REVIEW ARTICLE

Rickettsia felis, an emerging flea-transmitted human pathogen

Mohammad Yazid Abdad[1]*, John Stenos[1] and Stephen Graves[1,2]

[1]Australian Rickettsial Reference Laboratory, Geelong Hospital, Geelong, VIC, Australia; [2]Hunter Area Pathology Service, John Hunter Hospital, Newcastle, NSW, Australia

Rickettsia felis was first recognised two decades ago and has now been described as endemic to all continents except Antarctica. The rickettsiosis caused by *R. felis* is known as flea-borne spotted fever or cat-flea typhus. The large number of arthropod species found to harbour *R. felis* and that may act as potential vectors support the view that it is a pan-global microbe. The main arthropod reservoir and vector is the cat flea, *Ctenocephalides felis*, yet more than 20 other species of fleas, ticks, and mites species have been reported to harbour *R. felis*. Few bacterial pathogens of humans have been found associated with such a diverse range of invertebrates. With the projected increase in global temperature over the next century, there is concern that changes to the ecology and distribution of *R. felis* vectors may adversely impact public health.

Keywords: *Rickettsia felis*; *cat flea typhus*; *flea-borne spotted fever*; *Ctenocephalides felis*

Received: 8 February 2011; Revised: 5 May 2011; Accepted: 15 May 2011; Published: 1 July 2011

The human pathogenicity of the Spotted Fever group (SFG) rickettsiae varies widely between species. In spite of significant phenotypic variability between species, most members of the group are treated as potential human pathogens (1, 2). *Rickettsia felis* is a newly described species of the SFG (3). Previously, *R. felis* was classified as a member of Typhus group (TG) for over 10 years. The main vectors for *R. felis* (as with *R. typhi*) are fleas. Like all rickettsiae, *R. felis* is an obligate intracellular Gram-negative alpha-proteobacterium requiring a vertebrate and invertebrate host to survive and reproduce (4). There are proposals to re-organise the genus *Rickettsia* into four groups, instead of the traditional two, adding an Ancestral group (AG) and Transitional group (TRG) to the widely accepted SFG and TG (5). Should this new form of genotypic classification become generally accepted, *R. felis* would join the TRG alongside the related *Rickettsia akari*.

The geographic distribution of *R. felis* in arthropods, especially the cosmopolitan cat flea, *C. felis*, reinforces the hypothesis that *R. felis* can be found in most, if not all, human populations where domestic animals are kept as pets. The world-wide distribution of *R. felis* is probably due to the co-migration of humans and domestic animals harbouring *C. felis*.

First described by Adams et al. in 1990 (6), *R. felis* was originally named ELB agent after the laboratory from which it was first isolated, El Labs (ELB) in the United States. Its serendipitous discovery was by electron microscopy, showing a rickettsia-like organism, similar in morphology to *Rickettsia typhi*, the only species of *Rickettsia* known at the time to be flea-borne. Soon after, Azad et al. (7) described this new variant of rickettsiae, reporting on its 17 kDa and citrate synthase genes and classifying it as a TG rickettsia. The demonstration of the presence of the *omp*A gene in *R. felis* by Bouyer et al. (3), resulted in the re-classification *R. felis* as a member of the SFG. Re-analysis of the 17 kDA gene showed greater similarity to the SFG than TG.

The genome of *R. felis* has been sequenced and it was the first rickettsia to be described as having plasmids (8). Together with the two plasmids (pRF and pRFδ), the combined genetic material is the largest among *Rickettsia* sp. to date (5, 8). The plasmids of *R. felis* are highly variable (9).

1. Flea-borne spotted fever/cat-flea typhus

The names used to describe *R. felis* infection (flea-borne spotted fever/cat-flea typhus) may soon be deemed inaccurate with the recognition of other arthropods such as ticks and mites as potential vectors (10–12). However, until this is confirmed, the use of the names flea-borne spotted fever (FBSF) or cat-flea typhus are still warranted.

Citation: Emerging Health Threats Journal 2011, **4**: 7168 - DOI: 10.3402/ehtj.v4i0.7168
(page number not for citation purpose)

Clinical manifestations of human *R. felis* infection include fever, fatigue, headache, maculopapular rash, and eschar (13, 14). Observation of cases reported in the literature show a variability of presentation of clinical symptoms that can include a combination of some or all of the listed signs and symptoms (14–17). Thus far there have been no reports of flea-borne spotted fever causing either serious complications or death, and it appears to be milder than other rickettsioses (18). Due to shared symptoms with other rickettsial and viral infections, it is thought that many human cases are currently misdiagnosed.

The gold standard of rickettsial diagnosis is currently serology utilising an indirect immunofluorescence assay (19). There is considerable cross-reactivity between SFG and TG antibodies in human sera. In spite of this, serology remains the diagnostic tool of choice due to its quick turnaround time and ease of use. *R. felis* responds serologically as though it were a TG rickettsiae. This probably contributed to the earlier misdiagnoses of *R. felis* infections as *R. typhi*. There is a need to incorporate additional diagnostic assays such as polymerase chain reaction (PCR), to supplement serology for diagnosing *Rickettsia* infection. PCR as a diagnostic tool is not readily available to clinicians, as few diagnostic laboratories have access to a rickettsial PCR assay. Diagnostic protocols for rickettsiosis continue to rely on serological methods such as immunofluorescence assay (IFA) alongside clinical presentation of symptoms and epidemiological knowledge including a travel history (20).

The self-limiting nature of most rickettsioses can be another reason why these infections, in particular FBSF, are under-reported. This is further exacerbated by the overlapping endemic areas of *R. felis* and *R. typhi* along with shared vectors and hosts (21). The recent appearance in the literature and increasing reporting of cases and locations supports the designation of FBSF as an emerging disease (22). Recently, human infection occurred in Victoria, Australia, where a cluster of five patients between the ages of 4 and 63 years were exposed to fleas (*C. felis*) originating from their pet cat (17). All patients sero-converted to TG antigens. The detection of *R. felis* DNA from the cat fleas supported the FBSF diagnosis.

2. Invertebrate hosts

Infection by *R. felis* has been attributed to flea saliva rather than faeces. In this respect it is unlike *R. typhi* which is usually transmitted by inhalation of dried flea faeces (23, 24). FBSF was first described in 1990 and its main vector was identified as *C. felis*. Since its description, more than 12 flea species have been identified as hosts (Table 1). The expansion of *R. felis* hosts and potential vectors to include mites, lice, and ticks (both Ixodid and Argasid) further highlights the infancy of the field. Much work still needs to be done to fully understand the bacterium's ecology. The sharing of arthropod hosts between several pathogens, especially bacteria, of similar and different genera is well documented (Table 1). This diversity of hosts may have contributed to the earlier misdiagnosis of *R. felis* infection.

Maintenance of *R. felis* in *C. felis* is well documented with transstadial and transovarial transmission (6). The maintenance of *R. felis* within infected populations of *C. felis* has been documented for 12 generations with little adverse affect on the vector's fitness (25), unlike *Rickettsia rickettsii* and *Rickettsia prowazekii* that have been observed to adversely affect their vectors (26, 27).

Even though *R. felis* does not appear to diminish the fitness of *C. felis*, its presence leads to reduced microbiota diversity (28). One may assume that colonisation with *R. felis* limits the diversity of microbiota in the flea thus limiting its effectiveness in transmitting other bacterial pathogens; however, dual infections by *R. felis* and other flea-borne organisms has been reported (29).

In temperate climates, *C. felis* and *Ctenocephalides canis* activity on host animals are influenced mainly by temperature with trends showing peak activity during warm months and periods of high rainfall (30, 31). This was observed with several vector types and species.

The reporting of *R. felis* in *Rhipicephalus sanguineus* ticks points to possible horizontal transmission from flea to tick via a vertebrate host, presumably a dog (32). The global distribution of *R. sanguineus* has been attributed to the geographical spread of the dog. Other intracellular bacteria have also been reported from *R. sanguineus* such as *Rickettsia conorii* and *Coxiella burnetii*, the aetiologic agent for Mediterranean spotted fever and Q fever, respectively (33). *R. sanguineus* has never been implicated as a vector of either *R. felis* or *C. burnetii*. However, due to its world-wide distribution overlapping with that of *C. felis*, it may play the role of an amplifier for horizontal transmission to the more competent vector.

Although *C. felis* has been designated as the main vector of *R. felis*, the competency of all 24 species of fleas, ticks, mites, and lice as transmission vectors has yet to be demonstrated.

3. Human migration

Human migration may have led to the geographical spread of *R. felis* hosts, in particular *C. felis*, *C. canis*, *Pulex irritans,* and *Xenopsylla cheopis*. Occurrence of flea vectors in human settlements world-wide and among animals that are generally associated with human activity such as cats, dogs, and rodents support this view. Increased travel may have played a role in spreading these flea-associated pathogens in recent decades as travellers and their accompanying animals moved between countries (34).

Citation: Emerging Health Threats Journal 2011, **4**: 7168 - DOI: 10.3402/ehtj.v4i0.7168

Table 1. Invertebrate hosts of *Rickettsia felis*, some of which carry other potential bacterial pathogens

Invertebrate host	Vertebrate host	Location	Other potential pathogens[a]	Disease	Reference
Fleas					
Ctenocephalides felis	Dog, cat, rodents, monkey, opossums	Argentina, Australia, Brazil, Canada, Chile, Cyprus, France, Gabon, Germany, Israel, Mexico, New Zealand, Peru, Spain, Taiwan, Thailand, UK, United States, Uruguay	*Rickettsia typhi, Bartonella* sp.	Murine typhus, Cat-scratch disease	(47–66)
Ctenocephalides canis	Dog, cat	Algeria, Brazil, France, Spain, Thailand, Uruguay	*Bartonella* sp.	Cat-scratch disease	(50, 65–69)
Pulex Irritans	Human and mammals	DR Congo, United States	*Rickettsia typhi, Yersinia pestis*	Murine typhus, Plague	(24, 29)
Xenopsylla cheopis	Rodents, shrew	Indonesia, United States	*Rickettsia typhi, Yersinia pestis*	Murine typhus, Plague	(21, 70)
Anomiopsyllus nudata	Rodents	United States	–	–	(71)
Archaeopsylla erinacei	Hedgehog, dog, cat	Algeria, France, Germany	–	–	(50, 56, 68)
Echidnophaga gallinacean	Poultry, dog, cat	Australia, DR Congo	*Rickettsia* sp.	Spotted fever	(29, 49)
Spilopsyllus cuniculi	Cat, rabbit	Australia	–	–	(49)
Ctenophthalmus sp.	Rodent	Portugal	*Rickettsia typhi, Bartonella* sp.	Murine typhus, Cat-scratch disease	(72)
Xenopsylla brasiliensis	Rodent	Brazil	*Yersinia pestis*	Plague	(29)
Tunga penetrans	Human, dog, cat, pig	Brazil	–	–	(29)
Polygenis atopus	Dog, cat, opossum	Brazil	–	–	(73)
Ticks					
Haemaphysalis flava	Cat	Japan	*Rickettsia japonica*	Japanese spotted fever	(11)
Haemaphysalis kitaokai	Cattle, deer	Japan	–	–	(11)
Rhipicephalus sanguineus	Dog, horse	Brazil	*Rickettsia* sp., *Anaplasma* sp.	Spotted fever, Anaplasmosis	(32)
Amblyomma cajennense	Dog, horse	Japan	*Rickettsia* sp.	Spotted fever	(11)
Ixodes granulatus	Shrew	Taiwan	*Rickettsia* sp., *Ehrlichia* sp.	Spotted fever, Ehrlichiosis	(74)
Ixodes ovatus	Cat	Japan	*Rickettsia* sp.	Spotted fever	(11)
Carios capensis	Seabird	United States	*Coxiella* sp., *Rickettsia* sp.	Unknown, Spotted fever	(75)
Haemaphysalis sulcata	Sheep, goat	Croatia	–	–	(76)
Mites					
Trombiculid	Wild rodents	South Korea	*Orientia tsutsugamushi*	Scrub typhus	(10)
Leptotrombidium deliense	Rat	Taiwan	*Orientia tsutsugamushi*	Scrub typhus	(74)
Mesostigmata	Rat	Taiwan	–	–	(74)
Lice					
Liposcelis bostrychophila	–	Canada	–	–	(77)

[a]Multiple bacterial pathogens present in the same host are simplified with genus only. Fields with no bacterial pathogens listed denotes no record in the literature.

During the twentieth-century and the start of the twenty-first century, mass migrations in the form of refugees escaping conflict and persecution were common. A new form of transient migration has arisen with the advent of tourism with fast, low-cost travel. It is not uncommon to see reports of rickettsial infections in travellers returning to their home country (35, 36). Returning infected travellers increase the risk of horizontal transmission of rickettsiae to other endemic arthropods. The rate and efficiency of horizontal transmission of rickettsial organisms, in particular *R. felis*, has yet to be fully understood (22).

4. Climate change

The distribution of vectors and associated pathogen transmission rates can be affected by changes in the ambient temperature and climate. Such changes, whether caused by human activities or not, will cause (a) local vector populations to migrate to more favourable climates alongside vertebrate hosts and (b) alter the life cycle duration of vectors. Evidence has shown an average global temperature increase of 0.3–0.6°C in the last 100 years and that this has affected the hydrological cycle and humidity (37, 38). Arthropod vectors feeding activity, reproduction, and mortality rates are highly sensitive to slight temperature changes. An increase in temperature of 3°C (25 to 28°C) reduced the time needed for hatching, pupation, and development of two *Xenopsylla* flea species (39). The significant time reduction in major stages of the flea life cycle would probably result in an increased population density. As these flea species are potential reservoirs of *R. felis* the risk of human infection is likely to increase.

Fleas harbouring *R. felis* are dependent on hosts directly linked to human habitation (Table 1). Ticks, however, are more widely distributed and most of their vertebrate hosts involve native fauna. Increases in temperature due to climate change would probably see the range of many tick species widening and encroaching further into areas of human activity. Of the several tick species found to potentially transmit *R. felis*, *R. sanguineus* stands out as the most likely to mediate change due to its world-wide distribution and its tendency to harbour other rickettsial organisms (40). *R. sanguineus* prefers a warmer climate in general, thus increased humidity may also enhance the establishment of populations in new areas (41). *R. sanguineus* has been shown to be widely established in the Mediterranean and other similar regions due to adequate humidity and warm temperatures (42). However, populations of *R. sanguineus* have been rarely seen in northern and central Europe. With the projected increase in summer temperatures over the next few decades, there may be a spread of this tick into temperate Europe and the establishment of permanent populations. A recent report reinforces this hypothesis, where an increase in the affinity of *R. sanguineus* for humans during the warmer months in Europe was noted (43).

5. Conclusion

Long-term surveillance of vector densities and the emergence of diseases associated with those vectors should be established. With evidence of *R. felis* in every human settlement located within temperate zones worldwide, the need to make spotted fever and typhus group rickettsiosis part of diagnostic considerations is crucial for a prompt and proper medical response. As with all zoonotic diseases, overlapping activities between reservoir, vector, and humans would have a significant influence on transmission rates. The *R. felis* vector and reservoir animals have always overlapped with human habitation. Any increase in effective transmission is likely to result in a rise in human cases of FBSF.

There is a need to be vigilant in identifying both current and emerging vector-borne diseases in the environment. A good example to illustrate this is Lyme disease in North America, which was first reported in the literature 27 years ago. Since then it has become the most prevalent vector-borne disease on that continent. However, molecular analysis of specimens that predate the recognition of this major pathogen showed similar prevalences, indicating misdiagnosis and confusion with other illnesses with similar clinical symptoms (44, 45). This observation can be applied to other tick-borne diseases including *R. felis*. Only recently has *R. felis* been considered to be part of an infectious disease differential diagnosis. With the awareness of its human pathogenicity increasing, one would expect to see the number of FBSF cases rise.

With the long list of vector species potentially harbouring and transmitting *R. felis*, the situation is different to other vector-borne pathogens where the vector hosts and reservoir are limited to specific species. The implications of this are that unchecked expansion of vectors would potentially adversely affect human health. It is also of concern that these shared vectors contain other bacterial pathogens such as *Yersinia pestis*, *Ehrlichia* sp., *Bartonella* sp. and *Rickettsia* sp. (Table 1). The competency of implicated invertebrate hosts of *R. felis* listed in Table 1 need proper consideration and investigation. Most, if not all, of the invertebrate hosts are found around and within human populations. Thus, *R. felis* infections are inevitable. The transmission efficiency of this organism by its vectors needs to be investigated further.

Influence of climate change on temperature levels may be far-reaching. Not only could it affect arthropod life cycles but also human activities as well. Use of the land in affected areas will be influenced and long-term activities such as farming and tourism will indirectly affect transmission of arthropod-borne diseases (46).

Citation: Emerging Health Threats Journal 2011, **4**: 7168 - DOI: 10.3402/ehtj.v4i0.7168

FBSF poses one of the many challenges to human and veterinary medicine in the twenty-first century. In spite of it being a self-limiting disease with only modest severity, the likelihood of geographical range expansion is a cause for concern. Better understanding of this endemic disease will equip local doctors, veterinarians, and public health officials with the information needed to prevent outbreaks and provide proper treatment.

Conflict of interest and funding

The authors declare no ethical conflict of interest or bias.

References

1. Hechemy KE, Oteo JA, Raoult D, Silverman DJ, Blanco JR. New insights into rickettsioses: Genomics, proteomics, pathobiology, and the international threat of rickettsial diseases. Ann N Y Acad Sci. 2005;1063:xiii–xx.
2. Chosewood CL, Wilson DE, editors. Biosafety for microbiological and biomedical laboratories. 5th ed. HHS Publication No. (CDC) 21-1112. Washington, DC: U.S. Department of Health and Human Services; 2009. 1–416.
3. Bouyer DH, Stenos J, Crocquet-Valdes P, Moron CG, Popov VL, Zavala-Velazquez JE, et al. *Rickettsia felis*: Molecular characterization of a new member of the spotted fever group. Int J Syst Evol Microbiol. 2001;51:339–47.
4. Higgins JA, Radulovic S, Schriefer ME, Azad AF. *Rickettsia felis*: A new species of pathogenic rickettsia isolated from cat fleas. J Clin Microbiol. 199634(3):671–4.
5. Gillespie JJ, Beier MS, Rahman MS, Ammerman NC, Shallom JM, Purkayastha A, et al. Plasmids and rickettsial evolution: Insight from *Rickettsia felis*. PLoS One. 2007;2(3):266.
6. Adams JR, Schmidtmann ET, Azad AF. Infection of colonized cat fleas, *Ctenocephalides felis* (Bouche), with a rickettsia-like microorganism. Am J Trop Med Hyg. 1990;43:400–9.
7. Azad AF, Sacci JBJ, Nelson WM, Dasch GA, Schmidtmann ET, Carl M. Genetic characterization and transovarial transmission of a typhus-like rickettsia found in cat fleas. Proc Natl Acad Sci U S A. 1992;89:43–6.
8. Ogata H, Robert C, Audic S, Robineau S, Blanc G, Fournier PE, et al. *Rickettsia felis*, from culture to genome sequencing. Ann N Y Acad Sci. 2005;1063:26–34.
9. Fournier PE, Belghazi L, Robert C, Elkarkouri K, Richards AL, Greub G, et al. Variations of plasmid content in *Rickettsia felis*. PLoS ONE. 2008;3:e2289.
10. Choi YJ, Lee EM, Park JM, Lee KM, Han SH, Kim JK, et al. Molecular detection of various rickettsiae in mites (acari: trombiculidae) in southern, Jeolla Province, Korea. Microbiol Immunol. 2007;51(3):307–12.
11. Ishikura M, Ando S, Shinagawa Y, Matsuura K, Hasegawa S, Nakayama T, et al. Phylogenetic analysis of spotted fever group rickettsiae based on gltA, 17-kDa, and rOmpA genes amplified by nested PCR from ticks in Japan. Microbiol Immunol. 2003;47(11):823–32.
12. Cardoso LD, Freitas RN, Mafra CL, Neves CV, Figueira FC, Labruna MB, et al. Characterization of *Rickettsia* spp. circulating in a silent peri-urban focus for Brazilian spotted fever in Caratinga, Minas Gerais, Brazil. Cad Saude Publica. 2006;22(3):495–501.
13. Schriefer ME, Sacci JBJ, Dumler JS, Bullen MG, Azad AF. Identification of a novel rickettsial infection in a patient diagnosed with murine typhus. J Clin Microbiol. 1994;32(4):949–54.
14. Richter J, Fournier PE, Petridou J, Häussinger D, Raoult D. *Rickettsia felis* infection acquired in Europe and documented by polymerase chain reaction. Emerg Infect Dis. 2002;8(2):207–8.
15. Raoult D, La Scola B, Enea M, Fournier P-E, Roux V, Fenollar F, et al. A flea-associated rickettsia pathogenic for humans. Emerg Infect Dis. 2001;7(1):73–81.
16. Falkow S. The microbe's view of infection. Ann Intern Med. 1998;129(3):247–8.
17. Williams M, Izzard L, Graves S, Stenos J, Kelly J. First cases of probable *Rickettsia felis* (cat flea typhus) in Australia. Med J Aust. 2010;194(1):41–3.
18. Znazen A, Raoult D. Flea-borne spotted fever. In: Raoult D, Parola P, editors. Rickettsial diseases. New York: Informa Healthcare; 2007;87–96.
19. Hechemy KE, Stevens RW, Sasowski S, Michaelson EE, Casper EA, Philip RN. Discrepancies in Weil-Felix and microimmunofluorescence test results for Rocky Mountain spotted fever. J Clin Microbiol. 1979;9(2):292–3.
20. Brouqui P, Bacellar F, Baranton G, Birtles RJ, Bjoersdorff A, Blanco JR, et al. Guidelines for the diagnosis of tick-borne bacterial diseases in Europe. Clin Microbiol Infect. 2004;10(12):1108–32.
21. Eremeeva ME, Warashina WR, Sturgeon MM, Buchholz AE, Olmstead GK, Park SY, et al. *Rickettsia typhi* and *R. felis* in rat fleas (*Xynopsylla cheopis*), Oahu, Hawaii. Emerg Infect Dis. 2008;14:1613–5.
22. Reif KE, Macaluso KR. Ecology of *Rickettsia felis*: A review. J Med Entomol. 2009;46:723–36.
23. Azad AF. Epidemiology of murine typhus. Annu Rev Entomol. 1990;35:553–69.
24. Azad AF, Radulovic S, Higgins JA, Noden BH, Troyer JM. Flea-borne rickettsioses: Ecologic considerations. Emerg Infect Dis. 1997;3(3):319–27.
25. Wedincamp JJ, Foil LD. Vertical transmission of *Rickettsia felis* in the cat flea (*Ctenocephalides felis* Bouche). J Vector Ecol. 2002;27(1):96–101.
26. Snyder JC, Wheeler CM. The experimental infection of the human body louse, *Pediculus humanus corporis*, with murine and epidemic louse-borne typhus strains. J Exp Med. 1945;82(1):1–20.
27. Niebylski ML, Peacock MG, Schwan TG. Lethal effect of *Rickettsia rickettsii* on its tick vector (*Dermacentor andersoni*). Appl Environ Microbiol. 1999;65(2):773–8.
28. Pornwiroon W, Kearney MT, Husseneder C, Foil LD, Macaluso KR. Comparative microbiota of *Rickettsia felis*-uninfected and -infected colonized cat fleas. *Ctenocephalides felis* ISME J. 2007;1:394–402.
29. Sackal C, Laudisoit A, Kosoy M, Massung R, Eremeeva ME, Karpathy SE, et al. *Bartonella spp.* and *Rickettsia felis* in fleas, Democratic Republic of Congo. Emerg Infect Dis. 2008;14:1972–4.
30. Cruz-Vazquez C, Catro Gamez E, Parada Fernandez M, Ramos Parra M. Seasonal occurrence of *Ctenocephalides felis* felis and *Ctenocephalides canis* (Siphonaptera: Pulicidae) infesting dogs and cats in an urban area in Cuernavaca, Mexico. J Med Entomol. 2001;38(1):111–3.
31. Beck W, Boch K, Mackensen H, Wiegand B, Pfister K. Qualitative and quantitative observations on the flea population dynamics of dogs and cats in several areas of Germany. Vet Parasitol. 2006;137(1–2):130–6.
32. Oliveira KA, Oliveira LS, Dias CCA, Almeida MR, Almada G, Bouyer DH, et al. Molecular detection of *Rickettsia felis* in ticks and fleas from an endemic area for Brazilian spotted fever. Mem Inst Oswaldo Cruz. 2008;103(2):191–4.

33. Bernasconi MV, Casati S, Péter O, Piffaretti JC. Rhipicephalus ticks infected with *Rickettsia* and *Coxiella* in Southern Switzerland (Canton Ticino). Infect Genet Evol. 2002;2(2):111–20.
34. Soto SM. Human migration and infectious diseases. Clin Microbiol Infect. 2009;15:26–8.
35. Rahman A, Tegnell A, Vene S, Giesecke J. Rickettsioses in Swedish travellers, 1997–2001. Scand J Infect Dis. 2003;35(4): 247–50.
36. Jensenius M, Fournier PE, Fladby T, Hellum KB, Hagen T, Priø T, et al. Sub-acute neuropathy in patients with African tick bite fever. Scand J Infect Dis. 2006;38(2):114–8.
37. Zell R. Global climate change and the emergence/re-emergence of infectious diseases. Int J Med Microbiol. 2004;293:16–26.
38. Patz JA, Graczyk TK, Geller N, Vittor AY. Effects of environmental change on emerging parasitic diseases. Int J Parasitol. 2000;30:1395–405.
39. Krasnov BR, Khokhlova IS, Fielden LJ, Burdelova NV. Development rates of two *Xenopsylla* flea species in relation to air temperature and humidity. Med Vet Entomol. 2001;15: 249–58.
40. Dantas-Torres F. The brown dog tick, *Rhipicephalus sanguineus* (Latreille, 1806) (Acari: Ixodidae): From taxonomy to control. Vet Parasitol. 2008;152:173–85.
41. Silveira JA, Passos LM, Ribeiro MF. Population dynamics of Rhipicephalus sanguineus (Latrielle, 1806) in Belo Horizonte, Minas Gerais State, Brazil. Vet Parasitol. 2009;161(3–4):270–5.
42. Lorusso V, Dantas-Torres F, Lia RP, Tarallo VD, Mencke N, Capelli G, et al. Seasonal dynamics of the brown dog tick, Rhipicephalus sanguineus, on a confined dog population in Italy. Med Vet Entomol. 2010;24(3):309–15.
43. Parola P, Socolovschi C, Jeanjean L, Bitam I, Fournier P-E, Sotto A, et al. Warmer weather linked to tick attack and emergence of severe rickettsioses. PLoS Negl Trop Dis. 2008;2:e338.
44. Marshall WF III, Telford SR III, Rys PN, Rutledge BJ, Mathiesen D, Malawista SE, et al. Detection of *Borrelia burgdoferi* DNA in museum specimens of *Peromyscus leucopus*. J Infect Dis. 1994;170:1027–32.
45. Hubbard MJ, Baker AS, Cann KJ. Distribution of *Borrelia burgdoferi* s.l. spirochaete DNA in British ticks (*Argasidae* and *Ixodidae*) since the 19th century, assessed by PCR. Med Vet Entomol. 1998;12:89–97.
46. Gray JS, Dautel H, Estrada-Pena A, Kahl O, Lindgren E. Effects of climate change on ticks and tick-borne diseases in Europe. Interdiscip Perspect Infect Dis. 2009;2009:593232.
47. Oliveira RP, Galvao MAM, Mafra CL, Chamone CB, Calic SB, Silva SU, et al. *Rickettsia felis* in *Ctenocephalides* spp. fleas, Brazil. Emerg Infect Dis. 2002;8(3):317–9.
48. Nava S, Perez-Martinez L, Venzal JM, Portillo A, Santibanez S, Oteo JA. *Rickettsia felis* in *Ctenocephalides felis* from Argentina. Vector Borne Zoonotic Dis. 2008;8(4):465–6.
49. Schloderer D, Owen H, Clark P, Stenos J, Fenwick SG. *Rickettsia felis* in fleas, Western Australia. Emerg Infect Dis. 2006;12(5):841–3.
50. Bitam I, Parola P, De La Cruz KD, Matsumoto K, Baziz B, Rolain JM, et al. First molecular detection of *Rickettsia felis* in fleas from Algeria. Am J Trop Med Hyg. 2006;74(4):532–5.
51. Kamrani A, Parreira VR, Greenwood J, Prescott JF. The prevalence of *Bartonella*, *Hemoplasma*, and *Rickettsia felis* infections in domestic cats and in cat fleas in Ontario. Can J Vet Res. 2008;72(5):411–9.
52. Labruna MB, Ogrzewalska M, Moraes-Filho J, Lepe P, Gallegos JL, López J. *Rickettsia felis* in Chile. Emerg Infect Dis. 2007;13:1794–5.
53. Psaroulaki A, Antoniou M, Papaeustathiou A, Toumazos P, Loukaides F, Tselentis Y. First detection of *Rickettsia felis* in *Ctenocephalides felis* fleas parasitizing rats in Cyprus. Am J Trop Med Hyg. 2006;74:120–2.
54. Rolain J-M, Franc M, Davoust B, Raoult D. Molecular detection of *Bartonella quintana*, *B. koehlerae*, *B. henselae*, *B. clarridgeiae*, *Rickettsia felis*, and *Wolbachia pipientis* in cat fleas, France. Emerg Infect Dis. 2003;9(3):338–42.
55. Rolain JM, Bourry O, Davoust B, Raoult D. *Bartonella quintana* and *Rickettsia felis* in Gabon. Emerg Infect Dis. 2005;11:1742–4.
56. Gilles J, Just FT, Silaghi C, Pradel I, Passos M, Lengauer H et al. Rickettsia felis in fleas, Germany. Emerg Infect Dis. 2008;14:1294–6.
57. Bauer O, Baneth G, Ehskol T, Shaw SE, Harrus S. Polygenic detection of *Rickettsia felis* in cat fleas (*Ctenocephalides felis*) from Israel. Am J Trop Med Hyg. 2006;74:444–8.
58. Zavala-Velazquez JE, Zavala-Castro JE, Vado-Solis JA, Ruiz-Sosa JA, Moron CG, Bouyer DH, et al. Identification of *Ctenocephalides felis* fleas as a host of *Rickettsia felis*, the agent of spotted fever rickettsiosis in Yucatan, Mexico. Vector Borne Zoonotic Dis. 2002;2:69–75.
59. Kelly PJ, Meads N, Theobald A, Fournier PE, Raoult D. *Rickettsia felis*, *Bartonella henselae*, and *B. clarridgeiae*, New Zealand. Emerg Infect Dis. 2004;10(5):967–8.
60. Blair PJ, Jiang J, Schoeler GB, Moron C, Anaya E, Cespedes M, et al. Characterization of spotted fever group rickettsiae in flea and tick specimens from northern Peru. J Clin Microbiol. 2004;42(11):4961–7.
61. Marquez FJ, Muniain MA, Perez JM, Pachon J. Presence of *Rickettsia felis* in the cat flea from southwestern Europe. Emerg Infect Dis. 2002;8(1):89–91.
62. Tsai KH, Lu HY, Huang JH, Wang PJ, Wang HC, Huang CG, et al. *Rickettsia felis* in cat fleas in Taiwan. Vector Borne Zoonotic Dis. 2009;9(5):561–3.
63. Kenny MJ, Birtles RJ, Day MJ, Shaw SE. *Rickettsia felis* in the United Kingdom. Emerg Infect Dis. 2003;9:1023–4.
64. Williams SG, Sacci JBJ, Schriefer ME, Andersen EM, Fujioka KK, Sorvillo FJ, et al. Typhus and typhuslike rickettsiae associated with opossums and their fleas in Los Angeles County, California. J Clin Microbiol. 1992;30:1758–62.
65. Venzal JM, Perez-Martinez L, Felix ML, Portillo A, Blanco JR, Oteo JA. Prevalence of *Rickettsia felis* in *Ctenocephalides felis* and *Ctenocephalides canis* from Uruguay. Ann N Y Acad Sci. 2006;1078:305–8.
66. Parola P, Miller RS, McDaniel P, Telford SR, Rolain JM, Wongsrichanalai C, et al. Emerging rickettsioses of the Thai-Myanmar border. Emerg Infect Dis. 2003;9(5):592–5.
67. Horta MC, Chiebao DP, De Sousa DB, Ferreira F, Pinheiro SR, Labruna MB, et al. Prevalence of *Rickettsia felis* in the fleas *Ctenocephalides felis* felis and *Ctenocephalides canis* from two Indian villages in Sao Paulo Municipality, Brazil. Ann N Y Acad Sci. 2006;1078:361–3.
68. Gilles J, Just FT, Silaghi C, Pradel I, Lengauer H, Hellmann K, et al. *Rickettsia felis* in fleas, France. Emerg Infect Dis. 2008;14:684–6.
69. Blanco JR, Perez-Martinez L, Vallejo M, Santibanez S, Portillo A, Oteo JA. Prevalence of *Rickettsia felis*-like and *Bartonella* spp in *Ctenocephalides felis* and *Ctenocephalides canis* from La Rioja (Northern Spain). Ann N Y Acad Sci. 2006;1078:270–4.
70. Jiang J, Soeatmadji DW, Henry KM, Ratiwayanto S, Bangs MJ, Richards AL. *Rickettsia felis* in *Xenopsylla cheopis*, Java, Indonesia. Emerg Infect Dis. 2006;12(8):1281–3.
71. Stevenson HL, Labruna MB, Monteneiri JA, Kosoy MY, Gage KL, Walker DH. Detection of *Rickettsia felis* in a New World flea species, *Anomiopsyllus nudata* (Siphonaptera: Ctenophthalmidae). J Med Entomol. 2005;42(2):163–7.
72. De Sousa R, Edouard-Fournier P, Santos-Silva M, Amaro F, Bacellar F, Raoult D. Molecular detection of *Rickettsia felis*,

Rickettsia typhi and two genotypes closely related to *Bartonella elizabethae*. Am J Trop Med Hyg. 2006;75(4):727–31.
73. Horta MC, Labruna MB, Pinter A, Linardi PM, Schumaker TT. *Rickettsia* infection in five areas of the state of Sao Paulo, Brazil. Mem Inst Oswaldo Cruz. 2007;102:793–801.
74. Tsui PY, Tsai KH, Weng MH, Hung YW, Liu YT, Hu KY, et al. Molecular detection and characterization of spotted fever group rickettsiae in Taiwan. Am J Trop Med Hyg. 2007;77(5):883–90.
75. Reeves WK, Loftis AD, Sanders F, Spinks MD, Wills W, Denison AM, et al. *Borrelia*, *Coxiella*, and *Rickettsia* in *Carios capensis* (Acari: Argasidae) from a brown pelican (*Pelecanus occidentalis*) rookery in South Carolina, USA. Exp Appl Acarol. 2006;39:321–9.
76. Duh D, Punda-Polic V, Trilar T, Petrovec M, Bradaric N, Avsic-Zupanc T. Molecular identification of *Rickettsia felis*-like bacteria in *Haemaphysalis sulcata* ticks collected from domestic animals in Southern Croatia. Ann N Y Acad Sci. 2006;1078:347–51.
77. Behar A, McCormick LJ, Perlman SJ. *Rickettsia felis* infection in a common household insect pest, *Liposcelis bostrychophila* (Psocoptera: Liposcelidae). Appl Environ Microbiol. 2010;76(7):2280–5.

***Mohammad Yazid Abdad**
Australian Rickettsial Reference Laboratory
Geelong Hospital
Geelong, VIC 3220
Australia
Email: myazid@barwonhealth.org.au