verify TBT-freedom after treatments. Six islands out of nine were declared provisionally free of ticks from 2001 to 2003. TBT-freedom status was removed for St Kitts in

2004. Antigua and Barbuda, Nevis and Saint Maarten still remain with the “TBT-infested” status (Pegram et al., 2002a). CAP programme ended in 2008 at this situation.

Surveillance data were collected between 1997 and 2006 in a unique regional database. Surveillance data were analysed in four islands (Nevis, St Kitts, St Lucia, and Barbados) where control and surveillance followed the initial protocol and where enough data were collected. The evolution of TBT infestation levels and the efforts carried out throughout the surveillance period were described. Logistic regression identified factors associated with herds found infested with TBT (Ahoussou et al, 2010). Overall, treatment programmes were associated with a decrease in proportion of TBT-infested farms. High surveillance efforts were carried out throughout the 1997-2007 period for all island of interest, but inadequate level of surveillance was observed in several quarters especially for St Kitts. Third quarter of the year, as indication of adult TBT seasonality on livestock, was significantly associated with the risk of detecting TBT in Nevis and St Kitts livestock farms. Also, presence of cattle in Nevis farms was shown associated with an increasing probability of farms being declared TBT-infested. Outcomes of these analyses provide basis for recommendations to improve future national and regional control and surveillance activities. This analysis demonstrates the usefulness of long term and adequate surveillance data for control programmes and identification of factors associated with risk of having infested herds.

The CAP was the first multi-country approach of an animal health problem in the Caribbean and it promoted the creation of a regional animal health network named CaribVET in which veterinary services of the Caribbean and regional/international organizations work together to improve and harmonize the surveillance and control of animal diseases. The CAP ended in 2008 and was followed by a project of national veterinary epidemiologists/paraepidemiologists (VEP) funded by USDA-APHIS under the strategy of CaribVET. CaribVET working group on tick and tick borne disease met in Fort Collins 1-2nd October 2009. It gathered veterinary services from 12 Caribbean countries or territories including those from the previous CAP (Antigua, Barbados, Dominica, Nevis, St Lucia, St Maarten, St.Kitts, St.Vincent), French islands (Guadeloupe and Martinique) and USA territories (Florida and St Croix), plus experts on tick and tick borne diseases from CIRAD and CEAH, Fort Collins, US and previous CAP. Presentation were given by CIRAD Guadeloupe, USDA-VS-CEAH, Fort Collins, US, on the following: research needs for heartwater and TBT, surveillance planning and previous heartwater/CAP risk assessment, analysis of CAP data, spatial analysis and vector-borne diseases, habitat suitability models for three host ticks, mathematical framework for potential tick presence.

The group reviewed the current surveillance and control programs in the different Caribbean countries and in the USA, in particular reviewed the changes associated with the end of the CAP. A questionnaire sent before the meeting to all the countries helped to assess the current situation regarding animal population (evolution, main breeds, density, and exchange between countries), surveillance system (protocol, type of surveillance, level of surveillance), level of control, limiting factors for TBT surveillance and control. The group worked on the use of risk factor analysis, spatial analysis and modelling of tick population dynamic for improvement of surveillance and treatment. The group developed recommendations for surveillance and control protocols both regional recommendations and specific recommendations according to the current level of TBT prevalence. The group also worked on data to be collected by the countries for analysis purpose (spatial analysis, modelling).

The recommendations included

a) General recommendations:

- Establish country objectives for the control & surveillance of TBT (need for political will/ official program)
- Each country to write surveillance and control protocols
- Educate farmers & increase public awareness
- Identify risk factors for introduction, seasonality, and habitat risk
- If need for reducing treatment cost: seasonal treatment then treat just cattle, then just infested cattle.

b) Recommendations according to the level of infestation of the country

Non infested islands

- Target surveillance on animals not routinely sprayed
- Training to identify ticks: NVSL and CIRAD
- Incentive to send *Amblyomma* ticks
- Check antemortem at the slaughter house
- Identify risk factors for introduction including study on current cattle egret movements and exchange of ruminants
- Small mammals and dead bird surveillance (AI)
- If ticks found: establishing hot spot area, treatment

Low infestation islands

- Identify high risk period if seasonality has been demonstrated in country
- Maintain a surveillance program (active & passive) Active surveillance at least once/quarter or twice a year in fenced farms at least
- Encourage farmer peer support
- Pursue search and research for IPM (breed, vaccines against ticks, biological control)
- Need to set up contingency plan (if your maximum accepted prevalence is reached)

High infestation and heartwater situation

- A social economic analysis is needed to assess a control strategy
- TBT control voluntary by the farmers, cost recovery mechanism
- A minimum surveillance tool recommended is the record of Bayticol® sold (farmers, village…)
- Surveillance active or passive, random or targeted according depending of goals funding and staff

c) Recommendations regarding data collection for spatial analysis, modelling, genetic studies, surveillance

- Review TickINFO: requirements for improving data records for covariates (habitat, practices)
- Compile 3 years of rainfall data to find out if the period and evolution of wet season
- Define epidemiological units through better knowledge of roaming animal
- Produce maps representing spatial distribution of TBT and animal dispersion/distribution/density

It is believed that these recommendations will help the Caribbean region for the regional effort in the control of *Amblyomma* tick populations.

Key words: Ticks, tick-borne diseases, Carribean.

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3. Climatic and anthropogenic factors that may trigger the changing distribution of ticks in Europe and their relationships with tick-borne disease epidemiology

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There can be no doubt that ticks are highly sensitive to climate, specifically the thermal and moisture conditions that determine their rates of development and survival, respectively. In Europe, the most widespread and epidemiologically significant tick species is *Ixodes ricinus*, which requires a relative humidity of at least c.85% to maintain its water balance. At the same time, if temperatures during the middle part of the year (from about April to September) are too low, development from one stage to the next cannot be completed within one calendar year, forcing an additional over winter period with its attendant increase in mortality [1]. It is these constraints that determine the distribution of tick populations within certain latitudinal and altitudinal limits.

Furthermore, the seasonal activity of ticks of each life stage is differentially driven by the same climatic factors, causing variable degrees of synchrony between ticks of each life stage and thereby determining the transmission potential for a variety of pathogens. *Borrelia burgdorferi* s.l., for example, shows a long period of infectivity in its vertebrate hosts, so that larval ticks may feed some months after the infected nymphs and still allow transmission from nymphs to larvae via vertebrates. This, as well as the wide range of competent hosts, allows *B. burgdorferi* s.l. to circulate more or less wherever there are ticks. Some strains of these bacteria in North America, however, have been shown to have shorter periods of infectivity and therefore require greater degrees of synchrony between larvae and nymphs [2, 3]. These strains are indeed more prevalent in tick populations showing such synchrony [4]. This mirrors the situation for tick-borne encephalitis (TBE) virus in Europe, which has such a brief infective period (whether systemic or non-systemic) via transmission-competent rodents [5] that close larval-nymphal synchrony is needed for persistent cycles of transmission [6]. This has been shown to occur under certain seasonal temperature profiles, specifically where the rate of warming in the spring is sufficiently rapid to allow the higher threshold temperature for the onset of larval activity (c.10°C daily maximum) to follow soon after the lower threshold for nymphal activity (c.7°C). TBE distribution is therefore much more focal across it European range, a pattern that can be predicted from remotely-sensed climatic factors [7].

With the steep increase in temperatures that occurred in 1989 across most of Europe (at least 1°C mean annual daily maximum temperature, revealed by individual station records everywhere from northern Sweden to the Mediterranean and Ireland to Estonia) (see Ref 8 for typical patterns), we should not be surprised by the observed expansion of the tick's range beyond its previous northern latitudinal and altitudinal limits. Ticks were recorded further north in Sweden at the end of the 20th century [9] and in Finland in recent years [10], and have been recorded higher up mountains in Austria [11], Slovakia [12] and the Czech Republic [13]. In these regions, warming is unlikely to be accompanied by increased moisture stress, as is seen further south, and therefore more rapid development will not be countered by increased mortality. This warming, however, does not necessarily mean a greater rate of spring warming; observations show that the whole spring rise in temperature is usually shifted forward to slightly earlier in the year without any change in slope. Nevertheless, where thermal conditions are right for TBE virus transmission, human cases of TBE have started to appear at higher altitudes [11-13].

Therefore, it appears that the sort of changes in climate that have been recorded in Europe could indeed promote the incidence of tick-borne diseases. The salient question is whether this climate change is enough to explain the dramatic and abrupt emergence of tick-borne diseases that has occurred over the past two decades? Pathogens such as Rickettsia, Anaplasma and Babesia are now being revealed more commonly by improved surveillance activities; Lyme borreliosis is highly prevalent and recorded increasingly, but unreliably, since its identification in the 1980s; and TBE, that has been well known, well recognised and well recorded for several decades, showed remarkable step upsurges in incidence in central and eastern Europe (CEE) in the early 1990s and more gradual increases in western Europe (see time series in [14], with many newly identified foci, most recently north of Copenhagen in Denmark [15]. For Europe as a whole, the number of reported TBE cases doubled in 1993, influenced mainly by events in many CEE countries where the increase was between 3- (Estonia) and 28-fold (Lithuania and Poland) from 1988-92 to 1993-97. First it is clear that the number of recorded TBE cases in newly invaded mountainous regions is not sufficient to account for these upsurges. Factors operating within the core endemic regions must be identified. Secondly, the pattern of climate change is far too uniform to account for the highly heterogeneous pattern of changing TBE epidemiology; upsurges varied in degree and timing over small and large spatial scales [8]. Instead, a wealth of quantitative evidence compiled from many countries supports the notion that a variety of factors, acting independently with differential force in time and space, impacted synergistically on the virus, ticks, wildlife hosts and humans to generate heterogeneous patterns of emergence [16].

In summary, these factors included the following: abiotic changes (land cover associated with agricultural reorganization, as well as climate change); biotic changes (a greater abundance of large wildlife hosts for ticks, and better tick survival through reduced pesticide usage); and changing human activities associated with increased wealth and leisure on the one hand, and unemployment and poverty on the other hand. Both these anthropogenic factors operated most suddenly in CEE countries due to the socio-economic transition that followed independence from soviet rule and the adoption of free market economies. Recreation and the harvesting of fruits and fungi from forests, a deep cultural tradition in this part of Europe but now practiced more freely and sometimes for economic gain, brought people into greater contact with tick-infested habitats. In 2006, this was brought into sharp focus by an unusual spike in TBE incidence in some, but not all, western and CEE countries, apparently due to the exceptional weather conditions that favoured both mushroom growth and outdoor activity from June onwards [17]. As expected, human responses to such weather apparently varied according to cultural and socio-economic contexts.

A final significant point is that in Latvia, the 6-fold increase in 1993-94 has been followed by an equal, although slightly more gradual, decrease since 1999, reverting to levels typical of the 1970s and ‘80s. If climate change alone was the cause of the increase, what then was the cause of this decrease? Analyses suggest that a combination of better vaccination cover and changes in human behaviour in response to perceived risk have been responsible [18]. This indicates that when we identify correctly the causal factors underlying tick-borne disease dynamics, they may turn out to be amenable to immediate and effective intervention, targeted at the behaviour of vulnerable sections of the population, in ways that climate change is not.

Key words: Ticks, tick-borne diseases, Europe, climate, human behaviour.

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4. Surveillance of ticks in Europe: multiplicity of approaches

Surveillance of ticks in Europe based on tick presence reporting

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The ability for public and veterinary health agencies to assess the risks posed by tick-borne pathogens is reliant on an understanding of the main tick vector species (Jongejan & Uilenberg). Crucially the status, distribution and changing trends in tick distribution and abundance is an implicit requirement of any risk assessment, however this is contingent on the quality of tick distribution data. In many cases the status of a tick species is informed by historical records, field studies and anecdotal evidence. Retaining and updating this resource is a challenge, as the ongoing funding requirement to sustain and maintain active surveillance is prohibitive. Ideally longitudinal surveillance at a number of sites across a country or continent would provide information on the changing trends in tick abundance, but it tells us very little about their geographical distribution and host preference. Conducting a nationwide distribution (presence/absence) survey at a high resolution is undoubtedly the ultimate surveillance approach, however often it is hugely costly and for many health agencies is an unobtainable goal.

For those individuals involved in mapping the distribution of ticks, one of the few approaches achievable within a limited budget is the recording of presence data, through a variety of ‘passive’ recording and surveillance schemes. This approach has huge limitations in that the absence of data in a geographical location does not confirm absence of ticks but merely the absence of records or data (Zaniewski *et al*, 2002). However, the value of this data should not be overlooked, and the many benefits of this kind of surveillance are best explained through the description of a current UK case study.

Since 2005 the Medical Entomology group at Health Protection Agency (UK) has promoted an enhanced tick surveillance programme. Through engagement with a variety of public and veterinary health agencies and practitioners (e.g. clinicians and veterinarians), wildlife groups (deer society, zoos, animal refuge centres, academics) and amateur entomologists, more than 4000 ticks from 900 different locations across the UK have been submitted, representing 14 tick species (*Ixodes ricinus*, *I. hexagonus*, *I. acuminatus*, *I. arboricola*, *I. canisuga*, *I. frontalis*, *I. trianguliceps*, *I. ventalloi*, *Argas vespertilionis*, *Dermacentor reticulatus*, *Haemaphysalis punctata, Hyalomma marginatum* and *Amblyomma* species) including two non-native species.

This surveillance data has provided useful spatial and temporal data, particularly on the more common species like *I. ricinus* and *I. hexagonus*. As the majority of data on the former were submitted from humans and companion animals (particularly dogs) this provides a valuable resource to assess changes in seasonality between years, and provides sufficient spatial data to permit comparisons with historical datasets to illustrate distribution changes. The anecdotal spread of *I. ricinus* in south-west England for example can now be illustrated by comparing such current surveillance with historical records.

For some of the more geographically restricted species such as *D. reticulatus* this surveillance programme has permitted new foci to be found and tick control initiatives to be implemented to limit their spread and mitigate their establishment. In the case of the incursion of non-native species, this surveillance scheme has provided significant evidence for the absence of *Rhipicephalus sanguineus* in the UK (thus supporting the continuation of tick controls on travelling dogs) and the first occurrence of an adult *H. marginatum marginatum* (Jameson *et al*, 2010; Jameson & Medlock, 2009). Such information is crucial in assessing the risks from *Rickettsia* and Crimean-Congo Haemorrhagic Fever virus.

From a Public Health perspective such a passive surveillance scheme provides a forum for submission of ticks from the concerned public and particularly those infected with Lyme borreliosis. This has raised awareness among public health agencies of the increased peri-urban tick problem in Britain, and has necessitated the development of risk communication material on dealing with ticks in gardens.

Receiving tick samples from across the UK for identification validation also provides a considerable resource for pathogen analysis, which can be used to appraise the existence of previously unrecorded pathogens, or the geographical distribution of endemic pathogens such as *Borrelia burgdorferi* sensu lato.

Primarily this dataset acts as an important resource in the development of predictive mapping using Geographic Information Systems, but it also provides evidence and information for where ticks are becoming a nuisance. Often reporting from known 'endemic' foci is under-represented as ticks are known to be part of the local fauna, and generate less interest. In contrast however, new foci of tick activity and biting are rapidly identified, and this can be further enhanced by ensuring that such a surveillance scheme is communicated widely through web-based sources such as a surveillance website.

Key words: Ticks, surveillance, reporting.

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Surveillance of ticks in Europe based on indirect methods: the anti-tick ELISA test.

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Direct methods for tick surveillance are based on the capture and identification of specimens, either from vegetation (dragging method) or from animal hosts in the area sampled. While these procedures are useful for the surveillance of Ixodid ticks owing to the exophilous lifestyle and long feeding times (days) of ixodids, they will not work with argasid ticks. As a rule argasids are fast feeders and spend very little time (minutes) attached to their hosts; in addition, they are endophilous/nidicolous and live in both wild and domestic habitats hidden in holes, cracks and fissures inside and around animal burrows, animal premises (i.e., pigsties, poultry houses) and human dwellings. This means that vegetation dragging and removal from animals are inefficient as direct methods for argasid surveillance; instead it is necessary to explore all possible tick refuges in the area sampled before such an area can be considered tick-free (Oleaga-Pérez et al., 1990; Vial et al., 2006). Evidently, this is an impractical procedure for large-scale studies.

These drawbacks have encouraged development of serological tests (ELISA) as indirect methods for tick surveillance, especially for argasid ticks. Serological methods are based on the detection of specific antibodies against tick salivary proteins in serum samples taken from animal hosts -or humans- living in the area under study. The development of such methods requires the resolution of several issues such as: 1) the host species to be sampled; these are determined first by the host preference of the tick species investigated, and second by factors such as the availability and ease of management of the different animal hosts. Domestic instead of wild animals are preferred. 2) Demonstration that the tick species investigated induces a humoral immune response. 3) Characterization of the response in terms of how many tick bites are necessary to induce detectable antibody levels, and how long antibodies remain at detectable levels after the last tick-host contact. 4) Which antigen should be used and what its sensitivity and specificity are.

Such test have been developed for *Ornithodoros erraticus* in southern Europe. In Spain and Portugal *O. erraticus* lives in close association with swine on free-range pig farms, where it can transmit severe diseases such as human relapsing fever (caused by *Borrelia hispanica* and *B. crocidurae)* and African swine fever (ASF). Accordingly, elimination of the tick from pig farms would greatly improve the control of such diseases (Oleaga et al., 1990; Manzano-Román et al., 2007). As part of an ASF eradication campaign carried out in the 90's in Spain, an ELISA test was developed to detect specific antibodies against *O. erraticus* in pigs. Following the sequence of issues mentioned above, the authors of the test demonstrated that (i) all developmental stages of *O. erraticus* induced humoral responses in pigs; (ii) 10 bites were sufficient to induce high levels of anti-tick antibodies; (iii) after primary contact, anti-tick antibodies remained detectable for six weeks, and (iv) after secondary contact antibody levels were detectable for at least 3 months (Canals et al., 1990). These results supported the viability of pig serology as a method for the detection of *O. erraticus*-infested farms.

The authors then analysed the specificity of the antigen used in the test, which was a salivary gland extract (SGE) obtained from adult *O. erraticus* ticks. The composition of the SGE was similar in all the developmental stages of the tick and, in turn, similar to the salivary fluid secreted into the host (Baranda et al. 1997). SGE specificity was first analysed using a panel of sera from pigs infected experimentally with several pig ectoparasites that are common in Spain (4 ixodids, the sarcoptic mange mite *Sarcoptes scabiei*, the pig louse *Haematopinus suis* and the mosquito *Anopheles atroparvus*), and also with an African argasid (*O. moubata*). SGE gave 100% sensitivity and specificity with the experimental sera (Pérez-Sánchez et al., 1992). Subsequently, SGE was evaluated under field conditions using the sera of pigs from several free-range farms at which the presence or absence of the tick was also checked by direct sampling (Oleaga-Perez et al., 1994). This analysis revealed that negative field sera afforded high background reactivity, causing some false-negative results among the pigs actually bitten, but with low antibody levels. The low antibody levels were attributed to the fact that the farm harboured only a few specimens of *O. erraticus,* such that pig-tick contact was infrequent and hence the pigs either only developed a primary response, or the time between contacts was long and the levels of antibodies fell. Some false-positive sera due to cross-reacting carbohydrate epitopes were also observed, which were eliminated after deglycosiyation of SGE with sodium metaperiodate. It was concluded that SGE provided more than 90% sensitivity and specificity, and that deglycosylated SGE could be used to confirm doubtful positive results.

Subsequently the SGE-ELISA test was used to analyse anti-*O. erraticus* antibodies in more than 19,000 samples of pig sera from 3,478 farms located in 234 townships in the province of Salamanca (Spain). This allowed the identification of the farms infested with the argasid in the province, the establishment of a significant association between the presence of the tick and the persistence of ASF cases on such farms (Pérez-Sánchez et al., 1994), and consequently the application of specific control measures to avoid tick-pig contact on the tick-infested farms.

O. erraticus SGE is a suitable antigen for the serological surveillance of this tick by ELISA tests, but it does have some drawbacks. Its collection is time-consuming and difficult to standardise, and its composition is poorly known and may contain non-specific antigens, giving rise to unexpected cross-reactivity. The alternative to SGE would be the use of an individual salivary antigen of proven specificity. With this aim, Baranda et al. (2000) purified and analysed the diagnostic value of the main SGE antigens, and proposed that the best of them -the so called Oe260- should be obtained in recombinant form for diagnostic purposes. Regarding the use of anti-tick ELISA tests for ixodid surveillance, only a few studies have been carried out using similar SGEs as antigens and human sera (Schwartz et al., 1993; Lane et al., 1999; Nebreda et al., 2004). These studies also confirmed the suitability of the method to detect anti-ixodid tick antibodies but found a high degree of cross-reactivity among ixodid species. As in the case of *O. erraticus,* the use of a specific recombinant antigen would solve these problems.

Key words: Ticks, surveillance.

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Surveillance of ticks in Europe based on predicting tick distribution: « presence models »

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The basic concept underlying species occurrence modeling (SOM) is the width of the ecological niche: each species is found within specific ranges of environmental variables, enabling individuals to survive and reproduce. Species occurrence can be predicted through appropriate environmental variables modeling, commonly referred to as habitat suitability models. Environmental variables determine, in part, the geographic distribution of a species as well as how selective pressures vary within that distribution.

Ideally, SOM is based on points of known occurrence from throughout the entire range of the target element in the study area. Furthermore, to best reflect the species environmental preferences, such points should result from even application of sampling effort throughout the study area. Needless to say, these conditions are rarely if ever met and almost all distribution maps are based on opportunistically-collected occurrence data that include an unknown degree of sampling bias; i.e., some of the study area has been sampled much more intensively than the rest, whilst others received little or no sampling for the target element.

Most natural resource scientists are familiar with modeling the relationship between species occurrence and environmental gradients via simple and multiple linear regressions. Most have also been exposed to simple and multiple logistic regressions (Hosmer and Lemeshow 1989). Logistic regression has the advantage of modeling a binary response variable in terms of probability of presence or absence of the target element given the values of environmental predictor variables (see Pearce and Ferrier 2000). A problem in logistic regression modeling is the selection of a probability threshold such that sites with probability values above the threshold are denoted as suitable for the target element, and those with lower probabilities are denoted as unsuitable (Fielding and Haworth 1995). Threshold selection may be under the modeler’s control and require case-by-case considerations. Finally, note that logistic regression requires absence data in addition to presence data. The interested reader can check an important source of information in Cumming (2002).

CART modeling (Breiman et al. 1984) is a discriminant process wherein a set of points of known presence and a set of points of suspected absence that are successively split from one another. The environmental variable and the value of that variable that best divide all points into a “mostly present” subset and a “mostly absent” subset are chosen first. Those 2 subsets are then each split again into “mostly present” and “mostly absent” subsets using the variables that best do that for each set, and so on until the final subsets contain only points of known presence or only points of suspected absence. The final product, then, is a dichotomous tree that shows a series of cut-points on environmental variables that lead to suitable and unsuitable environments. The first variable in the output tree (the one that best divides the full point set into mostly-present and mostly-absent subsets) can be interpreted as the most important variable in determining species distribution. Other techniques, especially logistic regression, attempt to identify a single most-suitable environment as defined by a particular combination of variables. Thus, for many elements, CART may be a more biologically-realistic way to model distribution. If run in an unsupervised fashion CART will explicitly overfit occurrence data to all environmental variables, and the default output is a very long and complex decision tree that ends in subsets of purely-present and purely-absent points. It is up to the user to prune this tree back several levels to a more parsimonious model. There are certain variations of CART, in particular the “random forests” and “bagging trees” approaches that are emerging as preferred applications (Prasad et al. 2006). Both of these approaches are iterative, in that they build multiple output trees by continually resampling the presence and absence data and then present an “average” tree as the final output.

Maximum entropy analysis, or “MaxEnt”, is based on statistical mechanics methods for making predictions from incomplete information. It evolved from signal processing routines that maximize the signal to noise ratio in a data sample. MaxEnt estimates the most uniform distribution (maximum entropy) of occurrence points across the study area given the constraint that the expected value of each environmental variable under this estimated distribution matches its empirical average (Phillips et al. 2006). The raw output is a probability value (0-1) assigned to each map cell in the study area. These values are then converted to a percentage of the cell with the highest probability value, and termed the “cumulative value” in the output map. Thus, threshold selection here is similar to threshold selection in logistic regression. Comparative studies using MaxEnt suggest that it is more accurate than others. Elith et al. (2006), in their rather exhaustive comparison of several modeling techniques, concluded that MaxEnt is one of the best SOM algorithms available today. An example as applied to ticks can be found in Estrada-Peña et al. (2007).

The evaluation of a model focuses on predictive performance at sites. The most commonly used approach is to partition the data randomly into ‘training’ and ‘test’ sets, thus creating quasi-independent data for model testing (i.e. Fielding and Bell, 1997). However, this approach may not work with a small number of samples because the ‘training’ and ‘test’ datasets will be very small, which is common for many tick datasets. Therefore, the researcher might use a jackknife procedure (also called ‘leave-one-out’) in which model performance is assessed based on its ability to predict the single locality that is excluded from the ‘training’ dataset. Several statistics are commonly used, namely the area under the Receiver Operating Characteristic curve (AUC), correlation and Kappa, to assess the agreement between the presence-absence records and the predictions. AUC has been used extensively in the species’ distribution modeling literature, and measures the ability of a model to discriminate between sites where a species is present, versus those where it is absent. This provides an indication of the usefulness of the models for prioritizing areas in terms of their relative importance as habitat for the particular species. AUC has received recent criticism about bias (Lobo et al., 2008). The correlation between the observation and the prediction is similar to AUC but takes into account how far the prediction varies from the observation instead of being rank-based. Cohen’s Kappa, which is a chance-corrected measure of agreement, is commonly used in ecological studies with presence-absence data. It provides an index that considers both omission and commission errors.

In any case, it is important to select a range of variables with biological meaning as applied to the life cycle of the tick to be modeled, instead to “mass select” a rough set of variables that might provide a high noise/signal ratio, therefore dangerously biasing the model. An adequate knowledge of the biological parameters involved in the regulation of the tick populations seem necessary, as the opposite paradigm of inclusion of as many variables as possible looking for an adequate and perhaps casual association among explanatory variables and tick distribution.

Key words: Ticks, surveillance, modelling, spatial distribution.

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Surveillance of ticks in Europe based on predicting tick distribution: « multi-Criterial Decision Analysis »

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When few data observations are present the previous modelling tools may not be suitable. To this end, a second set of modelling techniques is based on expert advice. This encompasses techniques from multi-criteria decision analysis (MCDA). MCDA is based solely on expert advice and allows the modeller to delineate areas with higher or lower suitability based on defined species occurrence limits for each variable. In the simplest case, these limits are defined as sharp thresholds, e.g. the species cannot occur below 10°C. While this is appealing due to its simplicity, this may not reflect reality. Therefore current MCDA techniques include fuzzy membership functions that will specify the threshold as a continuous function rather than a strict threshold. During the MCDA process, the modeller also has to specify the variable importance for species occurrence. This can be done through literature research or through expert consultation. In order to streamline this process, techniques such as the Analytical Hierarchical Process (Saaty, 1980) can be applied.

MCDA was developed for commercial or managing purposes and has been secondarily adapted for livestock policies (Geber at al. 2008), health services planning (Lwasa 2007), and disease mapping or control (Clements et al. 2002, Robinson et al. 2002). It has been recently used to predict suitable habitats for arthropod vectors (*Aedes albopictus* mosquito and *Ornithodoros* ticks) in Europe (Schaffner 2009, Hendrickx et al. 2008). Concerning *Ornithodoros* soft ticks, insufficient presence data were available among European countries and information mainly dated from the 1960s and did not reflect the current risk concerning these different vector species (actually 9 species or sub-species transmitting human tick-borne relapsing fever in or close to Europe). However, some scientific papers informed about the ecological constraints of this tick group and expert knowledge was also available to determine important environmental variable and define threshold for each variable. A first model including two temperature-dependant and two rainfall-dependant variables was therefore developed and predicted suitable habitats for our set of *Orntithodoros* species with a 70% accuracy (Vial et al. in prep).

Key words: Ticks, surveillance.

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FleaTickRisk: a meteorological model developed to monitor and predict the activity and density of 3 tick species and the cat flea in Europe

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Mathematical modelling is a very active field in epidemiology. Geographical Information Systems (GIS) combined with Remote Sensing (data collection and analysis) provide valuable models, but the integration of climatologic data in parasitology and epidemiology is less common. The aim of the model, called “FleaTickRisk”, is to use accurate meteorological data in order to forecast and to monitor the activity and density of some arthropods throughout Europe.

The parasitological model uses the WRF (Weather Research and Forecasting) meteorological model integrating biological parameters. The WRF model provides a temperature and humidity picture four times a day (at 6:00, 12:00, 18:00 and 24:00 hours). Its geographical resolution is 27 x 27 km over Europe (area between longitudes 10.5°W and 30°E and latitudes 37.75°N and 62°N). The model also provides weekly forecasts. Past data are compared and revalidated using current meteorological data generated by ground stations and weather satellites. The WRF model also includes geographical information coming from USGS (United States Geophysical Survey) biotope maps with a 30’’ spatial resolution (approximately 900 x 900 m). WRF takes into account specific climatic conditions due to valleys, altitudes, lakes, and wind specificities.

The biological parameters of *Ixodes ricinus*, *Dermacentor reticulatus, Rhipicephalus sanguineus* and *Ctenocephalides felis* were transformed into a matrix of activity. This activity matrix is expressed as a percentage, ranging from 0 to 100, for each interval of temperature x humidity. The activity of these arthropods is defined by their ability to infest hosts, take blood meals and reproduce. For each arthropod, the matrix was calculated using existing data collected under optimal temperature and humidity conditions, as well as the timing of the life cycle. The mathematical model integrating both the WRF model (meteorological data + geographical data) and the biological matrix provides 2 indexes: an activity index (ranging from 0 to 100), calculated for the previous week and predictive for the coming week, and a cumulative index (ranging from 0 to 1000) which takes into account the past 12 weeks. The indexes are calculated twice a day for each geographical point all over Europe and are corrected based on 3 types of defined biotopes: urban and sub-urban areas, rural areas, and wilderness and forests. To clarify the presentation, indexes are calculated within intervals and are presented as colour maps grouping index isoclines.

It has been hypothesised that the populations of tick and flea hosts are not lacking and therefore do not affect the numbers of arthropods. However, microclimates and biotopes have a major impact, especially on tick populations, and the results provided by the model must therefore be adjusted to local conditions by specialists, such as local veterinarians. Where fleas are concerned, the model takes into account their outdoor activity and ignores their indoor life cycle. The accuracy of the data was verified throughout 2007 and 2008, using sentinel veterinary clinics and tick samples, as well as comparisons with published surveys. The maps constructed with the model are available to veterinary practitioners on www.FleaTickRisk.com. This model is not a GIS-biotope model but a meteorological model. It does not indicate a suitability index to predict the ability or not for different tick species to be present. It indicates the rate of activity (“turn-over”) in biotopes that are suitable for the concerned tick. Knowing the local biotopes and the importance of micro-biotope for ticks, an interpretation is necessary.

A one year survey was conducted in France from mid 2008 to mid 2009 in collaboration with the veterinary services from the French Army. Fifteen sites were selected for tick collect. The ticks were collected by flagging every 2 weeks using the same methodology (flags of 1 m^2, distance of 500 m in length) which is described for *Ixodes* ticks. The ticks were counted and identified. *Ixodes ricinus* ticks were abundant only in 5 sites whereas other tick species were also found: *Rhipicephalus sanguineus*, *Dermacentor reticulatus and D. marginatus*, *Haemaphysalis punctata* and *Ixodes hexagonus*.

Even by trying to be as rigorous as possible, it is known that the tick collect is highly variable, with highly aggregative distribution of the ticks. Only the adults and nymphs were taken into account. The counting is also variable depending on the timing (collects were done between 10 am and 16 pm) and the daily weather (especially under raining conditions).

Despite this very high variability, the activity (AI) and cumulative (CI) indexes and the tick counts for *Ixodes ricinus* were compared. The Indexes were calculated using the GPS location of the collects. When the Indexes were very low, always below 10 for the AI and 100 for the CI, there were no *Ixodes* found (locations in South of France) or very few (less than

22) in the case of the South-West site (Bordeaux), located in a pine forest. For the central and Eastern locations, the graphics are showing a good fit between ticks counts and Indexes. Non parametric Spearman's rank correlation rho tests showed a significant correlation between the indexes and the tick counts. A difference in the timing of the cumulative index decrease and the tick count decrease was seen. It is directly related to the mode of calculation of the cumulative index which takes into account the past weeks (which were still favourable). This mode of calculation induces a delay which will have to be corrected.
Those comparisons between the indexes and the tick collects will be done also with the collects that are ongoing in other countries (Belgium, The Netherlands, and UK). A next work will be to adapt and modify the biological matrix in order to improve the correlations and to verify that they are accurate for all geographical locations.

Key words: Ticks, surveillance, provisional model.

5. Networking around ticks and tick-borne diseases

G. Uilenberg, Integrated Control of Ticks and Tick-borne Diseases Switzerland

In the last few years, international organisations like the European Union (EU) increasingly finance the creation of networks of expertise in human and animal health, in order to evaluate the risk of the appearance of certain diseases, including vector-borne ones, and to assist developing countries in their control. The ICTTD (Integrated Control of Ticks and Tick-borne Diseases) is one of such important initiatives in the field of ticks and tick-borne disease. Financed by the EU, this project has included 43 participating institutes from 29 different countries and has been conducted for 14 years. But even before the European Union was created, the Commission of the European Communities (CEC), through the Joint Research Centre of the Directorate-General for Science, Research and Development, had financed research on ticks and tick-borne diseases, for example the STD contracts on the "*Control of livestock diseases associated with the tick Amblyomma variegatum*" and theorical patners like the Faculty of Veterinary Medicine in Utrecht (Netherlands), the Centre of International Cooperation in Agricultural Research for Development (CIRAD) (ex-IEMVT) (France), the Royal Veterinary College (UK) and many other subcontracted institutes in France, the UK, Chad, Senegal and the Antilles.

The Concerted Action Project ICTTD, financed by the INCO-DC programme of the EU, started in January 1996. The coordinator, Prof. Frans Jongejan at the Faculty of Veterinary Medicine in Utrecht, had the charge of organising a network of scientists working on tick-borne diseases, of taking care of a newsletter and of the internet website. ICTTD started with 24 participating laboratories (including most of those involved in the earlier contracts) in Europe and the developing world, and has developed into a large international network of researchers on ticks and tick-borne diseases. ICTTD was also involved in coordinating EU (INCO-DC)-funded research projects on cowdriosis (heartwater), carried out in collaboration between laboratories in Montpellier, Guadeloupe, Onderstepoort, Utrecht, Edinburgh, Dakar, Bobo-Dioulasso and Harare, and on tropical theileriosis, carried out by institutes in the UK, Tunisia and the Netherlands.

Three successive contracts were established: ICTTD-1 (Integrated Control of Ticks and Tick-borne Diseases) started in January 1996 to finish in July 2000. The decision to fund ICTTD-2 (International Consortium on Ticks and Tick-borne Diseases) came during that period, and ICTTD-2 officially extend from July 2000 to December 2004. In October 2004, during the final presentation of the results from ICTTD-2, ICTTD-3 (Integrated Consortium on Ticks and Tick-borne Diseases) has been launched until September 2008 and was extended twice until August 2010.

Several working groups were created at the start of ICTTD-3:

THPbase / GIS - A cluster of integrated databases for ticks, hosts and pathogens. Prevalence data on ticks and tick-borne pathogens linked to remotely sensed eco-climatic data to create predictive maps for geographical distribution of ticks and diseases in the (sub)tropics.

Biosystematics Forum - Biosystematics and molecular phylogeny of ticks and tick-borne pathogens.

Molecular Diagnostic Network - Molecular diagnostics used to conduct comparative epidemiological studies on tick-borne diseases.

Genomics and Vaccine Design - Proteomics data for ticks and tick-borne pathogens are exploited to design novel integrated vaccine strategies targeting ticks and pathogens to reduce dependency on chemical tick control. The CA acts as a focal point for setting up consortia on novel genomics projects particularly for ticks

Tick-borne zoonoses in the (sub)tropics - The human medicine section of the consortium, developing a database on zoonotic tick-borne pathogens occurring in the Tropics and Subtropics.

A newsletter was created, with an editor in chief, supported by co-editors in various subjects. This ICTTD newsletter bears the title “Newsletter on Ticks and Tick-borne Diseases of Livestock in the Tropics”, and is focussed on economically important ticks and tick-borne diseases (TBDs) of livestock in tropical regions. However, it is increasingly difficult to strictly separate ticks and TBDs of livestock from those of humans (zoonoses) and of companion animals, and results of studies on ticks and TBDs in temperate areas are often of relevance to those of tropical livestock. The first issue appeared in April 1996, and it has since been published and distributed by mail three times a year. It is also freely available on the ICTTD website (www.icttd.nl). The final issue will appear at the end of the ICTTD, before 31 August 2010. The newsletter is not only meant as a network between the various participating laboratories, but even more so as an information service for scientists and field personnel in developing countries, often with no access to a library or with limited libraries. Publications and information on ticks and tick-borne diseases are presented, where relevant with comments by the co-editors and/or editor. Information on specific developments within the framework of the ICTTD are given in each issue by the coordinator.

Key words: Ticks, tick borne disease, network, control.

6. Links and news

EUCALB (European Union Concerted Action on Lyme Borreliosis)

This action coordinates research on the ecology, molecular biology, taxonomy and geographical distribution of *Borrelia burgdorferi* in Europe. It is interested in the study of clinical and epidemiological characteristics of Lyme Borreliosis in Europe and on risk factors for human contamination. It also investigates prevention measures based on education programs in endemic southern regions. A website (http://meduni09.edis.at/eucalb/cms/) has been established in 1997 to present information on the activities of the EUCALB and provide up-to-date information on Lyme Borreliosis in Europe in the form of short reviews and latest publications. It also serves as a notice board for relevant scientific meetings. Although available to the general public, its primary targets are healthcare professionals, scientists and students.

The new *Ticks and Tick-Borne Diseases* Journal

Ticks and Tick-borne Diseases (http://shop.elsevier.de/artikel/1275676&_osg=834301&_hsg=833821) is an international, peer-reviewed scientific journal that will appear quarterly. It publishes research papers, short communications, state-of-the-art mini-reviews, letters to the editor, clinical-case studies, book reviews, announcements of international meetings, and editorials on ticks (biosystematics/taxonomy, morphology, evolution, ecology, physiology/biochemistry, behaviour, molecular biology, genomics/proteomics, and control), the tick-borne pathogens and the ecology/ecoepidemiology of tick-borne diseases in domestic animals, wildlife and humans.

A new formula for the 50th anniversary of the *Acarologia* journal

A few months ago, Dr Michel Bertrand announced his wish to retire and the need of a new Editorial team to ensure the future of Acarologia. He offered to Serge Kreiter from INRA, France, the position of the next Editor-in-Chief of this prestigious journal. A new editorial team was then constituted including several dynamic French and Canadian scientists involved in researches on mites and ticks, with the support of a scientific editorial board composed of very eminent acarologists from across the World.

Acarologia is fifty years-old in 2010 and is therefore the oldest Scientific Journal currently publishing and devoted exclusively to the Acari. This is time to change the format of the journal, which will become a free and open-access journal encouraging open-minded topics concerning Acari (http://www1.montpellier.inra.fr/CBGP/acarologia/).

TTP-7 (Tick and Tick-borne Pathogen Conference)

The *Tick and Tick-borne Pathogen* Conference is organised every three years. It is an international congress including any scientists concerned by tick and tick-borne diseases issues worldwide, including taxonomy/systematic, epidemiology, genetics, modelling, vaccine development, tick control and surveillance…

The next one, TTP-7, will be held in Zaragoza (Spain) (http://www.unizar.es/ttp7/Sitio_web/Main.html). The scheduled dates for the Conference are from August 28th to September 2nd, 2011. The main theme of the conference is “Integration: studies aimed toward inclusion of different strategies to solve pathogen-vector-host-habitat interaction problems in the complex world of ticks and tick-borne pathogens”.

EURAAC newsletter (EURopean Association of Acarologists)

EURAAC (http://euraac.boku.ac.at/index.php) was founded 1987 in Amsterdam. Its aims are: (i) to organize meetings in Europe at regular intervals for the dissemination of knowledge among acarologists, (ii) to provide a means for personal contact among workers in this field, (iii) to provide support for instructional workshops for those wishing to specialize in this discipline, (iv) to represent the views and interests of European acarologists to official bodies in scientific matters.

This was the 1st issue of the EURAAC Newsletter at the end of 2009. The next issues will appear two times per year in May and November. This Newsletter comprises six sections: 1) “Spotlight” to highlight recent findings on mites and ticks, 2) “Forum” for miscellaneous mite- or tick-related announcements or comments, 3) “Theses” introducing recently finished MSc and PhD theses on mites or ticks, 4) “Media” dedicated to announcements of new books, journals, CDs, videos, and webpages, 5) “Job openings” and 6) “Events” announcing scientific events of potential acarological interest.