3 Factors Influencing the Spread and Distribution of Ticks

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3.1 Climate Changes

Long-time series of historical data related to climatic factors and the geographical distribution of ticks and tick-borne pathogens are required to determine the impact of climate changes on the spread of these vectors and the pathogens they carry. To our knowledge, few such attempts have been made, mainly because of the lack of data collection over a sufficiently long period of time to allow for comparison in relation to existing climatic data. One of the most recent and long-term studies has been described by Jaenson et al. (2012). In this article it was shown that deer abundance and climate change seem to be the most important factors explaining the spread of *Ixodes ricinus* northwards in Sweden during the last 30 years. It is suggested that the milder climate has made it possible for roe deer to expand northwards and into northern Sweden. As the roe deer is, generally, the most important host of adults of *I. ricinus* in Sweden the expansion of this tick host has favoured the subsequent expansion of the tick into the same northern area (Jaenson et al., 2012).

It is possible, however, to affirm that despite some evidence it is difficult to implicate climate change as the main cause for an increase in tick-borne diseases. In order to predict future tick-borne scenarios, climate change models are required that take into account the dynamic biological processes involved in vector abundance and pathogen transmission which affect the complex ecology and epidemiology of tick-borne diseases such as Crimean-Congo haemorrhagic fever (CCHF), tick-borne encephalitis (TBE) and Lyme borreliosis. According to Gray et al. (2009), climate changes have influenced the survival of ticks (direct effect). Empirical proofs have been obtained that climate may be in part responsible for shaping the prevalence rates of *Borrelia burgdorferi s.l.* in questing nymphal *I. ricinus* (Estrada-Peña et al., 2011). However, studies on the dynamics of CCHF cases in Turkey did not show any influence of climate when sites where the disease had been reported were compared with sites where the disease was absent (Estrada-Peña et al., 2010).

Changes in climate and the length of the different seasons directly affect tick survival, activity and development, but there is limited evidence that rising temperature results in a greater abundance of ticks simply by increasing rates of development. Effects of the climate on the geographical distribution of a tick species are generally more evident along the border of its distribution, affecting the geographic range potentially suitable for the tick. A study by Jaenson and Lindgren (2011) has shown that a warmer climate in Northern Europe has extended the vegetation period

which has allowed ticks to be active for a longer time during the year; this seems to have enlarged the geographic range available for the tick. Then again, changes in development rates make tick cohorts available to different diapause windows (largely determined by day length), thus changing the patterns of seasonal activity and significantly altering generation length. Probably the most interesting tick species to work on and to explore the diversity of seasonal patterns is *I. ricinus*, the most abundant tick in Europe and an important pest of both animals and humans. However, a process-driven model, which is necessary to study such diverse seasonality patterns, is still not available.

The indirect effects of climate change are more complicated to evaluate. Climate changes can indirectly alter survival of the ticks by modifying the type of vegetation and, as mentioned above, the host abundance. For instance, climate will affect the vegetation, which in many ways may influence the number of infected ticks. In addition, dense humid vegetation will, for some tick species, be beneficial to tick survival and could lead to an increase in tick numbers as well. Such vegetation may also benefit pathogen-reservoir hosts such as rodents and shrews, and increase the survival and abundance of tick-maintenance hosts such as deer (Jaenson *et al.*, 2012). All these factors may boost the density of infected ticks, but the direct impact on animal and human infection rates is unknown and has not yet been evaluated for any of the many pathogens that the ticks can transmit.

The influence of mast years on rodent abundance and consequently on tick density is one example of how vegetation will indirectly affect the density of *Borrelia*-infected *Ixodes* ticks (Ogden *et al.*, 2005). After mast years, rodent populations significantly increase as a result of an extended breeding season and higher survival during winter. This is due to an increase in food supply and consequently in body fat. The higher host population density affects the tick density in the following year and possibly also the risk of disease transmission (Tack *et al.*, 2010).

Climate change may also influence the risk of infection by affecting human activities; for example, the long-term use of land, e.g. for agriculture or tourism, could be affected by climate change. Weather patterns also have an effect by influencing short-term human behaviour so that tick-bite risk may be linked to the seasonality of certain human activities such as hiking, hunting, and berry and mushroom picking. Generally climate effects are more easily noticeable close to the geographical distribution limits of both vector and pathogen, but the magnitude of the effects of climate change in an endemic area is the result of the interaction of many other parameters associated with socio-economics, human migration and settlement, ecosystems and biodiversity, bird migrations, land use and land cover, human culture and behaviour, and immunity in the human and animal populations (Gray *et al.*, 2009).

3.2 Changes in Land Use

Changes in land use often affect the host–tick relationship and consequently increase the transmission of tick-borne pathogens. For instance, during World War II, after the occupation of Crimea (1941–1944), normal agricultural activities were disrupted and the common sport of hunting European hares was abandoned. When Soviet troops reoccupied the hilly Crimean steppes in 1944, the hares had become excessively abundant and neglected pastures were overgrown with weeds. European hares are a reservoir of CCHF virus (CCHFV) and one of the primary hosts of immature *Hyalomma*, and with the expansion of the hare population came the first documented CCHF outbreak of the modern era (Ergönül, 2006). A similar explanation was suggested for an outbreak in Turkey as hunting and pasturing had been abandoned in the fields in the affected region from between 1995 and 2001 because of terrorist activities (Ergönül, 2006). In this period, the numbers of small mammals (e.g. hares) and wild animals (e.g. wild boars) increased, as did the population of *Hyalomma* ticks. When the fields became available again for hunting and pasturing, cattle, sheep and humans were exposed to virus-carrying ticks (Ergönül, 2006).

3.3 Movement of Animals

3.3.1 Migratory birds

The introduction and spread of tick species by migratory birds are documented for those tick species which are ornithophilic in the larval and nymphal stages. *Hyalomma* (*Hy.*) *marginatum* and *Hy. rufipes*, and to a lesser extent some species of *Amblyomma*, belong to this group of ticks. Their potential spread northwards and the establishment of permanent populations in the north are therefore of great importance, particularly as the immature stages of *Hyalomma* are frequently found on migratory birds flying northward to temperate Europe (e.g. Jaenson *et al.*, 1994; Molin *et al.*, 2011). The dispersal of ticks by birds may be restricted to a short distance during local post-breeding flights or over extremely long distances during migration flights. In studies conducted on birds migrating through Egypt between 1955 and 1973, it was discovered that birds migrating from Eurasia to Africa carried tick species that were characteristic of the fauna of Europe and Asia (Hoogstraal, 1963). As another example, the introduction of *Am. variegatum* in southern Italy and Greece by migratory birds has been sporadically reported (Albanese *et al.*, 1971; Papadopoulus *et al.*, 1996).

Hy. rufipes is the most common tick found on birds migrating northwards from sub-Saharan Africa to Eurasia in the spring (Hoogstraal, 1963; Linthicum and Bailey, 1994). The risk of diffusion of CCHFV into areas where the virus does not occur is linked to the possibility of infected *Hyalomma* ticks reaching and becoming established in such 'uninfected areas'. This probability is greater for ticks associated with migratory birds (Manilla, 1998a). Hoogstraal (1979) reported that many bird species are responsible for the intracontinental and intercontinental dissemination of ticks associated with CCHFV. While this fact is not the most important factor in the introduction of CCHFV to Europe, it has nevertheless been hypothesized that the outbreak of CCHF in Turkey in 2002 could have been caused by birds carrying CCHFV-infected ticks from the Balkans (Karti *et al.*, 2004). The occurrence of this disease in Turkey is under discussion, taking into consideration the available epidemiological data. It currently seems impossible that migrating birds from the Balkans could have introduced the disease into Turkey and have it spread in an interval of weeks. The current opinion is that the virus has been there many years and that some change/s favoured its contact with humans so that disease incidence increased (Ozdarendeli *et al.*, 2010).

3.3.2 Importation of exotic and wildlife species

There are many examples of exotic ticks that have been introduced into countries by the importation of exotic animals. Some reptile-associated African *Amblyomma* tick species were found on the American mainland, mainly as a result of the importation of tick-infested reptiles from Africa (i.e. infested by *Am. marmoreum* or *Am. sparsum*). Also, in Poland, *Am. latum* and *Am. transversale* were found on pythons and *Am. exornatum*, *Am. flavomaculatum*, *Am. latum* and *Am. nuttalli* on monitor lizards, both reptiles imported from Africa (Nowak, 2010). In addition, in the Netherlands, *Am. flavomaculatum* was collected from an African savannah monitor lizard (Nijhof *et al.*, 2007), and other tick species such as *Am. marmoreum*, *Am. dissimile* and *Hy. rufipes* have occasionally been collected from imported tortoises and snakes (Bronswijk *et al.*, 1979; Jongejan, 2001). Similarly, a constant threat for the introduction of heartwater into the American mainland exists mainly by the importation of livestock from the Caribbean Islands infested with *Am. variegatum* ticks, but also through the introduction of lightly infested wild ungulates and tick-infested reptiles from Africa, as mentioned above (Burridge *et al.*, 2002).

3.3.3 Movement of domestic animals

Ticks associated with pets are able to reach and establish themselves in areas far from their origins. One of the most typical examples is *Rhipicephalus* (*Rh.*) *sanguineus*, universally known as the 'kennel tick' (Manilla,

1998b; Walker et al., 2000; Estrada-Peña et al., 2004). This is a monotropic three-host tick strictly associated with the domestic dog. *Rh. sanguineus* is probably one of the most widely distributed tick species in the world. Travellers with dogs have brought this important vector species permanently into the latitudes approximately between 50°N and 30°S (Walker et al., 2000). Furthermore, *Dermacentor reticulatus* (the ornate dog tick, marsh tick or cattle tick) may have been introduced into north-western Europe in a similar way, in addition to the routes described previously.

D. reticulatus is a tick species that appears to be expanding its range in north-western Europe. A study performed in Germany by Dautel et al. (2006) in 2003 and 2004 showed that the distribution and abundance of D. reticulatus has increased on deer and vegetation. Populations have also been found over the last few years in the Netherlands and Belgium (Nijhof et al., 2007; Cochez et al., 2011). In the Netherlands, several populations have been found in freshwater tidal marshes, mainly in the south of the country; these were most likely established after the introduction of southern European cattle breeds. Ponies were exported to Belgium to manage vegetation, and these ponies then introduced this tick species to that country. In Belgium, D. reticulatus has been found on tick (flag or drag) cloth dragged in different nature reserves and peri-urban areas, and on dogs. Most of these areas are frequented by dogs, possibly explaining further spread of D. reticulatus, as no large mammals are present there.

The introduction of *Am. variegatum* into the Caribbean area is an example of how the movement of domestic animals can spread exotic ticks. The initial introduction of *Am. variegatum* into Guadeloupe and probably also into most of the West Indies islands was due to the importation of infested N'Dama cattle in the 1800s, or to tick-infested litter used during cattle transportation by ships from Senegal to the West Indies (Barré et al., 1987), or from East Africa to the Indian Ocean islands. Cattle transportation between islands also explains the introduction of the tick at least into Marie-Galante, Antigua and Martinique. But from the late 1960s, the rapid increase in the number of infested islands in the Caribbean area was linked to the presence and spread of the cattle egret in the West Indies. This cattle-associated African bird species was also introduced into the Caribbean area (Corn et al., 1993; Barré et al., 1995). The reinfestation of some countries, for example Puerto Rico, after a successful eradication campaign might also be due to the movement of this bird (Bokma and Shaw, 1993). *Am. variegatum* is thus the only African vector of cowdriosis that has established itself successfully outside the continent (Walker and Olwage, 1987). It remains a threat in areas where climatic conditions are suitable for its establishment, as it has already succeeded in colonizing new territories through the movement of migratory birds which cannot be controlled.

Rh. (Boophilus) microplus, the pantropical blue tick, is without a doubt one of the most important vectors of livestock pathogens in the world, mainly because of its large geographical distribution and its ability to transmit both Asiatic and African redwater babesiosis caused by *Babesia bovis* and *B. bigemina* (Coetzer and Tustin, 2004).

This tick species originates from Asia, but during the latter half of the 19th century it, and the babesiae it transmits, was spread by cattle transported to Australia, Madagascar, South Africa, Latin America, Mexico and the USA (Hoogstraal, 1956; Temeyer et al., 2004). *Rh. microplus* was eradicated from the USA in 1943 through the costly Cattle Fever Tick Eradication Program which started in 1906. The most resistant strain studied to date has been shown to survive the dipping procedure used at the USA–Mexico border as part of an importation barrier to prevent the re-entry of *Rh. microplus* into the USA (Temeyer et al., 2004).

Until recently, *Rh. microplus* was not present in West Africa, but this tick species has unfortunately been introduced into the Ivory Coast (Madder et al., 2007, 2011) and Benin (Madder et al., 2012) as a result of uncontrolled cattle imports for cattle improvement programmes. Because of the high adaptability of ticks and, more specifically, of *Rh. microplus*, the risk of the introduction of this species into the Mediterranean area and the establishment of local populations seems possible.

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