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Anaplasma phagocytophilum and
human granulocytic anaplasmosis in Portugal

Ana Sofia Pereira dos Santos

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Neutrophil with *Anaplasma phagocytophilum* morulae. Peripheral blood smear stained with Diff-Quik. Photograph kindly provided by Professor J Stephen Dumler, The Johns Hopkins University School of Medicine, Baltimore.

Neutrófilo com uma mórula de *Anaplasma phagocytophilum*. Esfregaço de sangue periférico corado com Diff-Quik. Fotografia gentilmente cedida pelo Professor J Stephen Dumler, The Johns Hopkins University School of Medicine, Baltimore.

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ORIENTAÇÃO:

Doutora Fátima Bacellar
Investigadora Principal Aposentada
Centro de Estudos de Vectores e Doenças Infecciosas
Instituto Nacional de Saúde Dr. Ricardo Jorge, Lisboa

Professor John Stephen Dumler
Professor Associado
Division of Medical Microbiology, Department of Pathology
The Johns Hopkins University School of Medicine, Baltimore

COMISSÃO TUTORIAL:

Doutora Margarida Collares Pereira
Investigadora Principal com Habilitação
Instituto de Higiene e Medicina Tropical
Universidade Nova de Lisboa, Lisboa

Professor Doutor Paulo Almeida
Professor Associado
Instituto de Higiene e Medicina Tropical
Universidade Nova de Lisboa, Lisboa

Doutora Fátima Bacellar
Investigadora Principal Aposentada
Centro de Estudos de Vectores e Doenças Infecciosas
Instituto Nacional de Saúde Dr. Ricardo Jorge, Lisboa

Na presente dissertação incluem-se resultados que foram ou estão a ser alvo de publicação em co-autoria. Para efeitos do disposto no nº1 do Despacho nº2303/2000 do Regulamento de Programas de Doutoramento do Instituto de Higiene e Medicina Tropical, Universidade Nova de Lisboa (Diário da República, 2ª série, nº23, de 28 de Janeiro de 2000), o autor da dissertação declara que interveio na concepção e execução do trabalho experimental, na interpretação dos resultados e na redacção dos manuscritos publicados, no prelo ou que aguardam submissão.

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Ana Sofia Pereira dos Santos

a Arminda

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ABSTRACT

Anaplasma phagocytophilum and granulocytic anaplasmosis are of increasing interest to the scientific community as indicated by the expanding number of reports published in the past two decades, and especially since the emergence of the first cases of human granulocytic anaplasmosis (HGA). The growing recognition of the Public Health importance of *A. phagocytophilum* in North America and in Europe, along with its recent detection in Portugal has signalled the need for more detailed studies that address the emergence of HGA and its causative agent in our country.

Initially based on a methodological training in research units dedicated to Anaplasmataceae, this work enabled the transfer of technology as currently applied to *A. phagocytophilum* research and made possible the development of a new line of investigation at *Centro de Estudos de Vetores e Doenças Infecciosas, Instituto Nacional de Saúde Dr. Ricardo Jorge (CEVDI/INSA)*. By establishing the foundations for concerted study on *A. phagocytophilum* and HGA, the work described herein has facilitated development of a broad approach toward fundamental issues in Anaplasmataceae ecobiology and disease by focusing attention on identification of potential ixodid vectors, mammals likely to be involved in the infectious agent's life cycles either as reservoirs or affected hosts, and garnered the evidence indicating the potential for human exposure in Portugal.

The studies conducted in ixodid ticks proves the involvement of two *Ixodes* species in *A. phagocytophilum* cycles, including *Ixodes ricinus* on Madeira Island and *I. ventalloi* on the mainland. The detection of *A. phagocytophilum* DNA in *I. ricinus* reinforces prior studies and suggests its persistence on Madeira Island. This thesis also adds new data to the understanding of the natural history of *A. phagocytophilum* by providing the first evidence of infections in *I. ventalloi* ticks. The fact that some infected arthropods infest domestic cats not only mandates the inclusion of these mammals on the national list of vertebrate hosts parasitized by *I. ventalloi* ticks, but also shows their potential complicity in *A. phagocytophilum* maintenance. Moreover, molecular data shows the existence of *A. phagocytophilum* variant genotypes in Portuguese ticks. Partial gene sequences from infected ticks demonstrates nucleotide polymorphisms that support a close relationship of *A. phagocytophilum* on Madeira Island *I. ricinus* to North American strains isolated from humans as well as genotypes detected in Central and Northern Europe. Yet, these variants diverge from those found in mainland *I. ventalloi*, which represents a new genotype of undetermined pathogenicity.

Serological evidence of exposure to *A. phagocytophilum* or a close related agent is shown in *Mus spretus* mice, horses, and dogs in mainland. Molecular analysis of biological samples from these animal populations provides the first definitive evidence of *A. phagocytophilum* active infection in Portuguese vertebrates with detection of its DNA in one seropositive horse from mainland Portugal, where the *A.*

phagocytophilum genotype found is closely related to strains isolated from humans, suggesting the potential for HGA in Portugal. This thesis further extends study to identification of another closely related *Anaplasma* species, and its potential for serological cross-reactions with *A. phagocytophilum*, as evident with the detection of *A. platys* DNA in seropositive dogs. These data also underscore the importance of veterinarians maintaining vigilance for detection of not only granulocytic anaplasmosis but also canine infectious cyclic thrombocytopenia as causes of tick-borne diseases in Portugal.

Both prospective and retrospective serological and molecular investigations of human exposure to *A. phagocytophilum* were performed on samples received at CEVD/INSA for the laboratory diagnosis of patients with suspected tick-borne diseases during 2000-2006. The results provide evidence for seropositive Portuguese patients, including cases that fulfil serological criteria for HGA, although active infections were not detected. Moreover some seropositive patients had additional evidence of other tick-borne agents or related bacteria infections, including Lyme borreliosis, Q fever and bartonellosis. Although possibly false positive cross-reactions to shared antigens, these reactions potentially could be the result of active dual infections, or past exposure to several agents transmitted by *Ixodes* species. Overall, these results argue for continued development of improved *A. phagocytophilum* diagnostics, especially direct detection techniques, and integrated analysis of diagnostic tests for patients with suspected *Ixodes*-borne disease.

Although many aspects introduced and explored here will require expanded and more detailed investigations, this thesis contributes positively to a fundamental understanding of the extent to which *A. phagocytophilum* occurs in Portugal and its potential as a disease agent. It is hoped that these beginning studies will help to delineate new lines of research that more fully address granulocytic anaplasmosis and other emerging *Ixodes*-borne diseases.

RESUMO

Anaplasma phagocytophilum e anaplasmoze granulocítica têm vindo a merecer um crescente interesse na comunidade científica, facto demonstrado pelo crescente número de publicações que surgiram nas duas últimas décadas, particularmente desde que foram documentados os primeiros casos de anaplasmoze granulocítica humana (AGH). O reconhecimento da importância de *A. phagocytophilum* em termos de Saúde Pública na América do Norte e na Europa, associado à recente detecção do agente em Portugal, pôs em evidência a necessidade de estudos mais detalhados sobre a emergência deste Anaplasmataceae e de AGH no nosso país.

Inicialmente baseado num treino metodológico em Unidades de Investigação especializadas em Anaplasmataceae, o presente trabalho permitiu a transferência da tecnologia correntemente aplicada ao estudo de *A. phagocytophilum* e conseqüentemente o desenvolvimento desta linha de investigação no Centro de Estudos de Vectores e Doenças Infecciosas, Instituto Nacional de Saúde Dr. Ricardo Jorge (CEVDI/INSA). Ao estabelecer as bases para um estudo concertado em *A. phagocytophilum* e AGH, este trabalho tornou possível uma abordagem abrangente a aspectos essenciais da ecobiologia deste Anaplasmataceae e da doença que lhe está associada, focando-se na identificação de potenciais ixodídeos vectores, de mamíferos envolvidos no ciclo natural do agente, quer como reservatórios quer como hospedeiros susceptíveis, recolhendo evidências que apontam para a possibilidade de exposição do homem a este agente em Portugal.

Os estudos levados a cabo nos ixodídeos demonstram o envolvimento de duas espécies de *Ixodes* no ciclo de *A. phagocytophilum*, concretamente *Ixodes ricinus* na Ilha da Madeira e *I. ventalloi* no continente. A detecção de ADN do agente em *I. ricinus* vem reforçar estudos anteriores, sugerindo a sua persistência na Ilha da Madeira. Esta tese acrescenta ainda um novo dado ao conhecimento da história natural de *A. phagocytophilum*, com a primeira detecção de infecção em *I. ventalloi*. O facto de alguns dos artrópodes infectados terem sido obtidos a partir de gatos domésticos, não só acrescenta este mamífero à lista nacional de hospedeiros vertebrados parasitados por *I. ventalloi* mas sugere também o seu potencial envolvimento no ciclo de transmissão de *A. phagocytophilum*. A análise molecular dos dados obtidos evidencia ainda a existência de diferentes génotipos deste Anaplasmataceae nos ixodídeos portugueses. As sequências nucleotídicas obtidas sugerem a proximidade genética entre *A. phagocytophilum* detectado em *I. ricinus* na Ilha da Madeira e estirpes isoladas de humanos na América do Norte, bem como de sequências detectadas na Europa Central e do Norte. No entanto estes génotipos divergem das sequências nucleotídicas obtidas a partir do *I. ventalloi* no continente, que representa um novo génotipo de patogenia não determinada.

São também apresentadas evidências serológicas da exposição a *A. phagocytophilum* ou a outro agente antigenicamente semelhante em ratinhos *Mus spretus*, cavalos e canídeos domésticos no continente. A análise molecular das amostras biológicas obtidas a partir das populações em estudo permitiu a detecção da primeira infecção activa por *A. phagocytophilum* em vertebrados portugueses, com a identificação de ADN do agente num dos cavalos seropositivos. Sendo as sequências nucleotídicas obtidas semelhantes à das estirpes associadas aos casos de infecção em humanos, é reforçada uma vez mais a possibilidade de AGH ocorrer em Portugal. Esta tese refere ainda a identificação de outra Anaplasmataceae filogenicamente próxima de *A. phagocytophilum* - *A. platys*, detectada em canídeos seropositivos, evidenciando a possibilidade de ocorrerem reacções cruzadas entre estes dois agentes. Estes dados salientam a importância da vigilância em termos veterinários da ocorrência não só de anaplasrose granulocítica mas também de trombocitopenia cíclica infecciosa canina como causa de doença associada a ixodídeos em Portugal.

Para averiguar a possibilidade de exposição humana a *A. phagocytophilum* foram realizados estudos serológicos e moleculares retrospectivos e prospectivos, em amostras biológicas recebidas no CEVDI/INSA durante 2000-2006 para o diagnóstico laboratorial de pacientes com suspeita de doença associada a ixodídeos. Os resultados provam a existência de reacções serológicas positivas na população estudada, incluindo alguns casos que satisfazem os critérios serológicos para definição de AGH, embora sem evidência de infecção activa. Adicionalmente, alguns dos doentes seropositivos apresentaram evidência de infecção causada por outros agentes transmitidos por ixodídeos ou por bactérias relacionadas, nomeadamente borreliose de Lyme, febre Q e bartonelose. Embora estes resultados possam ser interpretados como falsos positivos resultantes de reacções cruzadas, a possibilidade de se tratarem de co-infecções ou exposições anteriores a vários agentes transmitidos por ixodídeos do género *Ixodes* também deverá ser considerada. Em suma, estes resultados apontam para a necessidade de desenvolver o diagnóstico de *A. phagocytophilum*, nomeadamente no que diz respeito à aplicação de técnicas directas de detecção do agente, bem como à integração dos dados do diagnóstico laboratorial em casos de suspeita de doença associada a *Ixodes* spp.

Embora muitos dos aspectos focados neste trabalho requeiram uma investigação mais detalhada, esta tese contribui positivamente para a compreensão das questões fundamentais relacionadas com a ocorrência de *A. phagocytophilum* e o seu potencial como agente de doença em Portugal. Termina-se com a esperança de que estes primeiros passos ajudem a delinear novas linhas de investigação no âmbito do estudo da anaplasrose granulocítica e outras doenças emergentes associadas a espécies do género *Ixodes*.

GENERAL INDEX

Abstract / Resumo	xi
General index	xv
Figures index	xix
Tables index	xxiii
List of abbreviations and abbreviations	xxvii
Introduction	1
Outline and objectives	3
Dissertation plan	4
Chapter I. State of the art	7
1.1. Family Anaplasmataceae	9
1.1.1. Definition	9
1.1.2. Phylogeny and taxonomy	10
1.1.3. Historical perspective of human infection	12
1.2. <i>Anaplasma phagocytophilum</i>	17
1.2.1. Generalities	17
1.2.2. Life-cycle	18
1.2.3. Pathogenesis	21
1.2.4. Ecology	30
1.2.5. Other <i>Ixodes</i> -borne agents	33
1.2.6. Variant strains and disease	37
1.2.6.1. Tick-borne fever	40
1.2.6.2. Equine granulocytic anaplasmosis	40
1.2.6.3. Other granulocytic anaplasmosis	41
1.3. Human granulocytic anaplasmosis	43
1.3.1. Definition	43
1.3.2. Epidemiology	43
1.3.3. Clinical presentation	49
1.3.4. Complications and outcome	50

1.3.5. Confirmatory laboratory tests	53
1.3.5.1. Optical microscopy, molecular analysis and <i>in vitro</i> culture	53
1.3.5.2. Serology	58
1.3.5.3. Case definition	60
1.3.6. Treatment	61
1.3.7. Prevention	64
1.4. Anaplasmataceae in Portugal	67
Chapter II. Exchange technology in Anaplasmataceae field	71
2.1. Distribution of " <i>Ehrlichia walkerii</i> " in <i>Ixodes ricinus</i> (Acari:Ixodidae) from the Northern part of Italy. Journal of Medical Entomology 2005; 42(1):82-3	73
2.2. Detection of a non-pathogenic variant of <i>Anaplasma phagocytophilum</i> in <i>Ixodes ricinus</i> from La Rioja, Spain. Annals of New York Academy of Science 2005; 1063:333-6	79
Chapter III. <i>Anaplasma phagocytophilum</i> in ticks (Acari: Ixodidae)	85
3.1. Detection of <i>Anaplasma phagocytophilum</i> DNA in <i>Ixodes</i> ticks (Acari:Ixodidae) from Madeira Island and Setúbal District, mainland Portugal. Emerging Infectious Diseases 2004; 10(9):1643-8	87
3.2. Ticks Parasitizing wild birds in Portugal: Detection of <i>Rickettsia aeschlimannii</i> , <i>R. helvetica</i> and <i>R. massilliae</i> . Experimental and Applied Acarology 2006; 39(3-4):331-8	95
3.3. Ticks and tick-borne rickettsiae surveillance in Montesinho Natural Park, Portugal. Annals of New York Academy of Science 2006; 1078:137-42	105
3.4. Detection of <i>Rickettsia helvetica</i> and other spotted fever group rickettsiae in <i>Ixodes ricinus</i> from Tapada Nacional de Mafra, Portugal. In submission	113
3.5. PCR-based survey of <i>Anaplasma phagocytophilum</i> in Portuguese ticks (Acari: Ixodidae). In submission	125
Chapter IV. <i>Anaplasma phagocytophilum</i> in non-human vertebrate hosts	147
4.1. Detection of antibodies against <i>Anaplasma phagocytophilum</i> in wild-rodents, Portugal. In submission	149
4.2. Serological survey and molecular detection of <i>Anaplasma phagocytophilum</i> infection in Portuguese horses. In submission	169
4.3. Anaplasmataceae as the etiologic agents of canine tick-borne disease in Portugal. In submission	187

Chapter V. Human exposure to <i>Anaplasma phagocytophilum</i>	205
5.1. Human exposure to <i>Anaplasma phagocytophilum</i> in Portugal. Annals of New York Academy of Science 2006; 1078:100-5	207
5.2. Six years of Anaplasmataceae serodiagnosis in humans. Data from a state laboratory, Portugal. In submission	215
Chapter VI. Final remarks and future perspectives	241
References	257
Appendixes	281
Appendix 1. Carraças associadas a patologias infecciosas em Portugal. Acta Médica Portuguesa 2006; 19:39-48	283
Appendix 2. Ehrlichiose granulocítica humana. Conceitos actuais. Revista Portuguesa de Doenças Infecciosa 2004; Outubro/Dezembro:12-7	295

FIGURES INDEX

Chapter 1. State of the art

1.1. Family Anaplasmataceae

- Figure 1. Electron photomicrograph of a canine macrophage-like cell (DH82, ATCC CRL-10389) infected with *Ehrlichia canis* 9
- Figure 2. Current phylogeny and taxonomic classification of genera in the family Anaplasmataceae 12

1.2. *Anaplasma phagocytophilum*

- Figure 3. Representation of the intracellular cycle proposed for *A. phagocytophilum* 20
- Figure 4. Representation of *p44* genes 23
- Figure 5. Representation of NADPH oxidase 25
- Figure 6. Approximate geographic distributions of four medically important *Ixodes persulcatus/ricinus* complex ticks 31
- Figure 7. Schematic representation of *A. phagocytophilum* transmission cycle 34

1.3. Human granulocytic anaplasmosis

- Figure 8. Number of HGA cases reported to NETSS, US 1999-2004 45
- Figure 9. Total number of HGA cases reported to NETSS by State, US 1999-2004 45
- Figure 10. Total number of HGA cases reported in each European country since 1997 46
- Figure 11. Relative sensitivity of diagnosis tests used for laboratory confirmation of HGA 54
- Figure 12. *A. phagocytophilum* morulae in neutrophils: A- peripheral blood smear stained by Diff-Quik; B- spleen section stained by immunoalkaline phosphatase/ hematoxylin 55
- Figure 13. Immunofluorescence assay (IFA) using HL-60 cells infected with *A. phagocytophilum* Webster strain as antigen: A- negative sample; B- reactive sample evidenced by green fluorescence of *A. phagocytophilum* morulae 59

Chapter II. Exchange technology in Anaplasmataceae field

2.1. Distribution of "*Ehrlichia walkerii*" in *Ixodes ricinus* (Acari:Ixodidae) from the Northern part of Italy

- Figure 1. Map of Belluno and suburbs in northern Italy 76

Chapter III. *Anaplasma phagocytophilum* in ticks (Acari: Ixodidae)

3.1. Detection of *Anaplasma phagocytophilum* DNA in *Ixodes* ticks (Acari:Ixodidae) from Madeira Island and Setúbal District, mainland Portugal

Figure 1. Collection sites in Madeira Island and Setúbal District, mainland Portugal	90
Figure 2. Dendrogram showing the phylogenetic relationships of the <i>msp2</i> sequences of the newly identified strains and other representative sequences from North American <i>A. phagocytophilum</i> strains (Webster strain-Wisconsin and USG3 strain-eastern United States), and from <i>A. marginale</i> Florida strain (<i>msp2</i> and <i>msp3</i>)	92

3.3. Ticks and tick-borne rickettsiae surveillance in Montesinho Natural Park, Portugal

Figure 1. Montesinho Natural Park	111
---	-----

3.5. PCR-based survey of *Anaplasma phagocytophilum* in Portuguese ticks (Acari: Ixodidae)

Figure 1. Tick species and collection areas on the mainland Portugal and in the Madeira Archipelago (2002-2006)	140
Figure 2. Dendrogram showing the phylogenetic relationships between <i>A. phagocytophilum</i> sequences presented in this study and other Anaplasmataceae based on partial nucleotide sequences of the <i>msp2</i> (A), <i>rrs</i> (B), and <i>groESL</i> (C)	143

Chapter IV. *Anaplasma phagocytophilum* in non-human vertebrate hosts

4.1. Detection of antibodies against *Anaplasma phagocytophilum* in wild-rodents, Portugal

Figure 1. Total number of rodent studied by IFA and/or PCR, according to sampling area (trapping period)	167
--	-----

4.2. Serological survey and molecular detection of *Anaplasma phagocytophilum* infection in Portuguese horses

Figure 1. Number of <i>A. phagocytophilum</i> seropositive cases per total horses studied in each district (origin information was not available for nine animals)	182
Figure 2. Phylogenetic relationships between <i>A. phagocytophilum</i> sequences detected in this study and other Anaplasmataceae based on partial nucleotide sequences of the <i>groESL</i> (A) and <i>rrs</i> (B)	185

4.3. Anaplasmataceae as etiologic agents of canine tick-borne disease in Portugal

Figure 1. Phylogenetic relationships between <i>A. platys</i> sequences detected in this study other Anaplasmataceae based on partial nucleotide sequences of the <i>rrs</i> (A) and <i>groESL</i> (B)	201
--	-----

Figure 2. Dendrogram demonstrating the similarity among GroEL amino acid sequences derived from *A. platys*-infected Portuguese dogs compared to other Anaplasmataceae species 203

Chapter V. Human exposure to *Anaplasma phagocytophilum*

5.1. Human exposure to *Anaplasma phagocytophilum* in Portugal

Figure 1. Western blot results for *A. phagocytophilum* IFA-positive patients 213

5.2. Six years of Anaplasmataceae serodiagnosis in humans. Data from a state laboratory, Portugal

Figure 1. Number of patients that had at least one sera sample submitted to *CEVDI/INSA* with a request for *A. phagocytophilum* and/or *E. chaffeensis* diagnosis during 2000-2006 235

Figure 2. Light microscopic appearance of *C. burnetti* human isolate in HL-60 cells. Cytoentrifuge preparations of culture stained with Diff-Quik (A) and IFA (B) 236

TABLES INDEX

Chapter 1. State of the art

1.1. Family Anaplasmataceae

Table 1. Current classification of the family Anaplasmataceae 10

Table 2. Biological, ecological and epidemiological features of medically important Anaplasmataceae species 15

1.2. *Anaplasma phagocytophilum*

Table 3. Prevalence (%) of questing ticks detected with *A. phagocytophilum* infections by PCR-based methods 32

Table 4. *A. phagocytophilum* infection in wild mammals detected by PCR-based studies 35

Table 5. Members of *Ixodes persulcatus/ricinus* complex as potential and confirmed vectors for other tick-borne agents 36

Table 6. Prevalence of *A. phagocytophilum* coinfections in questing *Ixodes* ticks detected by PCR-based methods 38

1.3. Human granulocytic anaplasmosis

Table 7. Meta-analysis of *A. phagocytophilum* seroprevalence (%) among various human populations based in seropositivity obtained from immunofluorescence assay 47

Table 8. Clinical complications of HGA reported in North America and in Europe 52

Table 9. Results of confirmatory laboratory testing for 330 patients with HGA from case series or case reports in North America and Europe 56

Table 10. DNA targets that have been used for the detection of *A. phagocytophilum* in samples from infected patients 57

Table 11. Proposed case definition for human granulocytic anaplasmosis 61

Table 12. Recommended adult and pediatric antibiotic treatment for HGA 62

Chapter II. Exchange technology in Anaplasmataceae field

2.1. Distribution of "*Ehrlichia walkeri*" in *Ixodes ricinus* (Acari:Ixodidae) from the Northern part of Italy

Table 1. Prevalence of *E. walkeri* in seven sites around Belluno, Italy 77

Chapter III. *Anaplasma phagocytophilum* in ticks (Acari: Ixodidae)

3.1. Detection of *Anaplasma phagocytophilum* DNA in *Ixodes* ticks (Acari:Ixodidae) from Madeira Island and Setúbal District, mainland Portugal

Table 1. Results of PCR to detect <i>A. phagocytophilum</i> DNA in ticks	91
Table 2. PCR-positive results of ticks	92

3.2. Ticks Parasitizing wild birds in Portugal: Detection of *Rickettsia aeschlimannii*, *R. helvetica* and *R. massiliae*

Table 1. List of wild birds parasitized by ticks	100
Table 2. List of wild birds parasitized with ticks infected with rickettsial agents	101

3.3. Ticks and tick-borne rickettsiae surveillance in Montesinho Natural Park, Portugal

Table 1. Number of ticks by species and stage collected in <i>MNP</i> and detection assay results	109
Table 2. <i>Rickettsia</i> isolation results	111

3.4. Detection of *Rickettsia helvetica* and other spotted fever group rickettsiae in *Ixodes ricinus* from Tapada Nacional de Mafra, Portugal.

Table 1. Tick samples detected with <i>Rickettsia</i> DNA	123
---	-----

3.5. PCR-based survey of *Anaplasma phagocytophilum* in Portuguese ticks (Acari: Ixodidae)

Table 1. <i>A. phagocytophilum</i> PCR results from questing ticks, according to sampling area, species and gender	141
Table 2. <i>A. phagocytophilum</i> PCR results from ticks collected parasitizing vertebrate hosts, according to sampling area, species and gender	142

Chapter IV. *Anaplasma phagocytophilum* in non-human vertebrate hosts

4.1. Detection of antibodies against *Anaplasma phagocytophilum* in wild-rodents, Portugal

Table 1. <i>A. phagocytophilum</i> results obtained from mainland mice tested by both IFA and PCR and Madeira Island rodents tested by PCR alone	168
--	-----

4.2. Serological survey and molecular detection of *Anaplasma phagocytophilum* infection in Portuguese horses

Table 1. Breed, geographic origin, gender, age, and other infectious disease tests for Portuguese horses with <i>A. phagocytophilum</i> antibodies	183
Table 2. Univariate statistical analysis of <i>A. phagocytophilum</i> seropositive horses according to age, gender and origin	184

4.3. Anaplasmataceae as etiologic agents of canine tick-borne disease in Portugal	
Table 1. Dogs presented with active infections detected by IFA and PCR	200
Chapter V. Human exposure to <i>Anaplasma phagocytophilum</i>	
5.1. Human exposure to <i>Anaplasma phagocytophilum</i> in Portugal	
Table 1. Serologic testing results for <i>A. phagocytophilum</i> and <i>E. chaffeensis</i>	211
Table 2. Epidemiological and clinical data from patients with confirmed exposure to <i>A. phagocytophilum</i>	212
5.2. Six years of Anaplasmataceae serodiagnosis in humans. Data from a state laboratory, Portugal	
Table 1. Patients with positive results for <i>A. phagocytophilum</i> in serologic tests (2000-2006)	237
Table 2. Patients with positive results for <i>E. chaffeensis</i> in serologic tests (2000-2006)	239
Table 3. Patients with positive results for both <i>A. phagocytophilum</i> and <i>E. chaffeensis</i> in serologic tests (2000-2006)	240

LIST OF ABBREVIATURES AND ABBREVIATIONS

<i>ankA</i>	Gene encoding AnkA
AnkA	The 153-160 kDa protein with several tandemly repeated ankyrin motifs
ATCC	American Type Culture Collection
AT-rich	Adenine-thymine rich
BF	Boutonneuse fever [also referred as Mediterranean spotted fever (MSF)]
bp	Base pair
CDC	Centers for Disease Control and Prevention
<i>CEVDI</i>	<i>Centro de Estudos de Vetores e Doenças Infecciosas</i>
CICT	Canine Infectious cyclic thrombocytopenia
CSF	Cerebrospinal fluid
DH82	Canine macrophage-like cell line
DNA	Desoxiribonucleic acid
EDTA	Ethylenediaminetetraacetic acid
EGA	Equine granulocytic anaplasmosis
ELISA	Enzyme-linked Immunosorbent assay
FBS	Fetal bovine serum
FICT	Fluorescein isothiocyanate
<i>flgB</i>	Flagellin gene
GA	Granulocytic anaplasmosis
G+C	Guanine + cytosine
<i>gltA</i>	Citrate synthase gene
<i>groESL</i>	Heat shock operon
GroESL	Heat shock proteins, including 10-20 kDa GroES and 58-65 kDa GroEL (also named GroL) that act as chaperonins
HB	Human babesiosis
HGA	Human granulocytic anaplasmosis
HGE	Human granulocytic ehrlichiosis (presently human granulocytic anaplasmosis)
HL-60	Human promyelocytic leukaemia cell line
rHL-60	HL-60 cells induced to differentiate into functional granulocytes
HME	Human monocytic ehrlichiosis
<i>ICNB</i>	<i>Instituto de Conservação da Natureza e da Biodiversidade</i>

IFA	Immunofluorescence assay
IgG, IgM	Immunoglobulin G, immunoglobulin M
INSA	<i>Instituto Nacional de Saúde Dr. Ricardo Jorge</i>
kDa	Kilodalton
LB	Lyme borreliosis
LPS	Lipopolysaccharide
MEM	Minimum essential medium
MSF	Mediterranean spotted fever [also referred as boutonneuse fever (BF)]
<i>msp2</i>	Surface proteins gene family (also <i>p44</i>)
MSP2	Surface proteins family (also P44)
NETSS	National Electronic Telecommunications Systems for Surveillance
<i>OmpA</i>	Outer membrane protein A gene
<i>OmpB</i>	Outer membrane protein B gene
<i>p44</i>	Surface proteins gene family (also <i>msp2</i>)
P44	Surface proteins family (also MSP2)
PBS	Phosphate buffered saline
PCR	Polymerase chain reaction
RMSF	Rocky Mountain spotted fever
<i>rrs</i>	16S rRNA gene
Salp	Ticks salivary gland protein
<i>s.l.</i>	<i>Sensu lato</i>
<i>s.s.</i>	<i>Sensu stricto</i>
TBE	Tick-borne encephalitis
TBF	Tick-borne fever (also referred as pasture fever)
TNM	<i>Tapada Nacional de Mafra</i>
US	The United States of America (also abbreviated as USA)
vero E6	Epithelial-like cell line obtained from kidney epithelial cells of the african green monkey (<i>Cercopithecus aethiops</i>)
WB	Western blot

INTRODUCTION

OUTLINE AND OBJECTIVES

Ticks are obligate hematophagous acarines that present widespread distribution and parasitize a broad range of terrestrial vertebrates, including amphibians, reptiles, birds, domestic and wild mammals and humans. Its implication in infectious disease was first evident in veterinary medicine when *Boophilus annulatus* was linked to Texas cattle fever via transmission of *Babesia bigemina* (Smith & Kilbourne, 1893). In the beginning of the 20th century, ticks were additionally implicated in human disease with the description of tick-borne relapsing fever, caused by *Borrelia duttonii*, and its association with *Ornithodoros moubata* bites (Dutton & Todd, 1905), as well as recognition of the role that *Dermacentor andersoni* plays as vectors of *Rickettsia rickettsii*, the agent of Rocky Mountain spotted fever (Ricketts, 1909). Since then, ticks were linked to several other protozoal, bacterial and viral infections. The last three decades in particular have revealed the emergence of an increasing number of human tick-borne diseases, mostly due to the expanding knowledge of ticks, their pathogenic potential and the development of more reliable diagnostic tools.

Human infections caused by bacteria belonging to the family Anaplasmataceae represent some of the best examples of newly emergent tick-borne diseases. Some of these agents have been long known as veterinary pathogens but their implication in human cases has only recently been recognized, such as for *Anaplasma phagocytophilum* the etiologic agent of human granulocytic anaplasmosis (HGA). Disease caused by this microorganism was first recognized in 1932 in European sheep and cattle (Gordon *et al.*, 1932), and a similar agent was also later found to be the cause of equine pathology in the United States of America (US) (Gribble, 1969; Stannard *et al.*, 1969). However, only in the 1990's were the first cases of human infection described in US (Bakken *et al.*, 1994; Chen *et al.*, 1994) and in Europe (Petovec *et al.*, 1997). At present, HGA stands out as the most prevalent human disease caused by an Anaplasmataceae member, due to the number of cases that are reported annually in US; in some areas of the country HGA is the second most frequent vector-borne disease following Lyme borreliosis (LB)¹. Moreover, it is suggested that *A. phagocytophilum* is found broadly across several countries in Europe, Middle East and Asia, raising the possibility of human and animal infections over the same geographic regions.

¹ Lyme borreliosis (LB) is a tick-borne disease caused by the eubacteria *Borrelia burgdorferi sensu lato (s.l.)*.

Although the number of HGA cases outside the US is still limited, the possibility that this zoonosis is under-diagnosed owing to a lack of physician awareness or inavailability of current laboratory diagnostics is controversial and of great concern.

As HGA has now been readily recognized in other European countries, this thesis was undertaken to contribute to the fuller understanding of *A. phagocytophilum* ecobiology, with an emphasis on its potential importance to human health in Portugal.

In summary, the general aims of this thesis are:

- To investigate the role of Portuguese tick species as vectors of *A. phagocytophilum*;
- To search for potential reservoirs and affected vertebrate hosts in Portugal;
- To ascertain the importance of *A. phagocytophilum* in human disease;
- To develop methodological and technical approaches applied to HGA laboratory diagnosis;
- To isolate and/or characterize *A. phagocytophilum* strains circulating in the country.

DISSERTATION PLAN

The thesis is organized in six chapters:

The first chapter is the introduction to the theme providing general information about tick-borne bacteria belonging to the family Anaplasmataceae and a broad updated perspective of *A. phagocytophilum* and its role in HGA.

Chapter two reflects the collaborative work focused on Anaplasmataceae field, developed during the technology exchange and the acquisition of tools and knowledge that provided the basis for developing the proposed research plan.

Chapter three is devoted to the study of *A. phagocytophilum* vectors. It describes molecular-based analyses of Anaplasmataceae within several tick species obtained either questing or parasitizing vertebrates in several areas of the country.

Chapter four explores the possibility of non-human vertebrate exposure to *A. phagocytophilum* supported by serological and molecular-based analyses of biological samples obtained from both wild and domestic animals.

Chapter five addresses the epidemiological basis of HGA in Portugal based on serologic studies of patients with suspected or confirmed tick-borne diseases and in the application of serologic testing in routine diagnosis performed at the *Centro de Estudos de Vectores e Doenças Infecciosas, Instituto Nacional de Saúde Dr. Ricardo Jorge (CEVDI/INSA)*.

Finally, chapter six summarises the results presented and discussed in previous chapters in an integrated analysis, highlighting their implications in Public Health and delineating future research objectives.

CHAPTER I

STATE OF THE ART

1.1. FAMILY ANAPLASMATACEAE

1.1.1. DEFINITION

Members of the family Anaplasmataceae are non-motile, obligatory intracellular Gram-negative bacteria that reside in a membrane-bound cytoplasmic vacuole of the host cell, either singly or more often in characteristic microcolonies resembling mulberries, termed morulae (Latin *morum* = mulberry, Figure 1). They are represented by fifteen or sixteen species, classified in five distinct genera: *Aegyptianella*, *Anaplasma*, *Ehrlichia*, *Neorickettsia* and *Wolbachia* (Table 1). (Garrity *et al.*, 2004; Dumler *et al.*, 2005b).

Most Anaplasmataceae are etiologic agents of worldwide veterinary diseases, some of which are now also regarded as emerging human pathogens. The only exception is the genus *Wolbachia* that includes arthropod and nematode endosymbionts, but that may be involved in the pathogenesis of filariasis (Hoerauf *et al.*, 2001; Taylor *et al.*, 2005). In general, the biological cycle of Anaplasmataceae involves the infection of invertebrates (*Wolbachia*), and incidentally also vertebrates (*Neorickettsia*) or both invertebrate and vertebrate hosts (*Aegyptianella*, *Anaplasma* and *Ehrlichia*). Unique cell tropisms are displayed by these agents and depending on bacterial species, endothelial and/or hematopoietic lineage cells (erythrocytes, monocytes/ macrophages, granulocytes or platelets) are specifically infected in vertebrate hosts. The most important biological, ecological and epidemiological features of Anaplasmataceae with medical importance are showed in table 2.

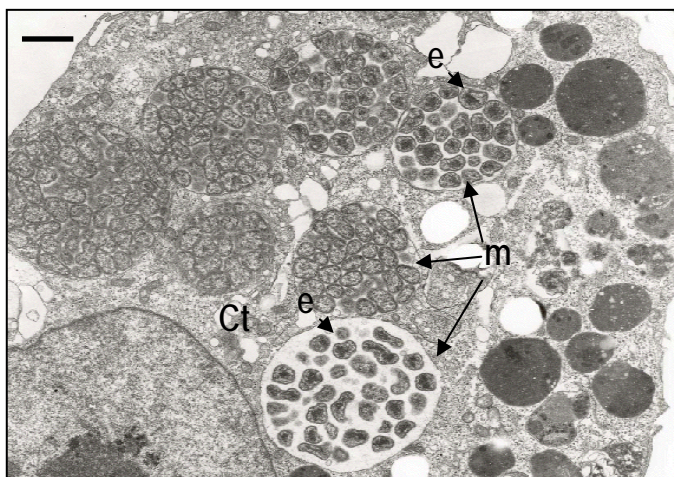


FIGURE 1. Electron photomicrograph of a canine macrophage-like cell (DH82, ATCC CRL-10389) infected with *Ehrlichia canis* (adapted from Popov *et al.*, 1998).

The cytoplasm (Ct) contains seven morulae (m) filled with ehrlichiae (e), showing coccoid to ellipsoidal, often pleomorphic shape. Bar 1 μ m.

TABLE 1. Current classification of the family Anaplasmataceae (adapted from Garrity *et al.*, 2004).

Family Anaplasmataceae				
Genus				
<i>Anaplasma</i>	<i>Aegyptianella</i> (<i>incertae sedis</i>)	<i>Ehrlichia</i>	<i>Neorickettsia</i>	<i>Wolbachia</i>
<i>A. bovis</i>	<i>A. pullorum</i>	<i>E. canis</i>	<i>N. helminthoeca</i>	<i>W. pipientis</i>
<i>A. caudatum</i>		<i>E. chaffeensis</i>	<i>N. risticii</i>	
<i>A. centrale</i>		<i>E. ewingii</i>	<i>N. sennetsu</i>	
<i>A. marginale</i>		<i>E. muris</i>		
<i>A. platys</i>		<i>E. ruminantium</i>		
<i>A. phagocytophilum</i>				

1.1.2. PHYLOGENY AND TAXONOMY

The family Anaplasmataceae is taxonomically classified in the Domain Bacteria, Phylum Proteobacteria, Class "Alphaproteobacteria" and Order Rickettsiales. For many years, Anaplasmataceae were categorized based solely on morphological, ecological, epidemiological and clinical characteristics such as infected host cells, infected mammalian species, geographic location, and antigenic cross-reactivity (Philip, 1957; Moulder, 1974; Weiss & Moulder, 1984). The development of molecular tools for phylogenetic studies and the improvement of methods for the cultivation of obligate intracellular bacteria has helped clarify the exact phylogenetic positions of Anaplasmataceae, which in turn has led to profound reorganization of this Family and other closely related *taxa* (Garrity *et al.*, 2004) (Figure 2).

The family Anaplasmataceae was first proposed in the seventh edition of Bergey's Manual of Determinative Bacteriology to include the genus *Anaplasma* composed of three species, *A. centrale*, *A. marginale* and *A. ovis* (Philip, 1957). Four additional genera, *Aegyptianella* (*A. pullorum*), *Eperythrozoon* (*E. coccoides*, *E. ovis*, *E. parvum*, *E. suis* and *E. wenyoni*), *Haemobartonella* (*H. canis*, *H. felis* and *H. muris*) and *Paranaplasma* (*P. caudatum* and *P. discoides*) were included in the revision that followed (Moulder, 1974). In the first edition of Bergey's Manual of Systematic Bacteriology *Paranaplasma* was assigned to the genus *Anaplasma*, and *P. caudatum* was renamed as *A. caudatum*, which represented the last categorization of this family based exclusively in phenotypic similarity (Weiss & Moulder, 1984).

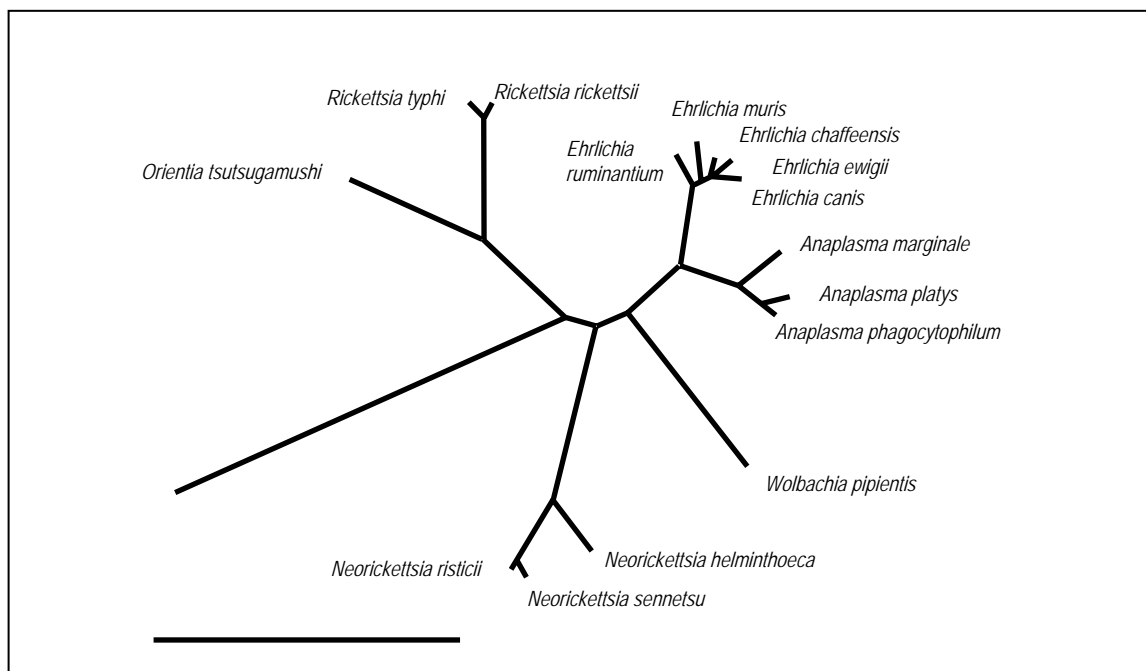
In the following years the analysis of conserved genes such as 16S rRNA (*rrs*), heat shock operon (*groESL*), and citrate synthase (*glfA*) sequences started to outline phylogenetic relationships of Anaplasmataceae and other closely related bacteria (Weisburg *et al.*, 1989, 1991; Dame *et al.*, 1992; O'Neill *et al.*, 1992; Wen *et al.*, 1995, 1996; Pretzman *et al.*, 1995; Rikihisa *et al.*, 1997; Zhang *et al.*, 1997; Sumner *et al.*, 2000; Inokuma *et al.*, 2001a, 2001b; Yu *et al.*, 2001). This approach has been widely used to both identify newly discovered bacteria as well as to redefine existing taxonomy, thus showing that the taxonomic classification of Anaplasmataceae needed to be restructured.

Molecular analysis has shown that *Eperythrozoon* and *Haemobartonella* species did not cluster with the other Anaplasmataceae, so their removal from the order Rickettsiales to Mollicutes was proposed (Rikihisa *et al.*, 1997). It has also been shown that some agents classified in the family Rickettsiaceae, especially those of the tribe *Ehrlichieae* and *Wolbachieae*, were closely related to *Anaplasma* (O'Neill *et al.*, 1992; Drancourt & Raoult, 1994; Wen *et al.*, 1995; Walker & Dumler, 1996; Sumner *et al.*, 2000; Inokuma *et al.*, 2001a, 2001b; Yu *et al.*, 2001). Based on an exhaustive analysis of *rrs*, *groESL* and surface protein gene sequences deposited in GenBank, Dumler and coworkers (2001) proposed a reorganization of the Order Rickettsiales. Concerning Anaplasmataceae, it was proposed: **i)** to include the closely related species of the family Rickettsiaceae (*Ehrlichia*, *Neorickettsia*, *Cowdria*, *Wolbachia*); **ii)** to expand the genus *Anaplasma* and incorporate *Ehrlichia bovis*, *Ehrlichia platys* and *Anaplasma phagocytophilum* (including *Ehrlichia phagocytophila*, *Ehrlichia equi* and human granulocytic ehrlichiosis [HGE] agent). The unification of *E. phagocytophila*, *E. equi* and HGE agent as a single species confirmed previous studies that suggested a close molecular (Chen *et al.*, 1994; Pretzman *et al.*, 1995; Goodman *et al.*, 1996; Sumner *et al.*, 1997; Zhang *et al.*, 1997; Inokuma *et al.*, 2001a, 2001b) and antigenic (Barlough *et al.*, 1995; Dumler *et al.*, 1995; Madigan *et al.*, 1995) similarity between those agents; **iii)** to fuse *Cowdria* with the genus *Ehrlichia* and place the sole species, *Cowdria ruminantium*, with the existing species *Ehrlichia canis*, *Ehrlichia chaffensis*, *Ehrlichia ewingii* and *Ehrlichia muris*; **iv)** to expand the genus *Neorickettsia* to include *Ehrlichia risticii* and *Ehrlichia sennetsu*; **v)** to exclude *Wolbachia persica* and *W. melophagi* from the genus *Wolbachia* and to include the genus *Wolbachia* with its sole member *Wolbachia pipientis*; **vi)** to retain provisional *Aegyptianella* as *Genus incertae sedis* due to the lack of molecular information.

Almost all the proposed reorganizations in family Anaplasmataceae were introduced in the second edition of Bergey's Manual of Systematic Bacteriology (Garrity *et al.*, 2001, 2002a, 2002b,

2003, 2004; Dumler *et al.*, 2005b). The heterogeneity of *W. pipientis* might also justify the revision of species concept with creation of additional *taxa* to include the distinct host-associated clades that have been described (Lo *et al.*, 2002; Fen *et al.*, 2006). Moreover, the *incertae sedis* classification of *Aegyptianella* has been called to question owing to its phenotypic similarities with *Anaplasma* spp., and later reinforced by genetic data (Rikihisa *et al.*, 2003). In future revisions new agents might be included in Anaplasmataceae, such as Candidatus *Neoehrlichia mikurensis* (*Ehrlichia walkerii*), *E. shimanensis*, and *Xenohalitotia californiensis* (Friedman *et al.*, 2000 ;Brouqui *et al.*, 2003; Kawahara *et al.*, 2004, 2006; Rikihisa, 2006a).

FIGURE 2. Current phylogeny and taxonomic classification of genera in the family Anaplasmataceae. The distance bar represents substitutions per 1,000 bp (adapted from Dumler *et al.*, 2005a).



1.1.3. HISTORICAL PERSPECTIVE OF HUMAN INFECTION

Our current knowledge of Anaplasmataceae started at the beginning of the 20th century with the descriptions of Theiler (1910) implicating *Anaplasma marginale* as the etiologic agent of anaplasmosis, a tick-borne disease of ruminants that is still associated to enormous worldwide annual economic losses. In the following years several other agents causing disease in domestic and wild animals were identified, such as *Anaplasma centrale* (Theiler, 1911); *Cowdria* (now

Ehrlichia ruminantium (Cowdry, 1925), *Ehrlichia* (now *Anaplasma*) *ovis* (Lestoquard, 1924), *Ehrlichia phagocytophila* (now *Anaplasma phagocytophilum*) (Gordon *et al.*, 1932; Foggie 1951), *Ehrlichia canis* (Donatien & Lestoquard, 1935), *Ehrlichia* (now *Anaplasma*) *bovis* (Donatien & Lestoquard, 1936), *Neorickettsia helminthoeca* (Philip *et al.*, 1953), *Ehrlichia equi* (now *Anaplasma phagocytophilum*) (Gribble, 1969; Stannard *et al.*, 1969), *Ehrlichia* (now *Anaplasma*) *platys* (Harvey *et al.*, 1978), *Ehrlichia* (now *Neorickettsia*) *risticii* (Holland *et al.*, 1985; Rikihisa & Perry, 1985), *Ehrlichia ewingii* (Ewing *et al.*, 1971; Anderson *et al.*, 1992), *Ehrlichia muris* (Wen *et al.*, 1995) (Table 2).

In spite of abundant reports in the veterinary field, no case of human infection by Anaplasmataceae was described before the 1950s. Sennetsu fever, documented in Japan in 1954 (Misao & Kobayashi, 1955), was formally the first known human disease caused by an Anaplasmataceae member, although it now commands little medical significance. In fact, the mononucleosis-like illness caused by *Neorickettsia* (formerly *Ehrlichia*) *sennetsu* occurs only in limited areas of the Far East, rarely outside Japan and Malaysia and is usually mild, with no deaths having ever been reported. However, in the last decade of the 20th century, the scientific community's view of Anaplasmataceae infections changed dramatically with the description of two new severe to fatal forms of disease in United States (US). In 1986, human monocytic ehrlichiosis (HME) was reported from Central Arkansas (Maeda *et al.*, 1987). This disease was caused by a new species named *Ehrlichia chaffeensis*, closely related to the veterinary pathogens *E. canis* and *E. ewingii* (Anderson *et al.*, 1991; Dawson *et al.*, 1991) and later proven to be also infective for animals, as summarized in Paddock and Childs (2003). In the early 1990's, cases of human granulocytic anaplasmosis (HGA) (formerly human granulocytic ehrlichiosis [HGE]) were reported from Minnesota and Wisconsin (Bakken *et al.*, 1994; Chen *et al.*, 1994). The exact nature of the causative agent, originally named "HGE agent", remained uncertain for several years until its unification with the animal pathogens *E. phagocytophila* and *E. equi* into a single species designation, *Anaplasma phagocytophilum* (Dumler *et al.*, 2001; Garrity *et al.*, 2003). Additionally, two other Anaplasmataceae of well known veterinary importance were also described as a cause of human infection. In 1996, *E. canis* - the etiologic agent of canine monocytic ehrlichiosis was isolated from an apparently healthy man (Perez *et al.*, 1996; Unver *et al.*, 2001b), and later associated with several symptomatic cases (Perez *et al.*, 2006) in Venezuela. More recently in 1999 *E. ewingii*, the etiologic agent of canine granulocytic ehrlichiosis, was also identified as a human disease agent in US, mostly in immunocompromised patients (Buller *et al.*, 1999).

HME and HGA are now considered the most important human diseases caused by Anaplasmataceae members. In the US, 1,223 cases were reported by 30 state health departments from 1986 to 1997, 742 (60.7%) categorized as HME, 449 (36.7%) as HGA and 32 (2.6%) not ascribed to a specific agent (McQuiston *et al.*, 1999; Paddock & Childs, 2003). In 1999, both diseases had become nationally notifiable and official reports show that HGA is more frequently recognized than HME (CDC, 2001, 2002, 2003, 2004, 2005, 2006). As an example, the average reported annual incidences during 2001-2002 were 14 and 6 cases per 10⁵ inhabitants for HGA and HME, respectively (Demma *et al.*, 2005). Moreover, worldwide investigation has revealed increasing evidence of a potential role of *E. chaffeensis* and especially *A. phagocytophilum* in human disease also outside the US. Serological studies have suggested the occurrence of HME in febrile illness patients from Europe (David de Morais *et al.*, 1991; Pierard *et al.*, 1995; Nutti *et al.*, 1998), Africa (Uhaa *et al.*, 1992), and South America (Da Costa *et al.*, 2006), but so far neither *E. chaffeensis* isolation nor DNA detection has been achieved in human cases to reinforce these data. Concerning HGA, the first patient with confirmed disease outside the US was reported from Slovenia in 1997 (Petrovec *et al.*, 1997) and more than fifty cases have been reported in Europe since then. The majority occurred in Northern and Central Europe, especially Slovenia (Lotric-Furlan *et al.*, 2006), but there are also individual case reports from other European countries, later discussed in detail. Polymerase chain reaction (PCR)-based studies of potential tick vectors and reservoir animals have also shown the wide distribution of *A. phagocytophilum* across Europe and in some parts of Middle East and Asia, which will be object of further revision.

It seems that human *A. phagocytophilum*-associated infections rather than *E. chaffeensis* are more commonly recognized over various continents. Thus, HGA possibly represents a widespread and significant public health problem of increasing but undefined magnitude in most countries, and that should be better investigated.

TABLE 2. Biological, ecological and epidemiological features of medically important Anaplasmataceae species.

Genus/Species	Vector/ Transmission	Host	Target Cell	Disease	Geographic Distribution	First Reference
<i>Anaplasma</i>						
<i>A. bovis</i>	Ixodid ticks/ Bite	Ruminants	Monocytes	Bovine "ehrlichiosis"	Africa, Middle East and Asia	Donatien & Lestoquard, 1936
<i>A. caudatum</i>	Ixodid ticks / Bite	Ruminants	Erythrocytes	Anaplasmosis	Worldwide	Ristic & Kreier, 1984
<i>A. centrale</i>	Ixodid ticks / Bite	Ruminants	Erythrocytes	Anaplasmosis	Worldwide	Theiler, 1911
<i>A. marginale</i>	Ixodid ticks / Bite	Ruminants	Erythrocytes	Anaplasmosis	Worldwide	Theiler, 1910
<i>A. ovis</i>	Ixodid ticks / Bite	Ruminants	Monocytes		Asia	Lestoquard, 1924
<i>A. platys</i>	Ixodid ticks / Bite	Canids	Platelets	Infectious cyclic thrombocytopenia	Worldwide	Harvey <i>et al.</i> , 1978
<i>A. phagocytophilum</i>	Ixodid ticks / Bite	Ruminants Equines Humans Canines Felines	Neutrophils	Tick-borne fever Equine granulocytic anaplasmosis Human granulocytic anaplasmosis	Europe America and Europe United States and Europe United States and Europe United States and Europe	Gordon <i>et al.</i> , 1932 Gribble, 1969; Stannard <i>et al.</i> , 1969 Bakken <i>et al.</i> , 1994; Chen <i>et al.</i> , 1994 Madewell & Gribble, 1982 Bjoersdorff <i>et al.</i> , 1999c
<i>Aegyptianella</i>						
<i>A. pullorum</i>	Argasid ticks /Bite	Birds	Erythrocytes		Worldwide	Carpano, 1928
<i>Ehrlichia</i>						
<i>E. canis</i>	Ixodid ticks/Bite	Canines Humans	Monocytes, macrophages	Canine monocytic ehrlichiosis	Worldwide; Venezuela	Donatien & Lestoquard, 1935 Perez <i>et al.</i> , 1996
<i>E. chaffeensis</i>	Ixodid ticks / Bite	Humans Canines	Monocytes, macrophages	Human monocytic ehrlichiosis	United States	Maeda <i>et al.</i> , 1987 Dawson <i>et al.</i> , 1996
<i>E. ewingii</i>	Ixodid ticks / Bite	Canines Humans	Neutrophils	Canine granulocytic ehrlichiosis	United States	Ewing <i>et al.</i> , 1971 Buller <i>et al.</i> , 1999
<i>E. muris</i>	Ixodid ticks / Bite	Rodents	Monocytes, macrophages		Japan	Wen <i>et al.</i> , 1995
<i>E. ruminantium</i>	Ixodid ticks / Bite	Ruminants	Endothelial cells, neutrophils	Heartwater disease	Africa and Caribbean region	Cowdry, 1925
<i>Neorickettsia</i>						
<i>N. helminthoeca</i>	Trematodes/ Ingestion	Canines	Monocytes, macrophages	Salmon poisoning disease	United States	Philip <i>et al.</i> , 1953
<i>N. risticii</i>	Trematodes/ Ingestion	Equines	Monocytes, macrophages	Potomac horse fever	America and Europe	Holland <i>et al.</i> , 1985; Rikihisa & Perry, 1985
<i>N. sennetsu</i>	Trematodes/ Ingestion	Humans	Monocytes, macrophages	Sennetsu fever	Japan and Malaysia	Misao & Kobayashi, 1955

1.2. ANAPLASMA PHAGOCYTOPHILUM

1.2.1. GENERALITIES

A. phagocytophilum is a small coccoid to ellipsoidal, often pleomorphic bacterium with a cell diameter ranging from 0.2 to 2.0 μm . Ultrastructurally, it contains a nucleoid with electron-dense DNA strands and ribosomes surrounded by two limiting membranes, an inner cytoplasmic membrane and a rippled outer cell wall. Like the majority of Anaplasmataceae, this microorganism forms characteristic microcolonies (morulae) in the cytoplasm of infected cells, as the result of the agent's binary fission in a confined area defined by membrane-bounded vacuole (Popov *et al.*, 1998).

The natural history of *A. phagocytophilum* involves both the infection of arthropods, especially *Ixodes* ticks, and several mammalian species, in which man is included as an incidental dead-end host. Depending on the infected host, different cell types are targeted by this agent in a replication cycle that is still not entirely understood. In vertebrates the microorganism has a marked tropism for polymorphonuclear leucocytes, preferentially infecting neutrophils, a characteristic feature often noted with disease. *A. phagocytophilum* causes a pathologic process commonly known as granulocytic anaplasmosis (GA). The designation based on cell tropism may become less useful as additional Anaplasmataceae members are recognized as pathogens and since more than one species may be responsible for the broad category of "granulocytic" disease. However, this nomenclature is firmly established in the literature, and to avoid confusion here it will be used to designate disease caused by *A. phagocytophilum*.

GA affects humans as well as several domestic animals including ruminants, horses, dogs and cats (Gordon *et al.*, 1932; Gribble, 1969; Madewell & Gribble, 1982; Bakken *et al.*, 1994; Chen *et al.*, 1994; Greig *et al.*, 1996; Bjoerdorf *et al.*, 1999c). The disease is generically characterized as a non-specific febrile illness accompanied by hematological abnormalities and hepatic injury. Historically, GA has been recognized by different designations, each of them associated with findings thought to be caused by a distinct etiologic agent. According to the affected host and implicated pathogen, the disease was named ruminant tick-borne fever (or pasture fever), equine granulocytic ehrlichiosis and human granulocytic ehrlichiosis as the result of infections by *E. phagocytophila*, *E. equi* and the HGE agent, respectively. The unification of these agents into a

single species proposed by Dumler and coworkers (2001) expanded the dimensions and broadened the perspective of this tick-borne disease.

Not cultivable in cell-free media or chicken embryos, the *in vitro* manipulation of *A. phagocytophilum* was initially based on direct purification from infected blood or short-term cultures of blood cells collected from infected animals. The development of cell culture systems able to mimic *in vivo* situations made the continuous propagation of the pathogen possible and allowed a more detailed analysis of its biological features. The first *in vitro* isolation of *A. phagocytophilum* was achieved by Goodman and coworkers (1996) after inoculation of a patient's blood in a human promyelocytic leukemia cell line (HL-60, ATCC CCL-240) developed by Gallagher and coworkers (1979). In addition to undifferentiated cell lines, other cells are also currently used for *A. phagocytophilum* cultivation, including HL-60 cells induced to differentiate into functional granulocytes (rHL-60), as well as embryonic *Ixodes scapularis* tick cell lines IDE8 and ISE6 (Goodman *et al.*, 1996; Munderloh *et al.*, 1996, 1999; Heimer *et al.*, 1997). Furthermore, the development of murine models that in part reproduced the infection process has greatly expanded the understanding of *A. phagocytophilum* pathogenesis. The use of inbred and targeted gene-deleted (knockout) mice has allowed insight into precise mechanisms of disease and host cell-pathogen interactions in the context of a whole organism, complemented studies based on *in vitro* tissue culture, *ex vivo* human and ruminant neutrophil cultures and *in vivo* large animal experiments (Borjesson & Barthold, 2002).

The complete genome sequence of *A. phagocytophilum* HZ strain has been recently achieved by Hotopp and coworkers (2006), illustrating the existence of a single circular chromosome of 1,471,282 bp with an average G+C content of 41%. Comparison analysis has shown that most genomic features of *A. phagocytophilum* are typical of other sequenced Anaplasmataceae, but also reveals new species-specific genes indicating particular niche adaptations (Hotopp *et al.*, 2006).

1.2.2. LIFE-CYCLE

The study of naturally- and experimentally-infected neutrophils as well as human and tick-derived cell cultures has allowed a detailed analysis of the intracellular replication cycle of *A. phagocytophilum* (Chen *et al.*, 1994; Goodman *et al.*, 1996; Munderloh *et al.*, 1996, 1999;

Popov *et al.*, 1998; Webster *et al.*, 1998). This bacterium undergoes a simple cycle involving three fundamental steps: invasion of host cells likely through receptor-mediated endocytosis; proliferation by binary fission in a membrane vacuole that does not fuse with lysosomes (parasitophorous vacuoles); exit via rupture of both *A. phagocytophilum*-containing vacuole and the adjacent host cell membrane when the morula is located at the periphery of the infected cell.

In general, morulae tend to be much larger and contain more microorganisms in tick cells than in neutrophils or HL-60 cells. Pathogen morphology is also more variable presenting a higher degree of pleomorphism (Munderloh *et al.*, 1996, 1999). Genome analysis has shown that *A. phagocytophilum* lacks genes for both lipopolysaccharide and peptidoglycan biosynthesis (Lin & Rikihisa, 2003; Hotopp *et al.*, 2006). The peptidoglycan layer is a polymer consisting of sugars and amino acids that form a homogeneous layer between the plasma membrane and the cell-wall of eubacteria, conferring structural strength to bacteria. The lack of this layer justifies the morphologic pleomorphism of *A. phagocytophilum* that should be expected to be higher in environments with less osmotic pressure than those experienced inside the body of invertebrate vector (Rikihisa, 2006b).

In both mammalian and tick cells, *A. phagocytophilum* presents two distinct ultrastructural forms: reticulate cells (RC) characterized by a loosely packed and randomly dispersed nucleoid and dense-cored cells (DC) with a condensed electron-dense protoplast. By temporal examination of *A. phagocytophilum* development in HL-60 cells, Webster and coworkers (1998) concluded that the early forms of the agent have the round reticular appearance while later structures are small and dense. In tick-cells the agent also presented the same temporal pattern; *A. phagocytophilum* colonies comprise appreciable numbers of condensing organisms in older tick-cell cultures (Munderloh *et al.*, 1996, 1999). This data suggests the existence of an intracellular biphasic development that undergoes from RC towards DC cells, similar to that observed for other closely related agents such as *A. marginale* (Blouin & Kocan, 1998) and *E. chaffeensis* (Zhang *et al.*, 2007), in which DC are the infective form and RC the metabolic active form that multiplies by binary fission (Figure 3). However, both the dense core and reticulate forms undergo binary fission *in vitro*, suggesting plasticity to any potential developmental or differentiation cycle (Popov *et al.*, 1998).

Depending on the infected host, *A. phagocytophilum* replication takes place in different cells types. In naturally infected ticks the agent has been detected in midgut cells, hemocytes and salivary gland cells (Magnarelli *et al.*, 1995b; Telford *et al.*, 1996; Alberti *et al.*, 1998; 2000;

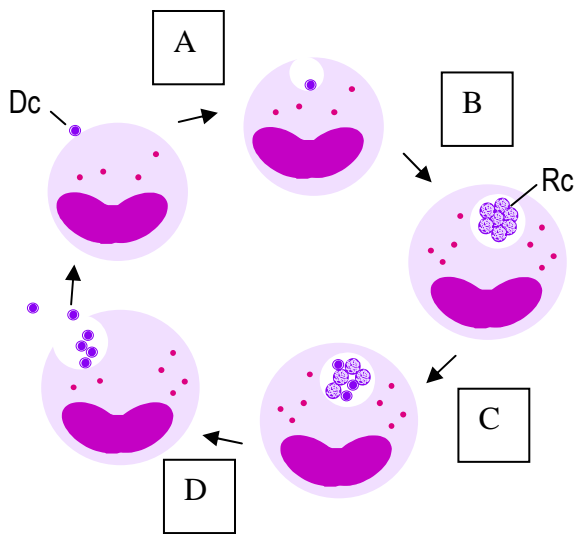


FIGURE 3. Representation of the intracellular cycle proposed for *A. phagocytophilum*.

A- Dense core (Dc) microorganism starts the cycle by attaching and entering into a susceptible host cell; B- Once inside the cell it remains within the vacuole that does not fuse with lysosomes. The microorganism differentiates into a metabolic active reticulated form (Rc) and multiplies by binary fission, forming characteristic dense packed microcolonies known as morulae; C- After multiple rounds of division Rc starts to differentiate into DC forms; D- Finally, by exocytosis or host cell lysis the infectious DC are released to initiate new cycles in new host cells (Blouin & Kocan, 1998; Zhang *et al.*, 2007).

Kim *et al.*, 2003; Ohashi *et al.*, 2005). These different locations are presumed to represent part of a life-cycle similar to that observed for *A. marginale* (Ge *et al.*, 1996; Kocan *et al.*, 2004). It is assumed that following ingestion in the blood meal by feeding ticks, *A. phagocytophilum* primarily infects midgut epithelial cells, passes through this barrier and, via circulating hemocytes, subsequently colonizes salivary gland cells from where it is transmitted to vertebrates via salivary emissions released during the next feeding. The infection of salivary glands seems to be an early event that may take place during or soon after the infective blood meal, since questing ticks already present *A. phagocytophilum* in acinus cells (Telford *et al.*, 1996; Ohashi *et al.*, 2005). Up to now, salivary glands are regarded as the most important organ for the agent's maintenance in vector ticks and subsequent transmission to vertebrate hosts. Other organs might also be infected by *A. phagocytophilum*, which may contribute to the agent's ability to persist in the vector tick, but it does not seem to include ovarian tissue. In fact, infected ticks show persistent bacteremia, with the agent surviving arthropod molts and being maintained in successive life stages (transstadial transmission) but with no, or inefficient offspring infection (transovarial transmission) (Richter *et al.*, 1996; Telford *et al.*, 1996; Des Vignes & Fish 1997; Hodzic *et al.*, 1998; Goethert & Telford, 2003). Of interest, Sukumaran and coworkers (2006) described an *Ixodes* tick salivary gland protein, Salp16, that in part determines successful colonization of salivary glands by *A. phagocytophilum* after acquisition of a blood meal from an infected mammalian host.

Once inside a mammalian host the agent targets cells derived from bone marrow precursors, most often neutrophils and band neutrophils. The infection is not localized, affecting circulating peripheral blood cells, but *A. phagocytophilum* has occasionally been detected in

spleen, lung, liver, bone marrow, lymph node and heart (Madigan *et al.*, 1995; Walker & Dumler, 1997; Bunnell *et al.*, 1999; Lepidi *et al.*, 2000; Martin *et al.*, 2000, 2001; Trofe *et al.*, 2001; Remy *et al.*, 2003; Bayard-Mc Neeley *et al.*, 2004). Both *ex vivo* and *in vitro* data have emphasized that pathogen tropism is especially directed to the mature granulocyte population (Heimer *et al.*, 1997; Klein *et al.*, 1998; Zeman *et al.*, 2002a; Bayard-Mc Neeley *et al.*, 2004) and its detection in several organs seems to reflect vascular perfusion or focal sequestration of infected neutrophils (Lepidi *et al.*, 2000). However, Walker and Dumler (1997) also discussed the possibility that the ligand recognized by *A. phagocytophilum* adhesion is broadly distributed over a wide variety of cells from different lineages, justifying the occasional detection of this agent in endothelial cells, fibroblasts and macrophages. Recent experimental studies have reinforced the hypothesis that other cell types might be involved in *A. phagocytophilum* cycle by the demonstration that the bacterium is capable of infecting endothelial cells and passing from the infected endothelium into neutrophils (Munderloh *et al.*, 2004; Herron *et al.*, 2005). As conjectured in those studies an endothelial reservoir cell may mediate the infection of blood cells and *A. phagocytophilum* spreads from the site of tick feeding, and offers opportunities for ongoing, direct cell-to-cell infection of neutrophils, avoidance of host immune effectors, and completion of the pathogen life-cycle by infection of circulating leukocytes available for transfer to blood-feeding ticks (Munderloh *et al.*, 2004; Herron *et al.*, 2005).

1.2.3. PATHOGENESIS

A. phagocytophilum undergoes substantial selection pressure to be able to survive and replicate in different environments during its life-cycle. In vector ticks, pathogens must survive extreme fluctuations in temperature, pH, osmotic pressure, and other factors related to the physiological status of these arthropods. In vertebrate hosts, they must overcome the highly developed inflammatory and immunologic defences of mammals. Moreover, *A. phagocytophilum* possesses an unusual intracellular lifestyle in that it colonizes neutrophils, the key cells in innate immunity and the first line of defence against invading pathogens. These short-lived, terminally differentiated cells ingest invading microorganisms and destroy them by various means, which include fusing the bacteria-containing phagosome with acidic lysosomes as well as directing toxic oxidative and proteolytic compounds into the phagosomal lumen (Mayer-Scholl *et al.*, 2004). The

specific cell tropism displayed by *A. phagocytophilum* is thus far known to be shared only by *E. ruminantium*, *E. ewingii*, and *Chlamydochila pneumoniae*, among eubacteria, and indicates that these microorganisms have developed strategies to evade and/or subvert neutrophil killing mechanisms in order to promote their survival and perpetuation. Recent investigations have been providing important data regarding *A. phagocytophilum* survival strategies and interactions with their host-cells, allowing a more complete understanding of granulocytic anaplasmosis pathogenesis (Borjesson & Barthold, 2002; Carlyon & Fikrig, 2003, 2006; Dumler, 2005; Dumler *et al.*, 2005a).

Lack of lipopolysaccharide

An adaptation of *A. phagocytophilum* that likely increases its chance of successful colonization of vertebrate neutrophils is the lack of lipid A and peptidoglycan biosynthesis genes (Lin & Rikihisa, 2003). Lipopolysaccharide (LPS) elicits profound innate immune responses via interactions with Toll-like receptor 4 and activating leukocytes and proinflammatory responses. Therefore, it is interesting to that comparative genomics among the Anaplasmataceae reveals cell-wall biosynthetic machinery only in *W. pipientis* and *A. marginale*, neither of which are associated with leukocyte infection (Hotopp *et al.*, 2006). Thus, LPS genes could have either been horizontally acquired in these microorganisms or were lost in the other Anaplasmataceae as an adaptation to successfully infect vertebrate immune cells (Hotopp *et al.*, 2006).

Antigenic variation

A. phagocytophilum has a genome with numerous repeats of functionally important genes, especially those of surface proteins. The whole genome sequence of *A. phagocytophilum* HZ strain demonstrates the existence of three outer membrane protein (*omp*)-1, one major surface protein (*m*sp)-2, two *m*sp2 homologs, one *m*sp4, and one hundred and thirteen 44-kDda surface protein(*p*44) loci belonging to the Omp-1/Msp2/P44 superfamily (Hotopp *et al.*, 2006)². The *p*44s represent the largest expansion of this surface protein superfamily and are annotated as full-length silent/reserve, truncated, and fragments that recombine to generate antigenic variation (Figure 4). The expression of as many as 65 different *p*44 genes (*p*44–1 to *p*44–65) has been reported in infected mammals and ticks (Felek *et al.*, 2004; Lin *et al.*, 2002; Wang *et al.*, 2002;

² Although established in the literature, the Omp-1/Msp2/P44 division is controversial, and some researchers defend that insufficient differences exist in the surface proteins to warrant the division, thus referring to them by the generic designation of Msp2.

Zhi *et al.*, 2002). Additionally, genome sequencing of *A. phagocytophilum* HZ strain has identified 23 novel *p44* genes (p44-66 to p44-88), but they have not yet been experimentally identified as being expressed (Hotopp *et al.*, 2006).

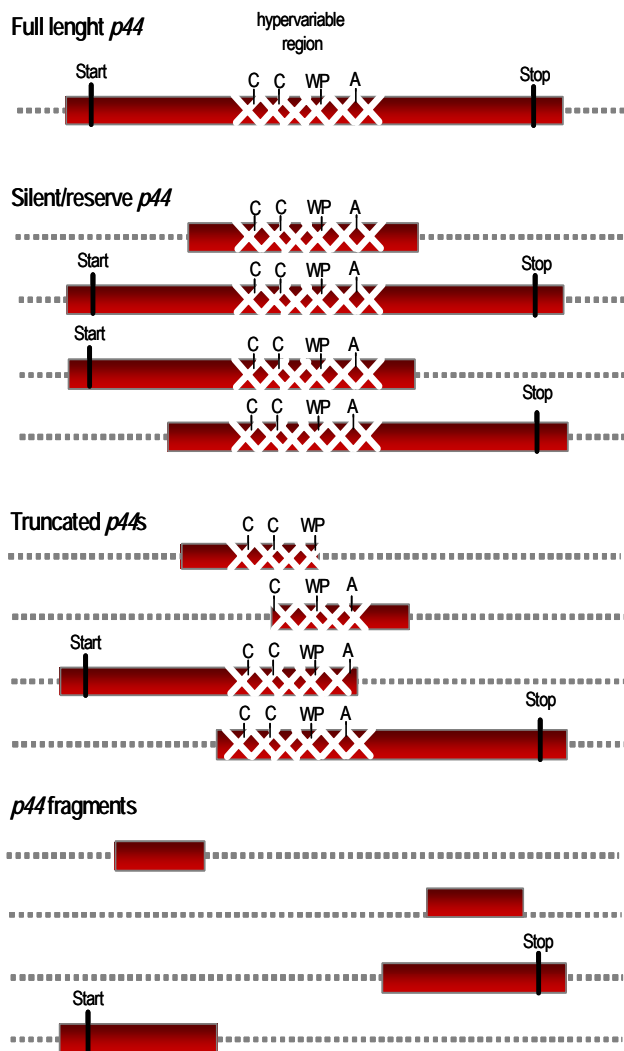


FIGURE 4. Representation of *p44* genes (adapted from Hotopp *et al.*, 2006).

The *p44*s consist of a central hypervariable region of approximately 280 bp containing a signature of four conserved amino acid regions (C, C, WP, A) and conserved flanking sequences longer than 50 bp. In *A. phagocytophilum* HZ strain there are 22 full-length *p44*s identified that have ORFs longer than 1.0 Kb with conserved start and stop codons. These genes recombine into one of three genomic expression loci (p44ES/APH_1221) [(Barbet *et al.*, 2003; Lin *et al.*, 2003) in Hotopp *et al.*, 2006]. Other 64 shorter *p44*s were identified presenting ORFs less than 1.0 Kb and likely serve as reserve/silent *p44*s. They may have either the conserved or alternative start and/or stop codons and are not likely to be expressed at their current genome location, but can recombine into the expression locus (p44ES/APH_1221). In addition 21 5' and 3' fragments and 6 truncations of *p44* genes larger than 60 nucleotides have been identified in the genome. Truncated *p44*s carry the complete hypervariable region, or a portion thereof, but only one of the two conserved regions. Fragments of *p44* have only a conserved region and no hypervariable region. Each annotated *p44* is longer than 60 bp, although smaller fragments can be identified throughout the genome. These, as well as *p44* truncations and fragments, are likely to be non functional remnants of previous recombination events.

Antigenic variation of surface proteins is regarded as a mechanism for promoting the pathogen's evasion of the immune system and persistence in the vertebrate host. This strategy is evident in other arthropod-borne agents such the extracellular *Borrelia hermsii* and *Trypanosoma brucei*, but also in the closely related intracellular *A. marginale* (Barbour & Restrepo, 2000 in Palmer *et al.*, 2006). Like those pathogens, *A. phagocytophilum* cannot be transovarially inherited in its arthropod vector and its persistence in vertebrates may be a mechanism for promoting

pathogen acquisition by ticks and transmission to new hosts. As surface proteins of *A. phagocytophilum* has been demonstrated to be adhesins, antigenic variation may also represent an ecological adaptation to different host environments or varying species host cells independent of immune selection. As showed by Zhi and coworkers (2002), transcription of specific *p44s* is dominantly expressed by *A. phagocytophilum* in mammals at an early stage of infection and in HL-60 cells at 37°C but differ from those associated to ticks that are upregulated in infected HL-60 cell at low temperatures of 24 to 25°C (Zhi *et al.*, 2002). Restricted transcription and expression of *p44* over many passages in cell culture and in tick salivary gland cells suggest selection by fitness for new niche, a finding underscored by the role of surface proteins to act as adhesins (Zhi *et al.*, 2002; Scorpio *et al.*, 2004a; Park *et al.*, 2003a; Dumler *et al.*, 2005a). However, more recent comprehensive studies do not confirm a restricted expression profile *in vitro* or *in vivo*, suggesting the concept that the changing expression of surface proteins does little to promote survival via antigenic variation among animals with a self-limited infection (Choi *et al.*, 2007).

Cell invasion by mediated-endocytosis and isolation of the parasitophorous vacuole

It has been suggested that *A. phagocytophilum* attaches to neutrophils by specific interaction between surface proteins and fucosylated, and possibly sialylated ligands, of surface proteins; platelet selectin glycoprotein ligand-1 (PSGL-1) has been chiefly implicated in this process (Goodman *et al.*, 1999; Herron *et al.*, 2000, Park *et al.*, 2003a). Such a receptor-mediated interaction seems to be determinant in *A. phagocytophilum* tropism for neutrophils and leads to the downstream events resulting in pathogen internalization by endocytosis and successful colonization of host cells (Mott *et al.*, 1999; Carlyon & Fikrig, 2003, 2006).

One of the primary means by which neutrophils destroy phagocytosed pathogens is through the production of toxic oxygen intermediates derived from superoxide anion (O_2^-). The pH change resulting from the O_2^- influx triggers a potassium-dependent release of proteases which along with reactive oxygen species (ROS) kill and degrade ingested microorganisms (Mayer-Scholl *et al.*, 2004). O_2^- is produced by the multi-component enzyme, NADPH oxidase that lies unassembled in resting cells and is activated by several stimuli, such as bacterial uptake (Figure 5). It has been shown that the addition of *A. phagocytophilum* to neutrophils elicits little or no detection of ROS *in vitro* (Mott & Rikihisa, 2000; Carlyon *et al.*, 2004; Ijdo & Mueller, 2004 Borjesson *et al.*, 2005). This likely stems from the fact that the pathogen enters its host-cell via non-opsonin phagocytic receptor-mediated endocytosis (Mott *et al.*, 1999), which presumably

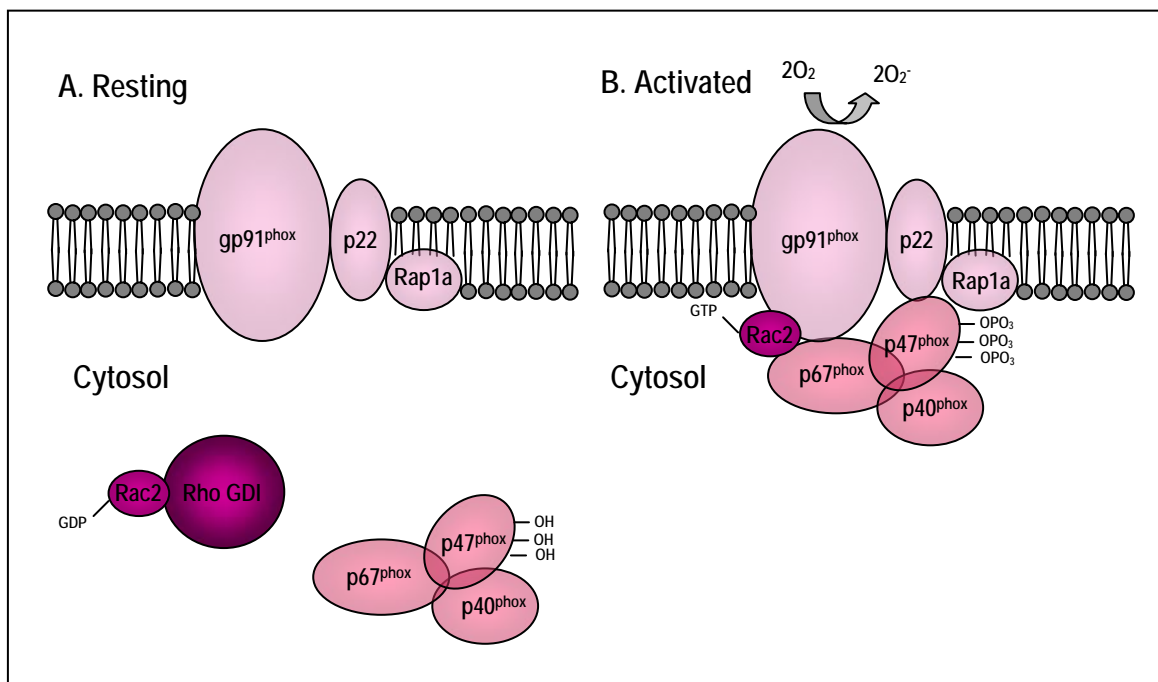


FIGURE 5. Representation of NADPH oxidase (adapted from Carlyon & Fikrig, 2003, 2006).

NADPH oxidase is a multi-component enzyme that lies unassembled in resting neutrophils (A). The cytochrome b_{558} , consisting of gp91^{phox} and p22^{phox}, is integrated into the membrane of secretory vesicles and specific granules. The additional subunits are present in the cytosol, and include p40^{phox}, p47^{phox}, p67^{phox} and Rac2. This latter component functions as the molecular switch for initiating the respiratory burst. Upon activation, either by the binding of opsonized microorganisms or by binding of high concentrations of chemoattractants to their cognate surface receptors, Rac2 dissociates from its inhibitor, RhoGDI, switches from a GDP- to a GTP-bound state and migrates to the site of oxidase assembly. The vesicle/granules fuse with the phagosomal or cell membranes to deliver cytochrome b_{558} to the site of oxidative formation. Concomitantly, p47^{phox} becomes phosphorylated and, along with the other cytosolic components translocate to join cytochrome b_{558} and form the functional enzyme (B). The redox center of assembled oxidase transfer electrons from NADPH to molecular oxygen to generate O₂⁻ outside the cell or within the lumen containing the ingested microorganism.

allows it to bypass the phagocytic route of oxidative stimulation. However, several studies have demonstrated that *A. phagocytophilum*-neutrophils interaction results in a dose-dependent stimulation of NADPH oxidase assembly and degranulation (Choi & Dumler, 2003; Carlyon *et al.*, 2004; Choi *et al.*, 2004). This suggests that the pathogen is able to directly detoxify O₂⁻, providing it with a means of protection from oxidative damage and contributing to the inability to detect ROS *in vitro* (Carlyon *et al.*, 2004; Borjesson *et al.*, 2005). Although the O₂⁻ scavenging mechanism is currently undefined, genomic location and transcriptional expression of a superoxide dismutase homologue (*sodB*) has been reported for *A. phagocytophilum* (Ohashi *et al.*, 2002). Superoxide dismutase is an enzyme that catalyses the rapid dismutation of O₂⁻ to H₂O₂ and O₂. The cotranscription of *sodB* with components of the type IV secretion system may also facilitate the transfer of molecules between the *A. phagocytophilum* and the host (Ohashi *et al.*, 2002;

Hotopp *et al.*, 2006). Moreover, genome sequencing has identified two other ortholog clusters of proteins potentially involved in response to oxidative stress - a putative heme copper oxidase and a putative flavohemoglobin (Hotopp *et al.*, 2006).

After entering the host cell, *A. phagocytophilum* resides in an endosome that ceases to mature and does not fuse with lysosomes. The nature of this parasitophorous vacuole is unique when compared with other vacuoles resulting from either phagocytosis or endocytosis. Several studies have showed that although *A. phagocytophilum* vacuoles are part of the endocytic pathway, they are somehow modified and do not colocalize with markers of either early or late endosomes (Webster *et al.*, 1998; Gokce *et al.*, 1999; Mott *et al.*, 1999). The vacuolar membrane also fails to colocalize with cytochrome b558, demonstrating that *A. phagocytophilum* continues to overcome the oxidative killing capacity by inhibiting the fusion of cytochrome b558-carrying vesicles/granules (Carlyon *et al.*, 2004; Ijdo & Mueller, 2004). It thus seems that *A. phagocytophilum* avoids destruction by isolating itself from host endocytic and exocytic vesicular traffic (Rikihisa, 2003). This phenomenon is restricted to *A. phagocytophilum*-containing vacuoles and is dependent on bacterial protein synthesis, as oxytetracycline treatment results in vacuole maturation into phagolysosomes (Gokce *et al.*, 1999; Ijdo & Mueller, 2004).

Subversion of host cell functions

Besides evading the host cell killing mechanisms as above mentioned, *A. phagocytophilum* subverts several biological functions of its host cell and thereby potentially promotes its intracellular survival and dissemination.

One of the most critical subversions elicited by *A. phagocytophilum* is the inhibition of NADPH oxidase activity in their host cells. Although not yet shown in neutrophils, HL-60 cells with established infections become severely inhibited in their ability to generate reactive oxygen species (ROs) (Banerjee *et al.*, 2000; Wang *et al.*, 2002). This phenomenon is time-dependent and has been linked to the inhibition of transcription of genes encoding two NADPH oxidase components, gp91^{phox} and Rac2 (Banerjee *et al.*, 2000; Carlyon *et al.*, 2002; Choi & Dumler, 2003). The mechanism by which the pathogen downregulates *CYBB* expression (gene encoding gp91^{phox}) has been already identified in HL-60 cells and is related to the inhibition of promoter activity (Thomas *et al.*, 2005). However the pathogen's determinants implicated in the process are currently unknown. An interesting observation regards the localization of *A. phagocytophilum* AnkA, a 153-160 kDa protein with at least 11 tandemly repeated ankyrin motifs with no homology with other proteins

(Caturegli *et al.*, 2000). Park and coworkers (2004) showed that this protein forms a complex with the chromatin of infected HL-60, binding to nuclear proteins and complexes to AT-rich nuclear DNA that lacks specific conserved sequences. As mentioned by Dumler and coworkers (2005b), the mere presence of AnkA in the nucleus of a cell in which gene transcription appears to be altered by infection compels further investigation of a direct pathogenesis role in regulation of eukaryotic gene expression.

Delayed apoptosis is another abnormal function of *A. phagocytophilum* infected neutrophils. Apoptosis is a process that regulates inflammation by programmed cell death of activated neutrophils usually within 24 to 48 hours (Dumler *et al.*, 2005a). *A. phagocytophilum* not only fails to activate the apoptosis program usually triggered by bacterial uptake, but it also delays spontaneous neutrophil programmed cell death by dysregulating and delaying the expression of apoptosis-associated genes (Yoshiie *et al.*, 2000; Scaife *et al.*, 2003; Borjesson *et al.*, 2005; Ge *et al.*, 2005). This phenomenon is not dependent on viable bacteria and is mediated, at least in part, by a heat-resistant surface molecule, as heat-killed *A. phagocytophilum* delays apoptosis as effectively as live bacteria (Borjesson *et al.*, 2005).

Additional dysregulations of neutrophil function by *A. phagocytophilum* includes reduction of adhesion to endothelial cells and inhibition of phagocytosis (Choi *et al.*, 2003, 2004; Garyu *et al.*, 2005). The adhesion defects have been associated with shedding of PSGL-1 and L-selectin as a result of cell degranulation (Choi *et al.*, 2003, 2004). The inhibition of phagocytosis seems to result from alterations of Rac2 expression and loss of important surface receptors (Garyu *et al.*, 2005).

Altogether the activated-deactivated phenotype of the *A. phagocytophilum*-infected neutrophil may benefit the bacterium by increasing concentrations of infected cells in the peripheral blood that are unresponsive to tissue recruitment and may have a prolonged lifespan. However, the cost to the host includes activation of neutrophils to participate in proinflammatory reactions while they are unable to act as microbicidal effectors or regulators of inflammation (Dumler *et al.*, 2005a). It has long been speculated that the antimicrobial capacities of granulocytes infected with *A. phagocytophilum* was altered, in large part this was due to early recognition that the pathogen in sheep and cattle exacerbates other diseases, including louping ill, listeriosis, pasteurellosis, staphylococcal abscesses, and parainfluenza 3 [(Gordon *et al.*, 1932; Foggie, 1951, 1956; Gronstol & Ulvund, 1977; Gilmour *et al.*, 1982; Batungbacal & Scott, 1982) in Borjesson & Barthold, 2002; Stuen *et al.*, 2003b]. Severe opportunistic infections have also been associated to fatal cases of

HGA, including invasive pulmonary aspergillosis, cryptococcal pneumonia, ulcerative *Candida* and herpes simplex esophagitis (Bakken *et al.*, 1994; 1996c; Hardalo *et al.*, 1995; Walker & Dumler, 1997; Jahangir *et al.*, 1998; Lepidi *et al.*, 2000). Although not directly proven, it is likely that loss of one of the primary means of host-mediated microbial killing contributes to the increased susceptibility to other infections (Carlyon & Fikrig, 2003).

Modulation of the inflammatory response

Two independent investigations have shown that neutrophils, bone marrow progenitors or HL-60 cells differentiated into neutrophil-like cells (rHL-60) infected with *A. phagocytophilum* produce striking quantities of CXC and CC chemokines, including monocyte chemotactic protein (MCP)-1, macrophage inflammatory protein (MIF)-1 α , MIF-1 β , regulated on activation normal T-cell expressed and secreted (RANTES) and interleukin (IL)-8, but not the classic pro-inflammatory cytokines IL-1, IL-6 and tumor necrosis factor (TNF)- α (Klein *et al.*, 2000; Akkoyunlu *et al.*, 2001). Chemokine production is induced specifically by a heat-stable *A. phagocytophilum* component independent of classic LPS stimulation (Klein *et al.*, 2000), suggesting a potential role for the pathogen in neutrophil activation. In fact, Akkoyunlu and coworkers (2001) dissected the biological relevance of chemokine production, especially the neutrophil chemoattractant IL-8, during *A. phagocytophilum* infection. They showed that bacterium induces IL-8 secretion from rHL-60 cells in a dose- and time-dependent fashion and the incubation with supernatants from *A. phagocytophilum*-infected, but not uninfected cells, results in chemotaxis of human neutrophils similar to that of recombinant IL-8. Human neutrophils respond to IL-8 through the receptors CXCR1 and CXCR2 (Mahalingam & Karupiah, 1999 *in* Carlyon & Fikrig, 2003). It was also showed that *A. phagocytophilum*-infected rHL-60 cells demonstrate elevated surface expression of CXCR2, and the antibody blockade of this receptor resulted in a decreased bacteremia (Akkoyunlu *et al.*, 2001). Moreover, *in vivo* experiments also showed the importance of neutrophil chemoattraction in *A. phagocytophilum* infection. Blockade of the murine homolog CXCR2 results in considerable decreases in bacterial load compared with control background (Akkoyunlu *et al.*, 2001; Scorpio *et al.*, 2004b). As an obligate intracellular bacterium, the successful maintenance of *A. phagocytophilum* is dependent on its transfer to new host-cells, thus inciting chemokine production could be a mechanism of attracting naïve neutrophils to sites of infection for further bacterial propagation (Carlyon & Filrig, 2003).

The disadvantage of inciting chemokine production to the host is that recruitment of inflammatory cells that are activated and could induce inflammation, leads to damage to tissues (Dumler *et al.*, 2005a). Sera from HGA patients (Dumler *et al.*, 2000) and experimentally inoculated mice (Akkoyunlu & Fikrig, 2000; Martin *et al.*, 2000) demonstrate elevated levels of interferon (IFN)- γ and IL-10, but lack TNF- α , IL-1 β , IL-4 and IL-6, which suggests a role for macrophage activation in recovery and disease (Dumler *et al.*, 2005a). It is well established that IFN- γ protects against infections by obligate intracellular bacteria and against *A. phagocytophilum* (Akkoyunlu & Fikrig, 2000; Martin *et al.*, 2001). However, there is a consequence to such protection as IFN- γ is also damaging against host cells (Fresno *et al.*, 1997 in Carlyon & Fikrig, 2003). Kinetic studies of the distribution of *A. phagocytophilum*-infected neutrophils and inflammatory injury in mouse models suggested a role of IFN- γ in restriction of infection but also in tissue injury (Martin *et al.*, 2000, 2001). As demonstrated by Martin and coworkers (2001) *A. phagocytophilum* IFN- γ knockout mice have a 6- to 7-fold increase in bacteremia compared to wild-type controls but with no histopathologic lesions. In contrast, IL-10 knockout mice, which poorly restrict IFN- γ production, present an identical bacterial load to that of wild-type mice although a substantially greater degree of inflammatory histopathologic injury (Martin *et al.*, 2001). Several other murine models have showed that host innate immune response plays a more important role in histopathologic lesions than does pathogen load. Indeed, the infection of mice in which innate immunity has been genetically altered, such as Toll-like receptor 2 (TLR2)-, Toll-like receptor 4 (TLR4)-, TLR adaptor molecule MyD88, TNF- α and *CYBB* knockout mice does not affect bacterial burden, yet abrogates inflammatory tissue lesions (Von Loewenich *et al.*, 2004; Scorpio *et al.*, 2005). Such findings suggest that disease relates to immune effectors that inadvertently damage tissue. Indeed, in HGA tissue histopathology and clinical illness are greater than predicted by bacterial burden (Walker & Dumler, 1997; Dumler & Bakken, 1998; Lepidi *et al.*, 2000). The disease processes appear to be immune and inflammatory in nature, not directly related to pathogen burden, and the result of triggering of a detrimental and poorly regulated host response (Dumler, 2005).

A. phagocytophilum modulation of host factors in order to promote survival and dissemination might not be limited only to vertebrates. A recent investigation performed by Sukumaran and coworkers (2006) has shown that the pathogen interacts with its vector tick modulating the gene expression of salivary proteins (Salps). In a comprehensive series of experiments, the authors measured the production of 14 Salps and documented a 55-fold

increase in Salp16 expression in salivary gland tissue of *I. scapularis* nymphal ticks infected with *A. phagocytophilum*. Production of ten other salivary proteins was not affected, whereas Salp10, Salp13 and Salp17 were downregulated (Sukumaran *et al.*, 2006). The study also showed that the inhibition of Salp16 affects pathogen survival in midgut and successful colonization of arthropod salivary glands (Sukumaran *et al.*, 2006). However, the mechanism by which *A. phagocytophilum* modulates Salp expression, the direct role of Salp16, or other salivary proteins in pathogen survival, or the consequences for the vector tick is so far unknown. The molecular aspects of arthropod–pathogen interactions are only beginning to be explored.

1.2.4. ECOLOGY

A. phagocytophilum has a circumglobal distribution within the Northern hemisphere, being maintained in enzootic cycles that correlate with the geographic distribution of vector ticks and competent reservoir hosts. Ticks from the *Ixodes persulcatus/ricinus* genospecies complex Oliver & Needham, 1992 (Camicas *et al.*, 1998), are considered the primary vectors for this agent, comprising *I. scapularis* and *I. pacificus*, respectively in Eastern and Western parts of North America, *I. ricinus* in Western, Central and Northern Europe (Macleod & Gordon, 1933; Richter *et al.*, 1996; Telford *et al.*, 1996) and most certainly *I. persulcatus* in Western Europe and Asia (Cao *et al.*, 2000, 2003, 2006; Morozova *et al.*, 2002; Kim *et al.*, 2003, 2006; Wen *et al.*, 2003; Rar *et al.*, 2005) (Figure 6). Other species of the genus *Ixodes* are also involved in perpetuation of *A. phagocytophilum* cycles, such as *I. spinipalpis* in Colorado (Zeidner *et al.*, 2000; Burkot *et al.*, 2001), *I. dentatus* in New England Coast (Goethert & Telford, 2003), and possibly *I. trianguliceps* in United Kingdom (Ogden *et al.*, 1998; Bown *et al.*, 2003). Although the direct role of these latter ticks in human and domestic animal disease is discussed due to their relative host specificity and limited questing potential, when compared with members of *I. persulcatus/ricinus* complex, they are regarded as important bridge-elements, maintaining parallel transmission cycles that would provide support for primary vector infections (Zeidner *et al.*, 2000; Bown *et al.*, 2003; Goethert & Telford, 2003). Additionally, *A. phagocytophilum* has also been detected in the salivary glands of questing *I. ovatus* in Japan, but the vector competence of this species still needs to be proven (Ohashi *et al.*, 2005). The same is true for almost all other non-*Ixodes* ticks and mites that have been sporadically reported with *A. phagocytophilum* DNA, including *Dermacentor variabilis*, *Dermacentor occidentalis*

and *Haemaphysalis leporispalutris* in US (Goethert & Telford, 2003; Holden *et al.*, 2003), *Haemaphysalis longicornis* in Korea (Kim *et al.*, 2003), *Hyalomma detritum* in Tunisia (Sarih *et al.*, 2005), *Dermacentor silvarum* in China (Cao *et al.*, 2006), the Trombiculidae mite *Neotrombicula autumnalis* in Spain (Fernandez-Soto *et al.*, 2001), Symbiophilidae quill mites *Torotroglia merulae* and *Syringophilopsis sturni* in Poland (Skoracki *et al.*, 2006). The majority of these arthropods were collected when feeding in vertebrate hosts. Thus the possible role of host infected blood in *A. phagocytophilum* positive results should not be excluded. Regarding *H. leporispalutris* and *D. variabilis*, experimental studies have already demonstrated that although these ticks are infected by *A. phagocytophilum* they are unable to either maintain the agent transstadially or to successfully transmit it to a susceptible vertebrate host, respectively, and are now considered incompetent vectors (Des Vignes *et al.*, 1999; Goethert & Telford, 2003).

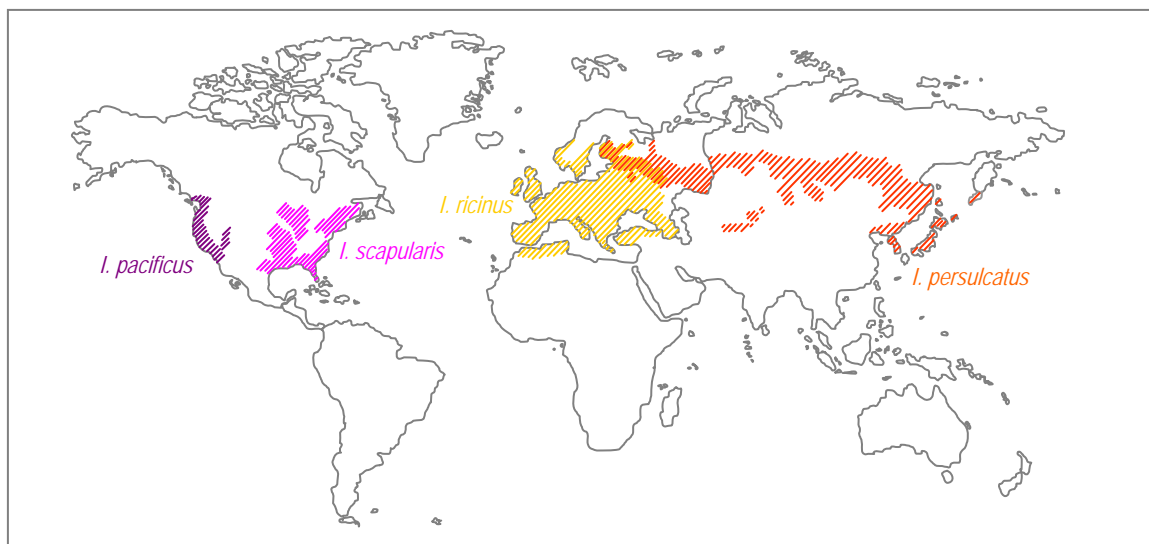


FIGURE 6. Approximate geographic distributions of four medically important *Ixodes persulcatus/ricinus* complex ticks (adapted from Swanson *et al.*, 2006).

Numerous PCR-based studies have assessed the prevalence of *A. phagocytophilum* infection among ticks in several countries. However, they are difficult to compare due to considerable differences in the methods of tick collection, specimen preparation, DNA extraction, selection of nucleic acid probes (primers), and in some cases the lack of further sequencing of positive samples. In general, these studies show pronounced differences according to spatial and temporal distribution, tick species and stage. Table 3 summarizes the prevalences of *A. phagocytophilum* in questing ticks according to different geographic location.

TABLE 3. Prevalence (%) of questing ticks detected with *A. phagocytophilum* infections by PCR-based methods*.

Region/Tick species	Comulative Analysis Mean prev (n ^{**})	Median Analysis	
		Median prev	Minimum-maximum prev
<u>Africa</u>			
<i>Ixodes ricinus</i>	0.5 (418)	0.5	0.0 – 1.0
<u>Asia</u>			
<i>Dermacentor silvarum</i>	0.7 (286)	0.7	
<i>Ixodes ovatus</i>	14.1 (64)	14.1	
<i>Ixodes persulcatus</i>	4.3 (1,876)	4.0	0.8 – 18.6
<u>Europe</u>			
<i>Haemaphysalis cocina</i>	2.1 (47)	1.6	0.0 – 3.1
<i>Ixodes ricinus</i>	4.7 (23,741)	4.3	0.0 – 57.1
<i>Ixodes persulcatus</i>	1.8 (563)	2.4	0.0 – 12.5
<u>North America</u>			
Eastern part <i>Ixodes scapularis</i>	12.5 (5,881)	11.5	0.0 – 50.0
Western part <i>Dermacentor occidentalis</i>	0.6 (651)	1	0.0 – 6.1
<i>Dermacentor variabilis</i>	4.4 (113)	7.6	0.0 – 15.2
<i>Ixodes pacificus</i>	3 (3,934)	5.2	0.0 – 33.3

*All the presented data comes from published reports:

African references - Sarih *et al.*, 2005;

Asian references- Cao *et al.*, 2000, 2003, 2006; Ohashi *et al.*, 2005; European references - Cinco *et al.*, 1997; Guy *et al.*, 1998; Ogden *et al.*, 1998; Fingerle *et al.*, 1999; Leutenegger *et al.*, 1999; Petrovec *et al.*, 1999; Pusterla *et al.*, 1999a; Alekseev *et al.*, 2001b; Christova *et al.*, 2001; Jenkins *et al.*, 2001; Liz *et al.*, 2001; Oteo *et al.*, 2001; Grzeszczuk *et al.*, 2002, 2004b; Oehme *et al.*, 2002; Morozova *et al.*, 2002; Santino *et al.*, 2002; Spitalska *et al.*, 2002; Derdakova *et al.*, 2003; Hildebrandt *et al.*, 2003; Makinen *et al.*, 2003; Sixl *et al.*, 2003; Skotarczak *et al.*, 2003; Hartelt *et al.*, 2004; Polin *et al.*, 2004; Stanczak *et al.*, 2004; Tomasiewicz *et al.*, 2004; Cisak *et al.*, 2005; De la Fuente *et al.*, 2005a; Rar *et al.*, 2005; Ferquel *et al.*, 2006; Grzeszczuk & Stanczak, 2006; Halos *et al.*, 2006; Mantelli *et al.*, 2006; Piccolin *et al.*, 2006; Shpynov *et al.*, 2006;

North American references - Magnarelli *et al.*, 1995b; Pancholi *et al.*, 1995; Barlough *et al.*, 1997a; Chang *et al.*, 1998; Daniels *et al.*, 1998; Varde *et al.*, 1998; Kramer *et al.*, 1999; Lane *et al.*, 2001, 2004; Fang *et al.*, 2002; Massung *et al.*, 2002, 2003a; Courtney *et al.*, 2003; Holden *et al.*, 2003; Adelson *et al.*, 2004; Dolan *et al.*, 2004; Caporale *et al.*, 2005; Fritz *et al.*, 2005; Schulze *et al.*, 2005;

**Total number of tested ticks.

The patchy distribution of *A. phagocytophilum* in nature is multifactorial and may depend on the existence of both competent vector ticks and reservoir hosts. In many regions *Ixodes* ticks are found beyond the areas of pathogen endemicity. The discrepancies between vector ticks and pathogen distribution are not well understood but might be related to feeding behaviour and reservoir-host dynamics (Swanson *et al.*, 2006). In fact, the apparent lack of *A. phagocytophilum* transovarial transmission in ticks directs attention to competent vertebrates, especially those which represent a feeding support for larvae and nymphs, as playing a critical role in the maintenance of agent's active cycles in nature.

Members of *I. persulcatus/ricinus* complex are usually characterized by a permissive feeding behaviour with a broad range of potential vertebrate hosts, including avian, reptilian, and numerous mammalian species (Sonenshine, 1991). Immature stages often parasitize rodents and other small animals, contrasting with adult ticks that quest medium to large-size mammals. The role of reptiles in *A. phagocytophilum* cycle is largely unknown. Several researchers support the idea that although birds seem to lack systemic infections, they promote agent exchange between cofeeding ticks and contribute to the dispersion of infecting ticks (Alekseev *et al.*, 2001a; Bjoersdorff *et al.*, 2001; Daniels *et al.*, 2002). However, a recent study has detected *A. phagocytophilum* in several bird blood specimens in Spain (De la Fuente *et al.*, 2005a). But the most relevant role is most certainly played by mammals, especially rodents and other small mammals that are often parasitized by immature stages of ticks. Several species of rodents have been already implicated in *A. phagocytophilum* cycle as primary reservoirs, especially *Peromyscus leucopus* in the Northeastern and North Central US (Telford *et al.*, 1996; Levin *et al.*, 2002), *Neotoma mexicana*, *N. fuscipes*, and *Peromyscus maniculatus* in Western US (Zeidner *et al.*, 2000; Burkot *et al.*, 2001; Foley *et al.*, 2002), *Myodes* (formerly *Clethrionomys*) *glareolus*, *Apodemus flavicollis* and *A. sylvaticus* in Europe (Odgen *et al.*, 1998; Liz *et al.*, 2000; Bown *et al.*, 2003), and *A. agrarius* in Asia (Chae *et al.*, 2003). Natural infections have also been reported from a wide range of other mammalians that may as well integrate the primary transmission cycle of *A. phagocytophilum* or even settle parallel cycles that would help to perpetuate the agent in nature (Table 4 and Figure 7). Examples of parallel transmission cycles have been observed between lagomorphs and rodents and their host-specific ticks, such as *Sylvilagus floridanus* and *I. dentatus* in Nantucket Island, Massachusetts (Goethert & Telford, 2003), *Neotoma sp.* and *I. spinipalpis* in Colorado (Zeidner *et al.*, 2000; Burkot *et al.*, 2001) and *Myodes glareolus*, *Microtus agrestis* and *I. trianguliceps* in United Kingdom (Bown *et al.*, 2003, 2006).

1.2.5. OTHER *IXODES*-BORNE AGENTS

A. phagocytophilum geographic distribution may overlap those of other pathogenic agents either because they share the same reservoir hosts and/or the vectors ticks. This latter aspect is of particular interest regarding the epidemiology of concurrent tick-borne diseases. Besides *A. phagocytophilum* transmission, members of *I. persulcatus/ricinus* complex are also potential or

confirmed vectors of several other agents with Public Health relevance, including *Anaplasma* spp., *Babesia* spp., *Bartonella* spp., *B. burgdorferi* s.l., *Coxiella burnetii*, *Francisella tularensis*, *Rickettsia helvetica*, *Toxoplasma gondii* and some tick-borne viruses (Table 5) (Rehacek *et al.*, 1994; Estrada-Pena & Jongejan *et al.*, 1999; Parola & Raoult, 2001b; Gray *et al.*, 2002; Sonogo *et al.*, 2003; Sroka *et al.*, 2003; Holden *et al.*, 2006). Moreover, newly described agents with unknown pathogenicity have also been associated to these tick species, such as candidate *Neoehrlichia mikurensis* (“*Ehrlichia walkerii*”), *Rickettsia monacensis* and IRS3 (Márquez *et al.*, 1998; Sekeyova *et al.*, 2000; Simser *et al.*, 2002; Brouqui *et al.*, 2003; Kawahara *et al.*, 2004).

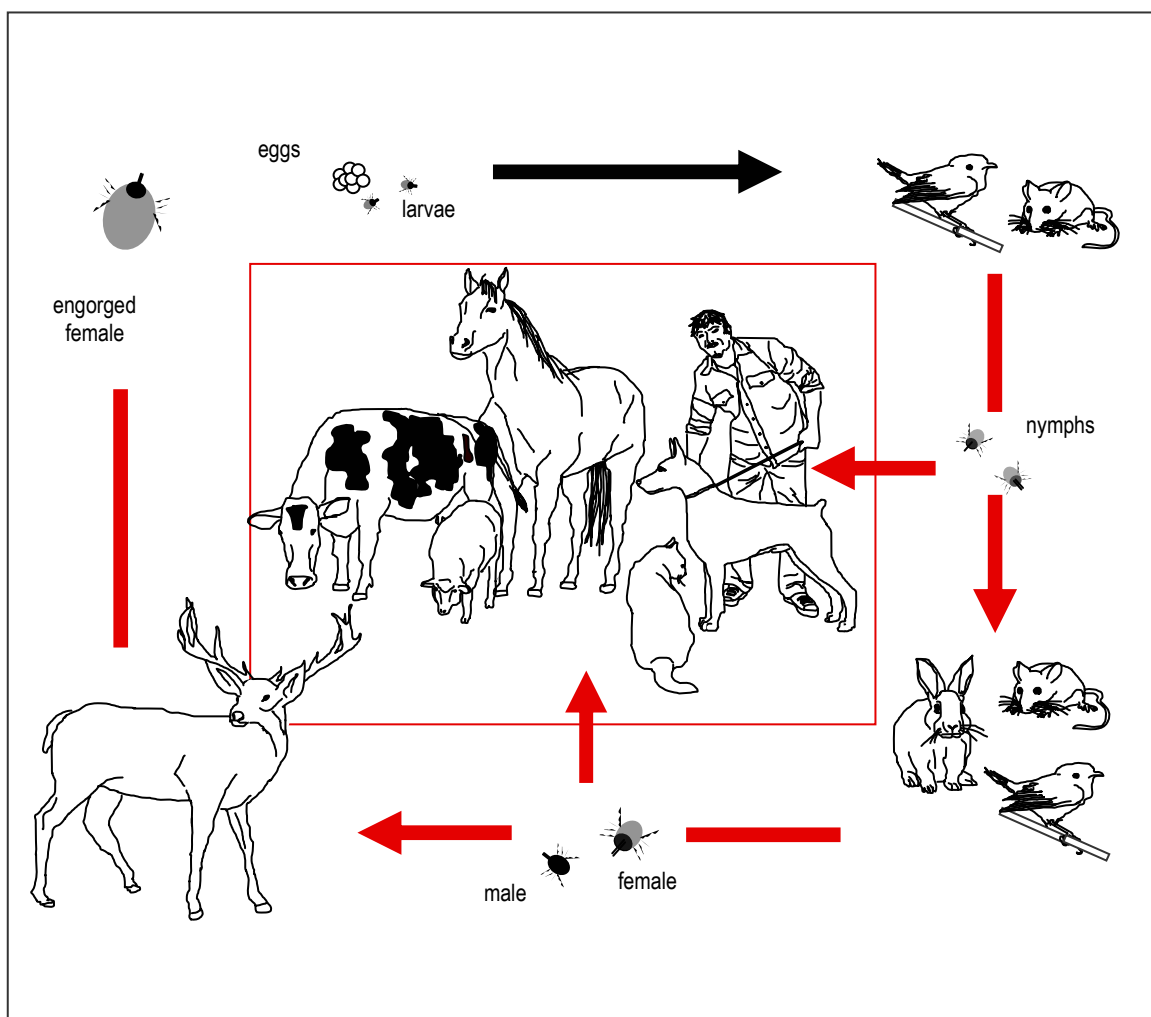


FIGURE 7. Schematic representation of *A. phagocytophilum* transmission cycle.

— potentially infected ticks; → potentially infective bite; — non-infected ticks; → non-infective bite.

TABLE 4. *A. phagocytophilum* infection in wild mammals detected by PCR-based studies.

Region/Order	Vertebrate species (common name)	References
Asia		
Artiodactyla	<i>Cervus nippon nippon</i> (wild sika deer) <i>C. nippon yesoensis</i> (wild sika deer)	Kawahara <i>et al.</i> , 2006
Rodentia	<i>Apodemus agrarius</i> (black-striped field mouse) <i>A. peninsulae</i> (korean field mouse) <i>Tamias sibiricus</i> (siberian chipmunk)	Chae <i>et al.</i> , 2003; Cao <i>et al.</i> , 2006; Kim <i>et al.</i> , 2006
Soricomorpha	<i>Crocidura lasiura</i> (ussuri white-toothed shrew)	Kim <i>et al.</i> , 2006
Europa		
Artiodactyla	<i>Capreolus capreolus</i> (roe deer) <i>Cervus elaphus</i> (red elk) <i>Rupicapra rupicapra</i> (chamois) <i>Sus scrofa</i> (wild boar)	Alberti <i>et al.</i> , 2000; Stuen <i>et al.</i> , 2001; Liz <i>et al.</i> , 2002; Petrovec <i>et al.</i> , 2002, 2003; Oporto <i>et al.</i> , 2003; Polin <i>et al.</i> , 2004; Skarphedinsson <i>et al.</i> , 2005
Rodentia	<i>Apodemus agrarius</i> (black-striped field mouse) <i>A. flavicollis</i> (yellow-necked mouse) <i>A. sylvaticus</i> (long-tailed field mouse) <i>Microtus agrestis</i> (field vole) <i>M. oeconomus</i> (tundra vole) <i>Myodes glareolus</i> * (bank vole) <i>Rattus rattus</i> (black rat)	Ogden <i>et al.</i> , 1998; Liz <i>et al.</i> , 2000; Bown <i>et al.</i> , 2003, 2006; Christova & Gladnishka, 2005; Grzeszczuk <i>et al.</i> , 2006a
Soricomorpha	<i>Sorex araneus</i> (eurasian shrew)	Liz <i>et al.</i> , 2000
North America		
Artiodactyla	<i>Cervus elaphus nannodes</i> (tule elk) <i>Odocoileus hemionus columbianus</i> (black-tailed deer) <i>O. hemionus hemionus</i> (mule deer) <i>O. virginianus</i> (white-tailed deer)	Belongia <i>et al.</i> , 1997; Foley <i>et al.</i> , 1998; Massung <i>et al.</i> , 2005a; Michalski <i>et al.</i> , 2006
Carnivora	<i>Canis latrans</i> (coyote) <i>Procyon lotor</i> (Raccoon) <i>Puma concolor</i> (mountain lion) <i>Ursus americanus</i> (american black bear)	Foley <i>et al.</i> , 1999b; Drazenovich <i>et al.</i> , 2006; Pusterla <i>et al.</i> , 2000; Levin <i>et al.</i> , 2002
Lagomorpha	<i>Lepus californicus</i> (black-tailed jackrabbit) <i>Sylvilagus audubonii</i> (desert cottontails rabbit) <i>S. floridanus</i> (eastern cottontails rabbit)	Goethert & Telford, 2003; Yabsley <i>et al.</i> , 2006
Rodentia	<i>Microtus ochrogaster</i> (prairie vole) <i>Myodes gapperi</i> ** (southern red-backed vole) <i>Neotoma fucipes</i> (dusky-footed wood rat) <i>N. mexicana</i> (mexican wood rat) <i>Peromyscus leucopus</i> (white-footed mouse) <i>P. maniculatus</i> (deer mouse) <i>P. truei</i> (pinyon mouse) <i>Reithrodontomys megalotis</i> (western harvest mouse) <i>Sciurus griseus</i> (western grey squirrel) <i>Spermophilus lateralis</i> (golden-mantled ground squirrel) <i>Tamias minimus</i> (least chipmunk) <i>T. striatus</i> (eastern chipmunk)	Walls <i>et al.</i> , 1997; Yeh <i>et al.</i> , 1997; Foley <i>et al.</i> , 1999b; Nicholson <i>et al.</i> , 1999; Stafford <i>et al.</i> , 1999; Zeidner <i>et al.</i> , 2000; Burkot <i>et al.</i> , 2001; Castro <i>et al.</i> , 2001; DeNatale <i>et al.</i> , 2002; Levin <i>et al.</i> , 2002; Massung <i>et al.</i> , 2002; Lane <i>et al.</i> , 2005; Drazenovich <i>et al.</i> , 2006; Nieto <i>et al.</i> , 2007

*Formerly *Clethrionomys glareolus*; **formerly *Clethrionomys gapperi*.

TABLE 5. Members of *Ixodes persulcatus/ricinus* complex as potential (*) and confirmed vectors for other tick-borne agents.

Pathogen	Disease	Affected hosts	Vectors
<u>Virus</u>			
CCHF virus	Crimean–Congo hemorrhagic fever (CCHF)	Humans	* <i>I. ricinus</i>
Looping ill virus	Looping ill	Sheep	<i>I. ricinus</i>
TBE virus	Tick-borne encephalitis (TBE)	Humans	<i>I. ricinus</i> , <i>I. persulcatus</i>
<u>Bacteria</u>			
<i>Anaplasma bovis</i>	Anaplasmosis	Bovines	* <i>I. ricinus</i>
<i>A. marginale</i>	Anaplasmosis	Bovines	* <i>I. ricinus</i>
<i>Bartonella henselae</i>	Bartonellosis	Humans/ animals	* <i>I. ricinus</i> , * <i>I. pacificus</i> , * <i>I. scapularis</i>
<i>Borrelia burgdorferi s.l.</i>	Lyme borreliosis (LB)	Humans/ animals	
<i>Borrelia afzelii</i>			<i>I. ricinus</i> , <i>I. persulcatus</i>
<i>B. burgdorferi s.s.</i>			All four species
<i>B. garinii</i>			<i>I. ricinus</i> , <i>I. persulcatus</i>
<i>B. lusitaniae</i>			<i>I. ricinus</i>
<i>B. valaisiana</i>			<i>I. ricinus</i>
<i>Coxiella burnetii</i>	Q fever	Humans/ animals	* <i>I. ricinus</i>
<i>Ehrlichia walkerii</i>	Unknown	Unknown	<i>I. ricinus</i>
<i>Francisella tularensis</i>	Tularemia	Humans/ animals	* <i>I. ricinus</i>
<i>Rickettsia helvetica</i>	Febrile illness	Humans	<i>I. ricinus</i>
<i>R. monacensis/ IRS3</i>	Unknown	Unknown	* <i>I. ricinus</i>
<u>Protozoa</u>			
<i>Babesia divergens</i>	Babesiosis	Humans/ bovines	<i>I. ricinus</i>
<i>B. microti</i>	Babesiosis	Humans	<i>I. scapularis</i>
<i>B. odocoilei</i>	Babesiosis	Wild ruminants	* <i>I. ricinus</i> , <i>I. scapularis</i>
<i>Toxoplasma gondii</i>	Toxoplasmosis	Humans/ animals	* <i>I. ricinus</i>

Several studies have attempted to identify simultaneous infection in *I. persulcatus/ricinus* complex but available data are essentially the result of focused detection of *B. burgdorferi s.l.* and *Babesia* spp. and/or *A. phagocytophilum* (www.pubmed.gov). Thus, the true prevalence of other coinfecting pathogens among *Ixodes* ticks remains largely unknown in the majority of geographic locations. These molecular studies have evidenced that although single infections are substantially more common, the possibility for coinfections exists. In a recent revision of published articles about this subject, Swanson and coworkers (2006) have shown that dual infection with any combination of *B. burgdorferi s.l.*, *B. microti*, and *A. phagocytophilum* occurs in 1% to 28% of *Ixodes* ticks from regions of LB endemicity in the US and in <1% to 13% of sampled European *Ixodes* ticks. Triple infection is rarely detected in geographic regions where all these tick-borne diseases are endemic and likely represents an incident occurrence of <1%. Moreover, *A. phagocytophilum* coinfection

with *Babesia odocoilei*, *Bartonella henselae*, *Bartonella* spp., and spotted fever rickettsiae have also been sporadically reported in ticks (Spitalska *et al.*, 2002; Holden *et al.*, 2003, 2006; Adelson *et al.*, 2004; Hartelt *et al.*, 2004; Halos *et al.*, 2006; Steiner *et al.*, 2006). Table 6 summarizes the prevalences of *A. phagocytophilum* coinfections detected in ticks.

1.2.6. VARIANT STRAINS AND DISEASE

A. phagocytophilum presents a minor degree of variation in the nucleotide sequences of conserved genes, such as *rrs*, *groESL*, and *ankA*² which has strengthened its unification into a single species (Sumner *et al.*, 1997; Caturegli *et al.*, 2000; Massung *et al.*, 2000; Dumler *et al.*, 2001; Yu *et al.*, 2001). Nevertheless, the existence of sequence polymorphisms has been a matter of interest in the scientific community suggesting the occurrence of variant strains with distinct geographic origin, reservoir hosts and pathogenicity (Shukla *et al.*, 2007).

Phylogenetic analysis of the *ankA* gene sequences has separated *A. phagocytophilum* into three distinct clades, representing the US Northeastern and Upper Midwestern strains, and European strains (Massung *et al.*, 2000). But more genetic heterogeneity may exist, as demonstrated by Von Loewenich and coworkers (2003a) with the description of unexpected *ankA* diversity in infected German ticks. The analysis of *groESL* has reinforced the association of variability with geographic origin but it also suggested the existence of distinct *A. phagocytophilum* lineages related with specific reservoir hosts, possibly the result of coevolution (Sumner *et al.*, 1997; Petrovec *et al.*, 1999; Chae *et al.*, 2000; Bjoersdorff *et al.*, 2002a; Petrovec *et al.*, 2002; Von Loewenich *et al.*, 2003a; Polin *et al.*, 2004). Moreover the analysis of the most conservative *rrs*, has shown that only two genotypes of *A. phagocytophilum* have thus far been associated with human disease: the prototype described by Chen and coworkers (1994), that occur in both Europe and North America (Northeast and Upper Midwest), and the strain described by Foley and coworkers (1999a) in California. These strains, referred to as Ap-ha (GenBank accession nos U02521; AF093788/ AF093789), are also pathogenic for horses, dogs and possible for cats, but less commonly associated with ruminants. The dominant genotype responsible for ruminant disease is referred to as Ap-variant 1 (GenBank accession no M73220) (Bjoersdorff *et al.*, 2002a;

² Gene encoding Anka, the 153-160 kDa protein with several tandemly repeated ankyrin motifs, as previously mentioned.

TABLE 6. Prevalence of *A. phagocytophilum* coinfections in questing *Ixodes* ticks detected by PCR-based methods.

Region	Reference	<i>Ixodes</i> species	No ticks sampled	Coinfecting agents*	Prevalence (%) of infection	Prevalence (%) of coinfection**
Asia						
China	Cao <i>et al.</i> , 2003	<i>I. persulcatus</i>	1,345	Ap/Bb	Ap 4.6; Bb 33.8	Ap/Bb 0.5
Europe						
Bulgaria	Christova <i>et al.</i> , 2001	<i>I. ricinus</i>	112	Ap/Bb	Ap 33.9; Bb 32.1	Ap/Bb 13.4
Germany	Fingerle <i>et al.</i> , 1999	<i>I. ricinus</i>	492	Ap/Bb	Ap 1.6; Bb 36.2	Ap/Bb 0.8
	Oehme <i>et al.</i> , 2002	<i>I. ricinus</i>	898	Ap/Bb	Ap 2.9; Bb 20.4	Ap/Bb 0.8
	Hildebrandt <i>et al.</i> , 2003	<i>I. ricinus</i>	305	Ap/Bb	Ap 2.3; Bb 11.1	Ap/Bb 0.7
Italy	Cinco <i>et al.</i> , 1997	<i>I. ricinus</i>	86	Ap/Bb	Ap 24.4; Bb 19.8	Ap/Bb 8.14
Poland	Skotarczak <i>et al.</i> , 2003	<i>I. ricinus</i>	514	Ap/Bb; Ap/Bm; Ap/Bb/Bm	Ap 4.7; Bb 15.8; Bm 13.0	Ap/Bb 1.4; Ap/Bm 0.8; Ap/Bb/Bm 0.6
	Stanczak <i>et al.</i> , 2004	<i>I. ricinus</i>	303	Ap/Bb; Ap/Bm	Ap 19.5; Bb 29.7; Bm 3.6	Ap/Bb 8.3; Ap/Bm 2.0
	Stanczak <i>et al.</i> , 2002	<i>I. ricinus</i>	424	Ap/Bb	Ap 19.2; Bb 11.6	Ap/Bb 5.0
Russia	Morozova <i>et al.</i> , 2002	<i>I. persulcatus</i>	150	Ap/Bb	Ap 8.0; Bb 38.0	Ap/Bb 6.0
Slovakia	Spitalska <i>et al.</i> , 2002	<i>I. ricinus</i>	137	Ap/RSFG	Ap 4.4; SFGR 10.9	Ap/SFGR 0.7
	Derdakova <i>et al.</i> , 2003	<i>I. ricinus</i>	60	Ap/Bb	Ap 8.3; Bb 38.3	Ap/Bb 5.0
Switzerland	Leutenegger <i>et al.</i> , 1999	<i>I. ricinus</i>	100	Ap/Bb	Ap 2.0; Bb 49.0	Ap/Bb 2.0
United Kingdom	Guy <i>et al.</i> , 1998	<i>I. ricinus</i>	60	Ap/Bb	Ap 7.0; Bb 37.0	Ap/Bb 1.7
North America						
California	Holden <i>et al.</i> , 2003	<i>I. pacificus</i>	776	Ap/Bb	Ap 6.2; Bb 5.7	Ap/Bb 1.0
	Lane <i>et al.</i> , 2004	<i>I. pacificus</i>	158	Ap/Bb	Ap 3.2; Bb 3.8	Ap/Bb 1.3
	Holden <i>et al.</i> , 2006	<i>I. pacificus</i>	168	Ap/Bh-like	Ap 28.6; Bh-like 6.5	Ap/Bh-like 3.0
New Jersey	Varde <i>et al.</i> , 1998	<i>I. scapularis</i>	100	Ap/Bb; Ap/Bm	Ap 17.0; Bb 43.0; Bm 5.0	Ap/Bb 6.0; Ap/Bm 2.0
	Adelson <i>et al.</i> , 2004	<i>I. scapularis</i>	107	Ap/Ba spp; Ap/Bb/Ba; Ap/Bm/Ba;	Ap 1.9; Bb 33.6; Ba 34.5; Bm 8.4	Ap/Ba 0.9; Ap/Bb/Ba 0.9; Ap/Bm/Ba 0.9
New York	Schulze <i>et al.</i> , 2005	<i>I. scapularis</i>	147	Ap/Bb	Ap 6.1; Bb 50.3	Ap/Bb 2.7
	Chang <i>et al.</i> , 1998	<i>I. scapularis</i>	229	Ap/Bb	Ap 9.0; Bb 54.0	Ap/Bb 4.0
	Daniels <i>et al.</i> , 1998	<i>I. scapularis</i>	1,268	Ap/Bb	Ap 13.5; Bb 15.1	Ap/Bb 2.2
	Schauber <i>et al.</i> , 1998	<i>I. scapularis</i>	188	Ap/Bb	Ap 42.6; Bb 66.0	Ap/Bb 28.2
Pennsylvania	Courtney <i>et al.</i> , 2003	<i>I. scapularis</i>	454	Ap/Bb	Ap 17.8; Bb 41.2	Ap/Bb 3.5
Wisconsin	Pancholi <i>et al.</i> , 1995	<i>I. scapularis</i>	89	Ap/Bb	Ap 7.9; Bb 11.2	Ap/Bb 2.2

* Ap *Anaplasma phagocytophilum*; Ba *Bartonella* spp.; Bb *Borrelia burgdorferi* s.l.; Bm *Babesia microti*; Bh-like *Bartonella henselae*-like; SFGR spotted fever group *Rickettsia* spp.;

** Coinfection data overlaps with the single-pathogen prevalence percentages.

Stuen *et al.*, 2002b, 2003a, 2003b, 2005; Von Loewenich *et al.*, 2003b; Poitout *et al.*, 2005; Massung *et al.*, 2006). Both Ap-ha and Ap-variant 1 have been detected in vector ticks and hosts but the existence of distinct enzootic cycles is suggested by the association of Ap-ha to small mammals and Ap-variant 1 to wild ruminants (Belongia *et al.*, 1997; Massung *et al.*, 1998, 2002, 2003a, 2003b, 2005a, 2006; Leutenegger *et al.*, 1999; Zeidner *et al.*, 2000; Petrovec *et al.*, 2002; Cao *et al.*, 2003; Courtney *et al.*, 2003; Sreter *et al.*, 2004; Tate *et al.*, 2005; Michalski *et al.*, 2006). However, the detection of coinfection in questing ticks indicates that those cycles are linked to some extent and both strains are capable of coexisting in the same tick vector (Massung *et al.*, 2002). Several other genetic variants of *A. phagocytophilum* have been described, some of those with unknown pathogenic potential (Walls *et al.*, 1997; Baumgarten *et al.*, 1999; Schouls *et al.*, 1999; Cao *et al.*, 2000, 2003; Massung *et al.*, 2002; Michalski *et al.*, 2006).

The distinction between ruminant and non-ruminant lineages of *A. phagocytophilum* was initially suggested by experimental cross-infections [(Barlough *et al.*, 1995; Madigan *et al.*, 1995; Stuen *et al.*, 1998 in Stuen *et al.*, 2002b); Pusterla *et al.*, 1999b, 2001]. A thorough understanding of the significance of *A. phagocytophilum* genetic variants is still far from complete, but their impact on both human and animal disease is already a matter of debate. Based on a 4-year field work study Massung and coworkers (2002) have hypothesized that variants strains of *A. phagocytophilum* may interfere with the maintenance and transmission of those causing human disease, resulting in a lower incidence of HGA in regions where different variants are common. Moreover, Stuen and coworkers (2005) have recently shown direct interference of *A. phagocytophilum* strains by the dominance of the genotype Ap-variant 1 over Ap-variant 2 in experimentally infected sheep. As discussed by those researchers, the reason for this dominance is unknown, but factors such as growth rate, immunogenicity, receptor competition, and antigenic variation may be involved in the infectivity and interaction of *A. phagocytophilum* variants. Further research is needed to investigate the role of competitive interactions between genetic variants of *A. phagocytophilum* that may modulate human and animal disease in each geographic area.

1.2.6.1. TICK-BORNE FEVER

(*A. phagocytophilum* synonyms: *Rickettsia phagocytophila*, *Cytoecetes phagocytophila*, *Ehrlichia phagocytophila*, *Anaplasma phagocytophila*)

Tick-borne fever (TBF) or pasture fever was first recognized in 1932 as a disease of sheep grazed on tick-infested pastures in Great Britain (Gordon *et al.*, 1932 in Dumler *et al.*, 2001). In the preceding years considerable information was acquired concerning the host range, pathogenicity and vector relationships. TBF affects domestic ruminants, chiefly sheep and cattle, in several European countries but is rarely reported in North America. Only a sporadic case of the disease was described in a llama (Barlough *et al.*, 1997b) which suggests that the North American Ap-Variant 1 or other ruminant strain have evolved into a less pathogenic form than the European counterparts. TBF is characterized by fever, apathy, anorexia, tachypnea, cough, nasal discharge, and reluctance to move [(Gordon *et al.*, 1932; Hudson, 1950; Foggie, 1951) in Dumler *et al.*, 2001]. Additionally, abortion commonly occurs if naïve pregnant sheep are introduced into pastures infested with vector ticks (Jones & Davis, 1995 in Borjesson & Barthold, 2002; Garcia-Perez *et al.*, 2003). Indirect losses are also associated with a decrease in milk production and reduced growth rate in both calves and lambs [(Gordon *et al.*, 1932; Hudson, 1950; Foggie, 1951) in Dumler *et al.*, 2001; Stuen *et al.*, 2002a]. The disease is usually moderate, but serious complications that may lead to death have also been observed. The most serious problem associated with TBF, especially in sheep, is the increase in severity of concurrent louping ill and the predisposition to secondary infections, such as staphylococcal abscesses, septicemia, and pasteurellosis, among others [(Gordon *et al.*, 1932; Foggie, 1951, 1956; Gronstol & Ulvund, 1977; Gilmour *et al.*, 1982; Batungbacal & Scott, 1982) in Borjesson & Barthold, 2002; Stuen *et al.*, 2003b].

1.2.6.2. EQUINE GRANULOCYTIC ANAPLASMOSIS

(*A. phagocytophilum* synonym: *Ehrlichia equi*, *Anaplasma phagocytophila*)

Equine granulocytic (formerly ehrlichiosis) anaplasmosis (EGA) was initially reported in 1969 associated to severe disease in horses in the foothills of the Sacramento Valley, California [(Gribble, 1969; Stannard *et al.*, 1969) in Dumler *et al.*, 2001]. Since then, the disease has been observed chiefly in California but sporadic cases are also reported in other parts of US and Europe (Engvall *et al.*, 1996; Madigan *et al.*, 1996; Pusterla *et al.*, 1998a; Bullok *et al.*, 2000;

Von Loewenich *et al.*, 2003b; Alberti *et al.*, 2005). EGA is usually a mild to moderately severe disease characterized by fever, depression, anorexia, icterus, limb oedema, petechiation, ataxia and reluctance to move.

1.2.6.3. OTHER GRANULOCYTIC ANAPLASMOSIS

The susceptibility of dogs and cats to *A. phagocytophilum* was first demonstrated in an experimental study (Lewis *et al.*, 1975 *in* Greig *et al.*, 1996) and later confirmed to occur naturally. In dogs, the disease was originally documented in California after the successful transmission of the agent from febrile, thrombocytopenic dogs to horses by blood transfusion (Madewell & Gribble 1982 *in* Greig *et al.*, 1996). Natural infection in domestic felines was initially recognized in Sweden (Bjoersdorff *et al.*, 1999c). In both cases, clinical disease was also found in other parts of North America and Europe (Engvall *et al.*, 1996; Greig *et al.*, 1996; Tozon *et al.*, 2003; Lappin *et al.*, 2004; Alberti *et al.*, 2005; Lester *et al.*, 2005; Shaw *et al.*, 2005). In general, the disease ranges from subclinical to mild febrile illness accompanied by depression, lethargy, and classic hematologic alterations.

Regarding human infection by *A. phagocytophilum* more detailed consideration is given below.

1.3. HUMAN GRANULOCYtic ANAPLASMOSIS

1.3.1. DEFINITION

A. phagocytophilum infection in humans, previously known as human granulocytic or granulocytotropic ehrlichiosis (HGE), is now called human granulocytotropic anaplasmosis (HGA). The synonym, HGE agent, was originally used to designate the etiology of the disease.

1.3.2. EPIDEMIOLOGY

Epidemiologic information regarding HGA is still limited. The available data seem to reflect the geographic distribution of *A. phagocytophilum* associated with human disease, competent tick vectors and reservoir hosts, their seasonal activity, and also human behavior that places persons at risk of tick attachment, and individual factors that determine the subsequent development of the disease. Understanding disease trends may help target prevention efforts and assist physicians in accurate and timely HGA diagnosis.

To date, HGA descriptions are restricted to the Northern hemisphere. As previously stated, the majority of patients have been diagnosed in the US, although a limited number of cases have also been reported from some European countries. In the US, HGA was originally described in 1994 from a series of patients residing in Wisconsin and Minnesota (Bakken *et al.*, 1994). In the following years, HGA was increasingly recognized also in other states, such as Connecticut, New York, Massachusetts and Rhode Island (Hardalo *et al.*, 1995; Telford *et al.*, 1995; CDC, 1995; Agüero-Rosenfeld *et al.*, 1996; Bakken *et al.*, 1996c; Goodman *et al.*, 1996; McQuiston *et al.*, 1999; Belongia *et al.*, 2001a; Gardner *et al.*, 2003). The disease became nationally notifiable in 1999 and is now in the rank of the 30th most important infectious diseases regarding the total number of incident cases reported to the Centers for Disease Control and Prevention (CDC, 2006). HGA cases are reported by State Health Departments to CDC through both the National Electronic Telecommunications System for Surveillance (NETSS) and Tick-Borne Rickettsial Disease Case Report Form (CRF). According to NETSS (CDC, 2001-2006), more than 2.000 cases have been reported in the six years of national surveillance representing an average annual incidence of 0.15

per 10⁵ inhabitants (Figure 8). The disease occurs mainly in the Upper Midwest, and parts of New England and the Mid-Atlantic States, which is consistent with previous surveillance reports (CDC, 1998; McQuiston *et al.*, 1999). In those areas, HGA is even more prevalent than other tick-borne diseases, such as Rocky Mountain spotted fever (RMSF)⁴ and HME, and is the second most reported tick bite-associated illness after LB (CDC, 2001-2006). The total number of HGA cases reported per state during 1999-2004 is presented in figure 9. Because nationally reportable diseases are recorded by state of residence rather than state of exposure, undoubtedly some cases might be incorrectly classified. Underreporting and inadequate diagnosis of HGA are also referred to as important limitations of the current passive surveillance system which might account for an incomplete overall distribution and regional prevalence of the disease (Ijdo *et al.*, 2000; Demma *et al.*, 2005).

The first European case of HGA was described in 1997 in Slovenia (Petrovec *et al.*, 1997), and more than 50 patients have been identified since then. The majority of cases have occurred in Central and Northern Europe, in areas at high prevalence of tick-borne encephalitis (TBE)⁵ and LB. Slovenia and Sweden account for the highest record of the disease (Bjoersdorff *et al.*, 1999a, 2002b; Laferl *et al.*, 1999; Arnez *et al.*, 2001; Karlsson *et al.*, 2001; Lotric-Furlan *et al.*, 2006) although sporadic cases have also been reported in Austria (Walder *et al.*, 2003a, 2006a), Czech Republic (Hulinska *et al.*, 2002), Croatia (Misić-Majerus *et al.*, 2006), Estonia (Prukk *et al.*, 2003), France (Remy *et al.*, 2003), Italy (Ruscio & Cinco, 2003; De la Fuente *et al.*, 2005b; Beltrame *et al.*, 2006; Mastrandrea *et al.*, 2006), Netherlands (Van Dobbenburgh *et al.*, 1999), Norway (Bjoersdorff *et al.*, 1999a, Kristiansen *et al.*, 2001), Poland (Tylewska-Wierzbanowska *et al.*, 2001; Grzeszczuk *et al.*, 2006b), and Spain (Oteo *et al.*, 2000; Garcia *et al.*, 2006). The geographic distributions of European HGA cases that have been reported since 1997 are presented in figure 10.

Seroepidemiological studies, however, suggest that human infection by *A. phagocytophilum* might be more common than clinical illness. The presence of antibodies against *A. phagocytophilum* has been reported from endemic areas in US and Europe and also from other European and Asiatic countries where HGA is not known to occur (Park *et al.*, 2003b; Ongut *et al.*, 2006; Walder *et al.*, 2006b). Reported seroprevalence rates range from zero or very low to up to 25% of the examined populations (Table 7). Generally, the proportion of seropositive persons increases with age and is higher for at-risk populations, such as forestry workers, persons with a

⁴ Rocky Mountain spotted fever (RMSF) is caused by the α -proteobacteria *Rickettsia rickettsii*.

⁵ Tick-borne encephalitis (TBE) is caused by the infection of a Flavivirus that received the same designation as the disease (TBE virus).

history of tick bite(s) and/or patients with LB and those with TBE, than in control subjects who are not (or who are less) exposed to ticks (Magnarelli *et al.*, 1995a; Bakken *et al.*, 1998b; Nuti *et al.*, 1998; Pusterla *et al.*, 1998b; Wittesjo *et al.*, 2001; Agüero-Rosenfeld *et al.*, 2002; Grzeszczuk *et al.*, 2004b).

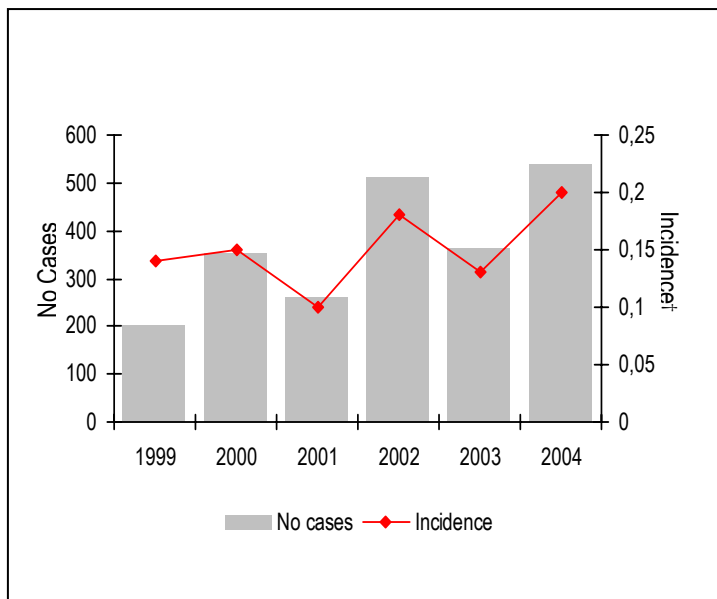


FIGURE 8. Number of HGA cases reported to NETSS, US 1999-2004 (adapted from CDC 2001-2006).

Available from:

<http://www.cdc.gov/mmwr/summary.html>

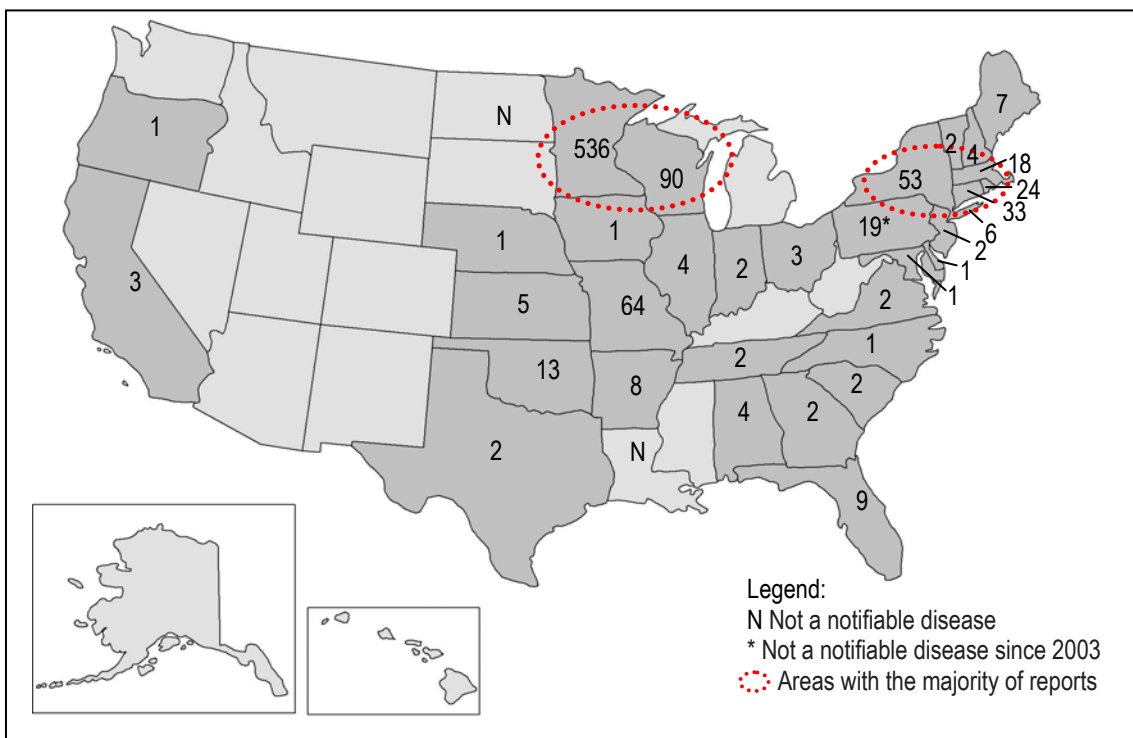
†Note. Incidence is presented per 100,000 inhabitants, based on data for the US total resident population. Population estimates are from the Bureau of the Census.

Available from: <http://www.census.gov/>

FIGURE 9. Total number of HGA cases reported to NETSS by State, US 1999-2004 (adapted from CDC 2001-2006).

Available from:

<http://www.cdc.gov/mmwr/summary.html>



Legend:

N Not a notifiable disease

* Not a notifiable disease since 2003

⋯ Areas with the majority of reports

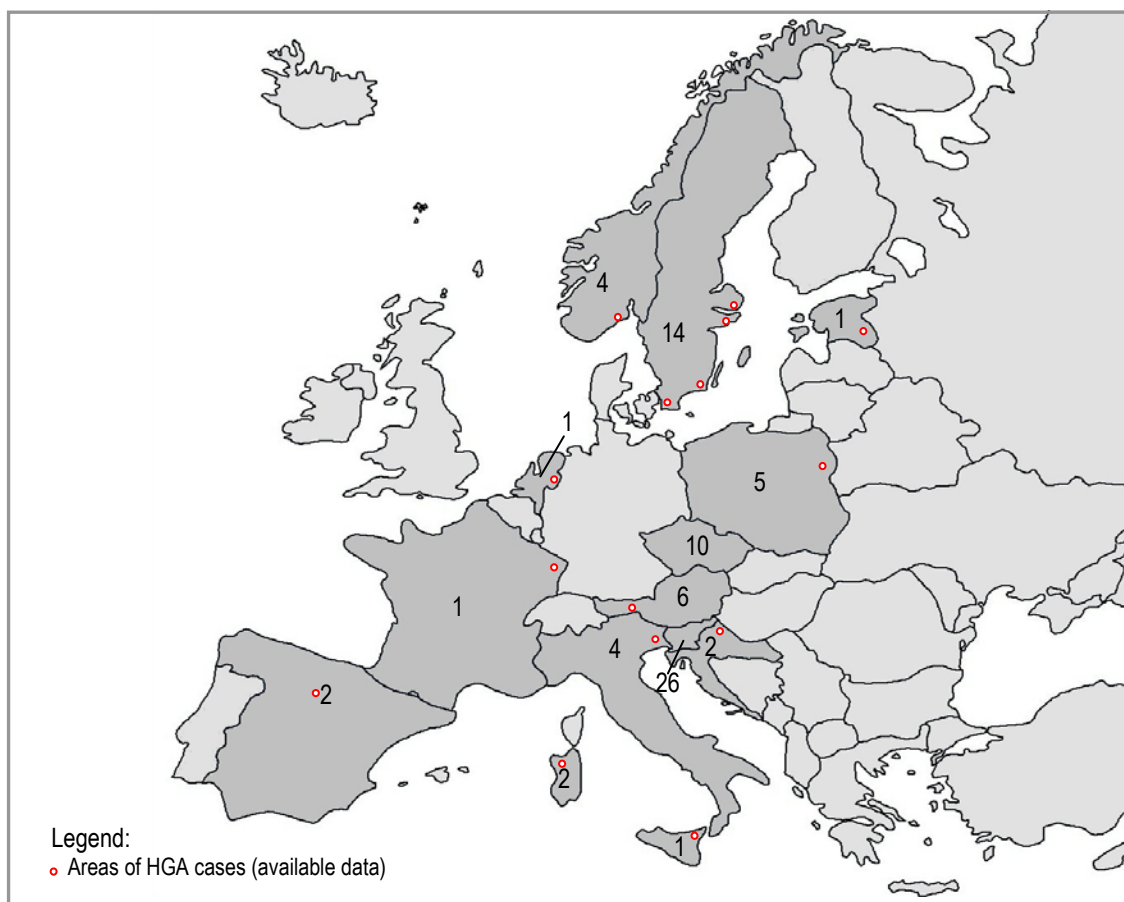


FIGURE 10. Total number of HGA cases reported in each European country since 1997 (based in a medline search <http://www.pubmed.gov>).

It is believed that asymptomatic or subclinical infections may contribute to the broad seropositivity. In four prospective serological studies up to 11% seroconversions were detected in individuals with a high degree of exposure without evidence of clinical illness, over a single tick season (Hilton *et al.*, 1999; Wittesjo *et al.*, 2001; Woessner *et al.*, 2001; Grzeszczuk *et al.*, 2004a). Nevertheless, it still remains unclear whether the discrepancy between the seroprevalence and incidence rate results from underdiagnosis of mild infections, asymptomatic serologic responses to *A. phagocytophilum* variants not associated with HGA, or even infections with other agents that produce cross-reactive serologic responses.

Exposure to tick bites is considered the most common route of human infection by *A. phagocytophilum*, although sporadic cases of HGA have been reported after perinatal transmission or contact with infected animal blood (Bakken *et al.*, 1996a; Horowitz *et al.*, 1998c). Transfusion transmission is also biologically plausible, but only a single possible case of transfusion-related HGA has been identified (McQuiston *et al.*, 2000; Kalantarpour *et al.*, 2000; Leiby & Gill, 2004).

TABLE 7. Meta-analysis of *A. phagocytophilum* seroprevalence (%) among various human populations based in seropositivity obtained from immunofluorescence assay* (adapted from Dumler, 2005).

	Cumulative Analysis Mean (Number of Subjects)	Median Analysis			Number Studies
		Median	Maximum	Minimum	
Overall					
Asia ^a	5.9 (816)	3.7	11.1	2.3	2
Europe ^b	7.0 (8,956)	7.3	23.0	0.0	26
North America ^c	9.7 (4,452)	8.6	35.6	0.0	14
At-risk^d					
Asia	11.1 (271)	11.1	11.1	11.1	1
Europe	9.3 (5,517)	8.8	23.0	0.0	22
North America	10.1 (3,693)	8.8	35.6	0.0	14
LB and/or TBE^e					
Asia	na ^f	na	na	na	0
Europe	10.8 (2,047)	9.7	23.0	0.0	13
North America	17.0 (393)	7.5	35.6	5.3	5

*All the data presented come from published reports:

^aReferences from Asia: Park *et al.*, 2003b; Walder *et al.*, 2006b;

^bReferences from Europe: Brouqui *et al.*, 1995; Bakken *et al.*, 1996b; Dumler *et al.*, 1997; Fingerle *et al.*, 1997; Lebech *et al.*, 1998; Nuti *et al.*, 1998; Pusterla *et al.*, 1998b; Bjoersdorff *et al.*, 1999b; Christova & Dumler, 1999; Hunfeld & Brade, 1999; Cizman *et al.*, 2000; Oteo *et al.*, 2001; Skarphedinsson *et al.*, 2001; Daniel *et al.*, 2002; Groen *et al.*, 2002; Guillaume *et al.*, 2002; Zeman *et al.*, 2002b; Topolovec *et al.*, 2003; Walder *et al.*, 2003b; Grzeszczuk *et al.*, 2004b; Santino *et al.*, 2004; Tomasiewicz *et al.*, 2004; Cisak *et al.*, 2005; ; Kowalski *et al.*, 2006; Ongut *et al.*, 2006; Stanczak & Grzeszczuk, 2006;

^cReferences from North America: Magnarelli *et al.*, 1995a, 1998; Pancholi *et al.*, 1995; Mitchell *et al.*, 1996; Fritz *et al.*, 1997; Wong *et al.*, 1997; Yeh *et al.*, 1997; Bakken *et al.*, 1998b; Wallace *et al.*, 1998; Hilton *et al.*, 1999; Ijdo *et al.*, 2000; Belongia *et al.*, 2001b; Aguero-Rosenfeld *et al.*, 2002; Leiby *et al.*, 2002;

^dIncludes adult and pediatric *B. burgdorferi* seropositive patients, farm workers, febrile patients, forest workers, patients with fever or undetermined origin, LB and TBE patients, individuals with tick bites or tick exposure;

^eIncludes adult and pediatric *B. burgdorferi* seropositive patients, LB and TBE patients;

^fna, not available.

The occurrence of HGA is seasonal, with the majority of cases being reported between late spring and fall (McQuiston *et al.*, 1999; Ijdo *et al.*, 2000; Belongia *et al.*, 2001a; Blanco & Oteo, 2002; Gardner *et al.*, 2003; Lotric-Furlan *et al.*, 2006). In US, a bimodal distribution has additionally been demonstrated with a first peak of the disease in July through August and a second peak in October and November (CDC, 2001-2006). The seasonal pattern might result in part from the increase in outdoor activities during April-September, either recreational pursuits (e.g., camping, hiking, fishing, hunting, gardening, and walking dogs) or occupational activities, which involve an increased risk to tick exposure. Moreover, it also overlaps the period of the year when nymphal-stage of *Ixodes* ticks are most active. Even though both adults and nymphs are able to transmit *A. phagocytophilum*, the diminutive size of the latter stage allows them to often feed undetected on

humans long enough to transmit the pathogen. For this reason, it is currently believed that nymphs of the *Ixodes* genus are the main stage involved in *A. phagocytophilum* transmission to humans.

Despite the characteristically geographic and temporal pattern, HGA distribution might be influenced by changes in ecological or environmental conditions. Increased development in suburban and rural sites can result in an additional risk of tick exposure and local increases in HGA cases. Moreover, an impact from climate warming on the vertical disease distribution should be expected as has been suggested for other *Ixodes* borne-disease (Zeman & Bene, 2004; Ogden *et al.*, 2006).

Cases of HGA have been reported in both sexes and in different age groups from <1 to ≥90 years, although older male adults (median age 40-60 years) appear to be at higher risk for developing the disease (Gardner *et al.*, 2003; CDC, 2001-2006). Pediatric cases are restricted to only a few reports (Horowitz *et al.*, 1998c; Arnez *et al.*, 2001; Krause *et al.*, 2003; Moss & Dumler, 2003). This tendency is still not well understood and could be multifactorial. The rates of clinical infection could be related to age and/or gender specific increased susceptibility to recognizable disease and/or greater risk of exposure to *A. phagocytophilum*. Moreover, the nonspecificity of signs and symptoms that characterize HGA and the reluctance to draw blood, especially convalescent samples, from paediatric patients may contribute to fewer-than-expected enrolled children and, hence, underdiagnosis of HGA cases in children compared to adults. Two cross-sectional studies in endemic areas (Slovenia and Westchester County, New York) have indicated that up to 15% of children and younger adults (age, ≤24 years) have serologic evidence of previous exposure to *A. phagocytophilum* antigens, suggesting that infection might be more common than previously recognized (Cizman *et al.*, 2000; Aguero-Rosenfeld *et al.*, 2002).

Co-infections with *A. phagocytophilum* and other *Ixodes*-borne agents have occasionally been reported in humans, including *B. burgdorferi s.l.* and less frequently *Babesia* sp. in US and both *B. burgdorferi s.l.* and TBE virus in Europe (Nadelman *et al.*, 1997; Horowitz *et al.*, 1998a; Krause *et al.*, 2003; Moss & Dumler, 2003; Hermanowska-Szpakowicz *et al.*, 2004; Lotric-Furlan *et al.*, 2005, 2006; Grzeszczuk *et al.*, 2006b). Dual infections may result from a single tick bite and simultaneous transmission of different pathogens, from multiple tick bites or even from sequential infections that took place at different times (Levin & Fish, 2000, Des Vignes *et al.*, 2001; Belongia *et al.*, 2002). Although a rare event, coinfection should be taken into account in the clinical evaluation, diagnosis and treatment of patients potentially exposed to *Ixodes* ticks, a topic that will be further mentioned.

1.3.3. CLINICAL PRESENTATION

HGA is clinically variable ranging from mild self-limited flu-like illness, in the majority of cases, to severe multisystemic disease (Blanco & Oteo, 2002; Strle, 2004; Dumler, 2005). The undefined localization and nonspecific presentation defines a disease that is usually difficult to differentiate from many other infectious and non-infectious conditions.

Onset occurs after an incubation period of 1 to 2 weeks and clinical manifestations are dominated by fever, headache, myalgia and malaise (Aguero-Rosenfeld *et al.*, 1996; Bakken *et al.*, 1996c; Horowitz *et al.*, 1998a; Lotric-Furlan *et al.*, 2006). A minority of patients may also present with arthralgia or involvement of the gastrointestinal tract (nausea, vomiting, diarrhea and abdominal pain), respiratory tract (cough, pulmonary infiltrates), liver, or central nervous system. Despite the observation of stiff neck and other signs and symptoms that may suggest meningeal involvement, very little evidence supports invasion of the central nervous system by *A. phagocytophilum* (Dumler, 2005), although cases of lymphocytic meningitis have been described in coinfection with TBE (Grzeszczuk *et al.*, 2006b; Lotric-Furlan *et al.*, 2006). Some patients may present with conjunctivitis or lymphadenopathy, findings that are especially common in HGA European series (Laferl *et al.*, 1999; Arnez *et al.*, 2001; Karlsson *et al.*, 2001; Prukk *et al.*, 2003; Lotric-Furlan *et al.*, 2006). Local skin reactions at the site of the tick bite have not been described, and nonspecific skin-rashes have been reported only occasionally. The presence of erythema migrans has been documented in concurrent LB (Nadelman *et al.*, 1997; Horowitz *et al.*, 1998a; Grzeszczuk *et al.*, 2006b).

Variable changes in blood cell counts and chemistry parameters are reported (Hossain *et al.*, 1999; Bakken & Dumler, 2000; Bakken *et al.*, 2001; Lotric-Furlan *et al.*, 2006). Most patients develop transient depletion in platelet and total leukocyte (WBC) concentrations, usually accompanied by mild increases in serum hepatic transaminase concentrations (aspartate aminotransferase, alanine aminotransferase) or lactate dehydrogenase. Elevation of inflammatory markers, such as C-reactive protein and the erythrocyte sedimentation rate have also been found in the many HGA patients (Bakken *et al.*, 2001; Lotric-Furlan *et al.*, 2002). Other less common laboratory findings include anaemia, elevated serum creatinine and blood urea nitrogen levels. Although total WBC, absolute neutrophil, and lymphocyte counts may be below normal, patients with HGA often have a left shift during the first week of illness. Neutrophil counts gradually return to normal thereafter accompanied by relative and absolute lymphocytosis. The hematological

abnormalities tend to normalize by the end of the second week of illness, even in the absence of antimicrobial therapy. Thus, as stated by Bakken and Dumler (2000), caution is advised against dismissing HGA from the differential diagnosis if blood cell counts are normal at the time of presentation, especially for patients who have been ill for more than one week.

The results of physical examination are often unremarkable. Interestingly, several European cases of HGA have been presented as atypical pneumonitis, a fact that has also been mentioned in US literature (Bakken *et al.*, 1994, 1996c; Hardalo *et al.*, 1995; Lepidi *et al.*, 2000; Karlsson *et al.*, 2001; Remy *et al.*, 2003; Bayard-Mc Neeley *et al.*, 2004; Lotric-Furlan *et al.*, 2006; Mastrandrea *et al.*, 2006). Additionally, Halasz and coworkers (2005) have reported the association of HGA and Sweet Syndrome.

In regions where several *Ixodes*-borne diseases are known to occur, distinguishing between concurrent infections in the early stages of illness can be difficult. Infections with different agents can complicate disease presentation, and unusual signs, symptoms and laboratory abnormalities may be present. According to Krause and coworkers (2002), patients with LB and HGA and/or human babesiosis (HB)⁶ experience more persistent flu-like symptoms with leukopenia and thrombocytopenia than those with LB alone. Acute LB is readily diagnosed when the pathognomonic erythema migrans is present, but some cases can lack that characteristic rash, overlapping HGA and HB clinical spectrum (Belongia *et al.*, 1999; Krause *et al.*, 2002). Likewise, HGA has a remarkably similar clinical and laboratory presentation to the initial phase of infection by TBE virus. However, prospective studies performed by Lotric-Furlan and coworkers (2000, 2002) have found statistically significant differences in the frequency of arthralgia and elevated concentration of C-reactive protein in patients with acute HGA than those with the initial phase of TBE. To sum up, the likelihood of coinfection should be considered when pursuing laboratory testing or selecting antimicrobial therapy.

1.3.4. COMPLICATIONS AND OUTCOME

HGA is usually an uncomplicated disease but nearly half of identified patients require hospitalization (Blanco & Oteo, 2002; Strle, 2004; Bakken & Dumler, 2006). In the US up to 17% of

⁶ Human babesiosis is the general designation for infections caused by the tick-borne protozoan species *Babesia microti* and *B. divergens*. Cases of *B. microti* and *B. divergens* are chiefly reported from US and Europe, respectively.

patients are admitted to an intensive care unit (Bakken & Dumler, 2006). The severity of the disease appears to correlate with advanced age, immunosuppressive therapy, chronic inflammatory illnesses, or underlying malignant diseases (Bakken & Dumler, 2000). Delayed diagnosis and onset of specific antibiotic therapy are also risk factors for an adverse outcome. Severe complications have been described in the literature and are listed in table 8. Even though the fatality rate of HGA is low (<1%), at least 5 deaths have been identified in the US, three of which were the result of opportunistic infections, including exsanguination after ulcerative *Candida* esophagitis, ulcerative herpes simplex virus esophagitis with cryptococcal pneumonia, and invasive pulmonary aspergillosis (Bakken *et al.*, 1994; 1996c; Hardalo *et al.*, 1995; Walker & Dumler, 1997; Jahangir *et al.*, 1998; Lepidi *et al.*, 2000). As previously mentioned, this might result from the potential role of *A. phagocytophilum* in suppressing host defense or immune function. The risk of contracting HGA in immunocompromised patients, such as organ transplant recipients and persons infected with human immunodeficiency virus, is unknown. However, several cases have been described and severe manifestations may occur (Hardalo *et al.*, 1995; Adachi *et al.*, 1997; Trofe *et al.*, 2001; Vannorsdall *et al.*, 2002; Springer *et al.*, 2003; Bayard-Mc Neeley *et al.*, 2004). Regarding European cases, the disease appears to be generally milder and resolves sooner, even in the absence of specific antimicrobial therapy (Laferl *et al.*, 1999; Arnez *et al.*, 2001; Remy *et al.*, 2003; Lotric-Furlan *et al.*, 2006). Complications are unusual. No opportunistic infections have been described so far and only one case of fatal infection was reported in an article from Czech Republic (Hulinska *et al.*, 2002).

Ultimately, the immunosuppressive nature of HGA may also affect the clinical course of concurrent infection. Experimental studies have provided results with regard to the effect of *A. phagocytophilum* on *B. burgdorferi* dissemination, pathogen burden and host immune response (Thomas *et al.*, 2001; Holden *et al.*, 2005; Nyarko *et al.*, 2006). Nevertheless, the potential contribution of concurrent infections toward a more severe clinical course in humans remains to be defined. The available data is limited to few cases and in some instances are paradoxical. So far only two patients with TBE and HGA have been reported and both presented a relatively mild illness with uneventful recovery (Lotric-Fulan *et al.*, 2005, 2006). Regarding concurrent LB and HGA, although the diversity and duration of symptoms reported by patients with dual infections exceeds that for patients with LB alone, the frequencies of disseminated blood, skin, joint, cardiac, and neurologic disease and of hospital admission appear to be similar (Krause *et al.*, 2002).

TABLE 8. Clinical complications of HGA reported in North America and in Europe.

Clinical Complications	Reference(s)
<u>North America</u>	
Acute abdominal syndrome	Greshel, 2000; Lepidi <i>et al.</i> , 2000
Acute renal failure	Modi <i>et al.</i> , 1999
Acute respiratory distress syndrome (ARDS) and pneumonitis	Bakken <i>et al.</i> , 1994; Hardalo <i>et al.</i> , 1995; Bayard-Mc Neeley <i>et al.</i> , 2004
Carditis (pancarditis, pericarditis, myocarditis)	Goodman <i>et al.</i> , 1996; Jahangir <i>et al.</i> , 1998
Coagulopathy and hemorrhage	Bakken <i>et al.</i> , 1994, 1996c
Neuropathies	Horowitz <i>et al.</i> , 1996; Bakken <i>et al.</i> , 1998a; Lee <i>et al.</i> , 2000
Opportunistic infections	Bakken <i>et al.</i> , 1994, 1996c; Hardalo <i>et al.</i> , 1995
Rhabdomyolysis	Shea <i>et al.</i> , 1996
Septic or toxic shock-like syndrome	Bakken <i>et al.</i> , 1994
<u>Europe</u>	
ARDS and pneumonitis	Bjoersdorff <i>et al.</i> , 1999a; Karlsson <i>et al.</i> , 2001; Tylewska-Wierzbanowska <i>et al.</i> , 2001; Remy <i>et al.</i> , 2003; Lotric-Furlan <i>et al.</i> , 2006
Rhabdomyolysis	Van Dobbenburgh <i>et al.</i> , 1999

In general, the HGA outcome is favourable and disease resolves either after specific antibiotic therapy or even spontaneously (Lotric-Furlan *et al.*, 2001). Complete resolution of HGA can take only a few days, although biphasic courses with recurrent fever may occur in the absence of appropriate antibiotic therapy (Horowitz *et al.*, 1998d; Karlsson *et al.*, 2001; Walder *et al.*, 2003a, 2006a). This condition in humans seems to be rare but is not totally unexpected, since *A. phagocytophilum* is known to cause relapsing illness in ruminants (Tuomi, 1967 in Horowitz *et al.*, 1998d). In general, patients respond to treatment within 24 to 48 hours, but some with advanced infections may take longer or present persistent residual symptoms and signs, reflecting slow resolution of inflammation or accumulated tissue injury (Dumler, 2005).

Relapses or chronic infections have never been reported, even for those patients who were never treated with an active antibiotic. Reinfection, albeit rare, may occur, and was demonstrated in one US case (Horowitz *et al.*, 1998a). Persistence of *A. phagocytophilum* in humans is rarely observed in convalescent patients (Dumler & Bakken 1996; Ijdo *et al.*, 2000). Only two patients are known to have developed chronic sequelae following HGA (Horowitz *et al.*, 1996; Dumler & Bakken, 1998). Both patients received appropriate antibiotic therapy, and in each case, the irreversible neurological or tissue damage was believed to be caused by the acute inflammatory response elicited by the microorganism rather than by persistent infection. According

to Ramsey and coworkers (2002), some patients may also develop an apparently post-infectious syndrome, with persistent constitutional symptoms 1-3 years after treatment, such as fevers, fatigue, sweats, body pain, but without functional disability, but such conditions require much more study.

1.3.5. CONFIRMATORY LABORATORY TESTS

Confirmatory laboratory testing is required for a definitive diagnosis of HGA, as this is virtually impossible based only on epidemiologic, clinical and routine laboratory findings. Confirmatory methods include direct and indirect tests that allow the detection of *A. phagocytophilum* (microscopy, molecular analysis, *in vitro* culture) and antibodies elicited by infection (serological assays), respectively. The sensitivity of each confirmatory test regarding the disease onset is represented in figure 11.

Guidelines for HGA diagnosis have been published recently as the result of joint effort of epidemiologists, infectious disease clinicians, microbiologists, and pathologists to develop criteria for case definition and a consensus approach for laboratory testing (Walker *et al.*, 2000; Brouqui *et al.*, 2004).

1.3.5.1. OPTICAL MICROSCOPY, MOLECULAR ANALYSIS AND *IN VITRO* CULTURE

Direct tests are useful to confirm HGA during active disease, prior to the initiation of effective antimicrobial therapy. Data based on observations of human and animal infection show that bacteremia occurs for a limited period of time that may persist for up to two weeks or until the administration of effective antibiotic therapy, and diminishes rapidly to become undetectable thereafter (Bakken *et al.*, 1996c; Dumler, 2003). Since *A. phagocytophilum* infects granulocytic leukocytes, mostly mature neutrophils, direct tests are routinely performed in peripheral blood obtained at initial presentation to physician. Other available samples, including bone marrow aspirates and tissue specimens obtained at biopsy or autopsy may also be used. Blood-samples should be collected in ethylenediaminetetraacetic acid (EDTA) and kept refrigerated until processed, preferably within 24 to 48 hours. The use of heparin as an anticoagulant should be

avoided because of its ability to compromise PCR-based detection methods. Aseptic conditions for collection and preparation of samples is required if bacterial culture is to be done.

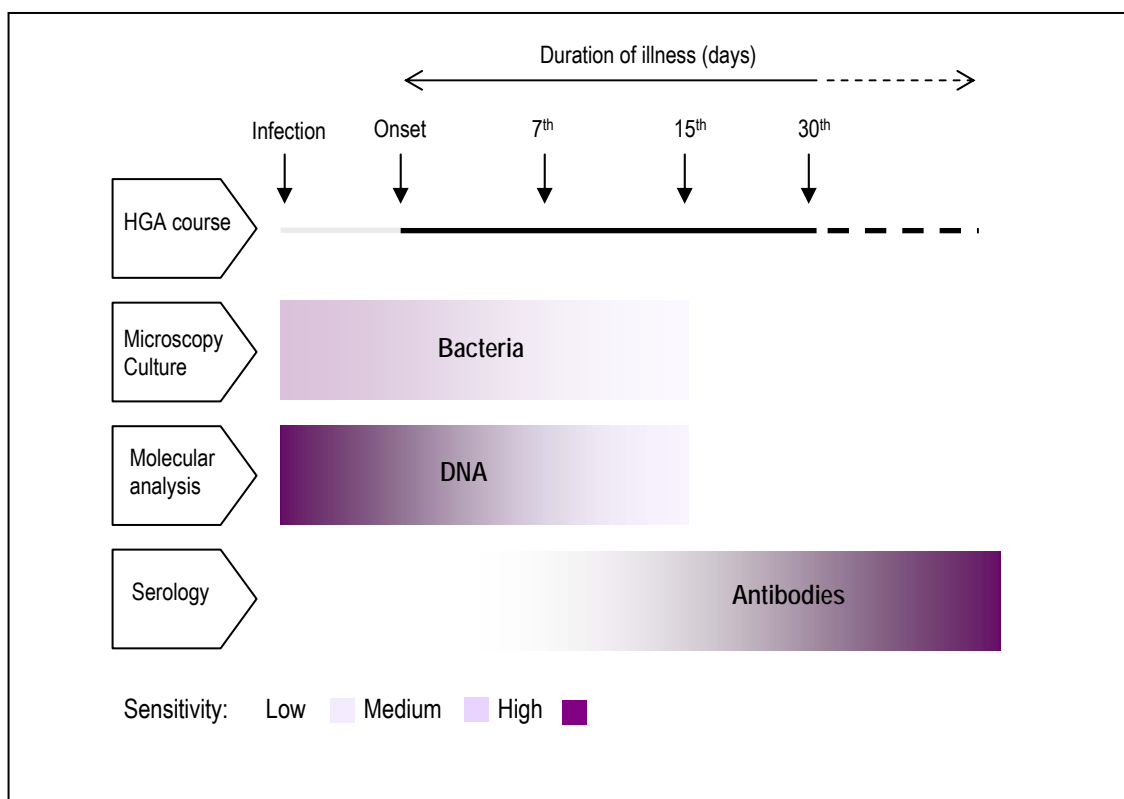


FIGURE 11. Relative sensitivity of diagnosis tests used for laboratory confirmation of HGA (Houpikian & Raoult, 2002; Bakken & Dumler, 2006).

Microscopic detection of *A. phagocytophilum* in blood is best achievable if smears are prepared immediately after sample collection. Buffy coat smears are preferred to regular whole-blood preparations, as most patients are leukopenic at the time of presentation and very few leukocytes are usually infected. Light microscopic examination of samples is performed under 400X or 1000X magnification and at least 800 to 1,000 granulocytes should be observed before considering a negative result (Aguero-Rosenfeld, 2000). The characteristic mulberry-shaped intraleukocytic morulae of *A. phagocytophilum* typically appear as dark blue to purple cytoplasmic densities after staining with eosin-azure (Romanovsky)-type dyes (including, Wright, Diff-Quik, Giemsa and Leishman stains) (Figure 12A). Although microscopy has been routinely applied for blood-smear testing, the examination of other available samples might also be useful. In severely ill patients, *A. phagocytophilum* morulae have been detected in bone marrow and other tissue samples, such as spleen, lung, liver and heart (Bakken *et al.*, 1994; Walker & Dumler, 1997;

Jahangir *et al.*, 1998; Lepidi *et al.*, 2000; Trofe *et al.*, 2001; Remy *et al.*, 2003; Bayard-Mc Neeley *et al.*, 2004). The examination of bone marrow smears should be performed after sample staining with eosin-azure (Romanovsky)-type dyes (Remy *et al.*, 2003; Bayard-Mc Neeley *et al.*, 2004). Other tissue specimens can be tested either fresh, following formalin fixation and paraffin embedding, using immunohistochemistry techniques (Figure 12B) (Bakken *et al.*, 1994; Walker & Dumler, 1997; Lepidi *et al.*, 2000).

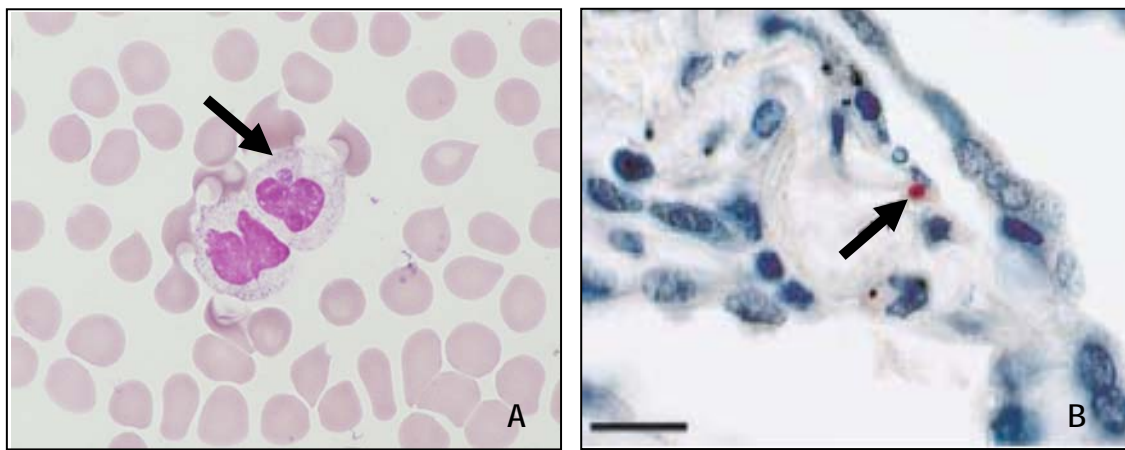


FIGURE 12. *A. phagocytophilum* morulae in neutrophils: A- peripheral blood smear stained by Diff-Quik; arrows- infected neutrophils, 1000X magnification (courtesy of JS Dumler); B- spleen section stained by immunoalkaline phosphatase/ hematoxylin; arrows- infected neutrophils within splenic red pulp sinusoids, bar- 20 μ m (adapted from Lepidi *et al.*, 2000).

Observation of blood smears is the most inexpensive and fastest laboratory test, but is also the least sensitive. *A. phagocytophilum* morulae may be sparsely distributed and difficult to detect, even by experienced observers and a negative result should not rule out HGA. Case series describing US patients with culture-confirmed HGA report only 60% morulae visualization, and although as much as 40% of peripheral granulocytes may contain *A. phagocytophilum* inclusions, the majority of patients with positive smears had less than 1% infected granulocytes (McQuiston *et al.*, 1999; Bakken *et al.*, 2001). In Europe the detection of *A. phagocytophilum* in peripheral-blood smears seems to be an infrequent finding, observed only in four patients (Van Dobbenburgh *et al.*, 1999; Remy *et al.*, 2003; Beltrame *et al.*, 2006; Garcia *et al.*, 2006) (Table 9). Moreover, false positive interpretations may also occur due to toxic granulations, Döhle bodies, or superimposed platelets, contaminant particles, or other inclusions which may be mistaken for organisms. Thus, microscopic examination of samples should be always conducted in parallel with other tests to confirm HGA diagnosis (Walker, 2000; Brouqui *et al.*, 2004).

TABLE 9. Results of confirmatory laboratory testing for 330 patients with HGA from case series or case reports in North America[†] and Europe[‡].

Confirmatory test	No. (%) patients with positive test result		Total
	North America [†] n=277	Europe [‡] n=53	
Morulae in neutrophils	116/238 (48.7)	4/43 (9.3)	120/281 (42.7)
Positive PCR result	112/185 (60.5)	31/47 (65.9)	143/232 (61.6)
Isolation of <i>A. phagocytophilum</i> in cell-culture	39/64 (60.9)	-	39/64 (60.9)
Seroconversion or ≥four-fold change in antibody titer ^a	232/273 (85.0)	50/58 (86.2)	282/331 (85.2)

[†]References of 277 HGA patients (representing 266 confirmed and 11 probable cases): Aguero-Rosenfeld *et al.*, 1996, 2000; Goodman *et al.*, 1996; Horowitz *et al.*, 1998b; Wallace *et al.*, 1998; Belongia *et al.*, 1999; Foley *et al.*, 1999a; Bakken *et al.*, 2002;

[‡]References of 53 HGA patients: Laferl *et al.*, 1999; Van Dobbenburgh *et al.*, 1999; Oteo *et al.*, 2000; Arnez *et al.*, 2001; Karlsson *et al.*, 2001; Kristiansen *et al.*, 2001; Tylewska-Wierzbanowska *et al.*, 2001; Bjoersdorff *et al.*, 2002b; Prukk *et al.*, 2003; Remy *et al.*, 2003; Rusio & Cinco, 2003; Walder *et al.*, 2003a, 2006a; De la Fuente *et al.*, 2005b; Beltrame *et al.*, 2006; Garcia *et al.*, 2006; Grzeszczuk *et al.*, 2006b; Lotric-Furlan *et al.*, 2006; Mastrandrea *et al.*, 2006; Misić-Majerus *et al.*, 2006;

^aIndirect immunofluorescence assay for acute- and convalescent-phase samples.

The detection of *A. phagocytophilum* DNA is now becoming the standard complement for serologic assays (Dumler 2003; Brouqui *et al.*, 2004). As for other direct tests, the most appropriate sample for molecular analysis is EDTA-anticoagulated whole-blood or buffy coat, although the usefulness of other available samples, such as serum, cerebrospinal fluid (CSF), and skin biopsies, has been described (Massung *et al.*, 1998; Comer *et al.*, 1999b; Lee *et al.*, 2000; Halasz *et al.*, 2005). Several primer sets are described in the literature for the amplification of specific nucleic acid sequences of *A. phagocytophilum* by PCR in simple or nested reactions (Table 10). Among the targeted genes are the *rrs*, *groESL*, *ankA*, *msp2* (*p44*) (Chen *et al.*, 1994; Pancholi *et al.*, 1995; Goodman *et al.*, 1996; Sumner *et al.*, 1997; Massung *et al.*, 1998; Walls *et al.*, 2000; Caspersen *et al.*, 2002). However, PCR-based methods are not yet standardized and may yield discrepant results. Sensitivity might be dependent on sample quality, target sequence (that may have multiple copies in *A. phagocytophilum* genome, as in the case of *ankA* and *msp2* and in the amplicon length (Dumler, 2003; Brouqui *et al.*, 2004). The detection limits of 13 published PCR assays have been assessed, and those targeting fragments of the outer surface proteins homologues or *rrs* were found to be the most sensitive (Massung & Slater, 2003), but this study was conducted prior to the availability of many other gene targets, application of real time PCR, and the publication of the genome sequence. Whichever DNA target is chosen, sequencing of PCR products is strongly encouraged to confirm their identity.

TABLE 10. DNA targets that have been used for the detection of *A. phagocytophilum* in samples from infected patients.

Target gene	Primer pair	PCR method/ amplified fragment	Detection Limit/ Specificity†	Reference
<i>ankA</i>	LA1/LA6	regular/ 444-bp	2.5/ –	Walls <i>et al.</i> , 2000
<i>groESL</i>	HS1/HS6; HS43/HS45	nested/ 442-bp	2.5/ Ec	Sumner <i>et al.</i> , 1997
<i>msp2 (p44)</i>	MSP465f/MSP980r	regular/ 550-bp	NT	Caspersen <i>et al.</i> , 2002
<i>rrs</i>	GE9f/GE10r	regular/ 919-bp	2.5/ –	Chen <i>et al.</i> , 1994
	Ehr521/Ehr747	regular/ 247-bp	0.25/ Bh, Ec, Rk	Pancholi <i>et al.</i> , 1995
	Ehr521/Ehr790	regular/ 293-bp	0.25/ Ec	Kolbert, 1996
	PER1/PER2	regular/ 451-bp	2.5/ Ec	Goodman <i>et al.</i> , 1996
	GER3/GER4	regular/ 151-bp	NT	Goodman <i>et al.</i> , 1996
	GE3a/GE10r; GE9f/GE2	nested/ 546-bp	0.25/ –	Massung <i>et al.</i> , 1998
	EC9/EC12; GE9f/GE10r	nested/ 919-bp	2.5/ –	Chen <i>et al.</i> , 1994

†According to Massung & Slater, 2003:

Detection limit was estimated by the minimum number of *A. phagocytophilum* infected cells that could be detected per test sample. Sensitivity was detected using template DNA from *Bartonella henselae* strain Houston-1 (Bh), *Ehrlichia chaffeensis* strain Arkansas (Ec), and *Rickettsia rickettsii* strain Sheila Smith (Rk); NT- not tested; – no detection of *B. henselae*, *E. chaffeensis* or *R. rickettsii*, DNA.

Since the first report of *A. phagocytophilum* isolation in HL-60 cells by Goodman and coworkers (1996), several investigators have used this modality of direct HGA diagnosis. Cells are maintained in antibiotic-free RPMI-1640 medium, supplemented with 2 mM glutamine and fetal bovine serum 5% v/v, and incubated at 37°C in an atmosphere of 5% CO₂. For isolation assays, 0.1 to 0.5 ml anticoagulated whole-blood or buffy coat is inoculated straight into HL-60 cells that are maintained at a final concentration of 2x10⁵ cells/ml. Cultures are evaluated every 2 to 4 days to adjust cell concentration and detect any microbial growth. Infection can be assessed by direct observation of cytocentrifuged culture aliquots after staining by eosin-azure type dyes. To date, almost all human isolates of *A. phagocytophilum* came from US patients, with the exception of one isolate obtained from a Slovenian patient (JS Dumler, personal communication), and in the majority of cases they were obtained from blood-samples. Only two reports describe the isolation of *A. phagocytophilum* from CSF and bone marrow samples (Lee *et al.*, 2000; Bayard-Mc Neeley *et al.*, 2004). According to Aguero-Rosenfeld (2002), most of the cultures from patients showing morulae on blood smears become positive during the first week of incubation, and for patients with negative smears it can take two weeks or more. Culturing of *A. phagocytophilum* is regarded as the most specific method to confirm the diagnosis of HGA although it is still not widely available. Only a

limited number of research institutions are currently able to perform culture assays. Even so, this might not be a constraint; Kalantarpour and coworkers (2000) have showed that *A. phagocytophilum* can remain viable in infected blood kept for up 18 days under refrigerated conditions thus biological samples can be easily transported to a referral laboratory where the appropriate assays can be carried out. The only limitation is that cultures will require more time to become positive (Kalantarpour *et al.*, 2000).

1.3.5.2 SEROLOGY

In most cases definitive HGA diagnosis relies on the demonstration of a serologic response to *A. phagocytophilum*. Indirect immunofluorescence assay (IFA) is currently the best overall option. Other serological methods include enzyme immunoassay and immunoblotting methods that employ purified antigens or recombinant proteins, but to date no standardization of these tests exists, and all are performed at the research level.

IFA testing is performed with serum or plasma samples, using *A. phagocytophilum* strains as a source of antigen, and most laboratories detect IgG and IgM separately, or total immunoglobulins. Antibody titer values are expressed as the reciprocal of the representative serum dilution at which unequivocal apple-green fluorescence of microbial inclusion bodies is focally located in the cytoplasm of the infected cells (Figure 13). Slide examination is performed in an UV microscope under 400X or preferably 1000X magnification. The cut-off value should be determined in each laboratory based upon well-characterized sera from patients with proven HGA and an uninfected control population (Walker *et al.*, 2000). Samples reactive at a dilution of 1:64 or 1:80 are usually considered positive (Dumler *et al.*, 1995; Bakken *et al.*, 1998b), and serial dilutions are done to determine the end-point titer.

In general, IFA testing of acute and convalescent-phase samples is the most sensitive laboratory tool for diagnosis confirmation of HGA (Table 9). The lack of humoral response has been described only in few cases and is still not well-understood (Aguero-Rosenfeld *et al.*, 1996, 2000; Bakken *et al.*, 2002; De la Fuente *et al.*, 2005b, Lotric-Furlan *et al.*, 2006). One possible explanation is that early therapy may abrogate antigenic mass sufficiently to preclude a detectable antibody response (Aguero-Rosenfeld *et al.*, 2000; Bakken *et al.*, 2002).

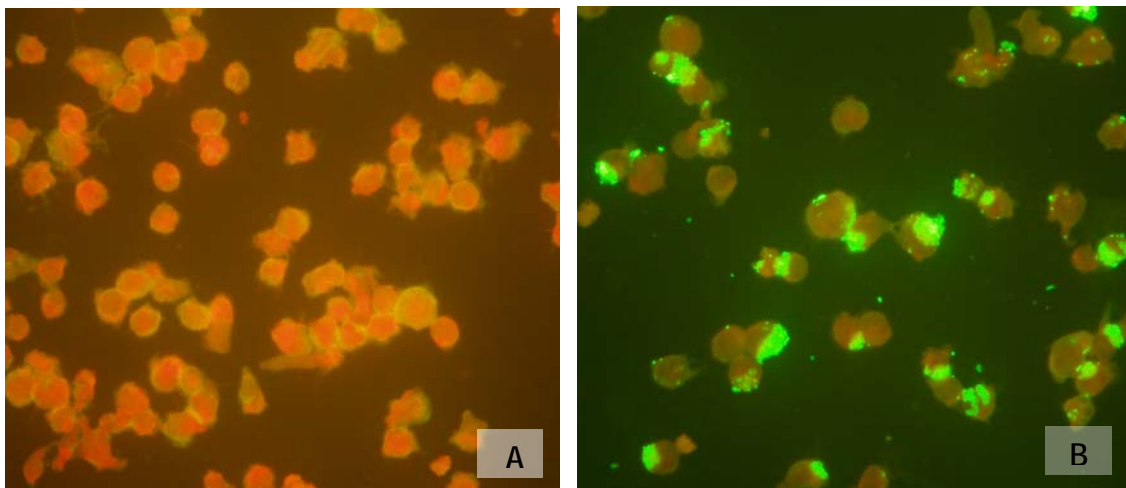


FIGURE 13. Immunofluorescence assay (IFA) using HL-60 cells infected with *A. phagocytophilum* Webster strain as antigen, 1000X magnification: A- negative sample; B- reactive sample evidenced by green fluorescence of *A. phagocytophilum* morulae.

The major disadvantage of IFA is that diagnosis confirmation is usually achieved retrospectively. Antibodies usually appear within two weeks after the onset of disease, reaching the highest titer during the first month of illness, and may remain detectable for a year or more (Aguero-Rosenfeld *et al.*, 2000; Lotric-Furlan *et al.*, 2001; Bakken *et al.*, 2002). Therefore, a negative serologic result in an acutely ill patient is typical and does not exclude HGA. Diagnostic confirmation usually depends on the availability of paired serum samples from acute and convalescent phases (obtained 2 to 4 weeks apart) to show seroconversion or a four-fold increase in antibody titer. Several studies have showed that only 20-40% of patients with confirmed HGA had antibodies detected by IFA at the time of initial presentation to the physician; however, more than 90% patients developed titers exceeding the cut-off within the first month of illness (Comer *et al.*, 1999a; Aguero-Rosenfeld *et al.*, 2000; Lotric-Furlan *et al.*, 2001; Bakken *et al.*, 2002).

Another limitation of IFA testing is cross-reactivity that might be present between antigens from other pathogens not only in the same genus but also from different genera. Cross-reactivity between *A. phagocytophilum* and *E. chaffeensis* is suspected to occur in approximately 10-20% of patients tested (Wong *et al.*, 1997; Walls *et al.*, 1999; Comer *et al.*, 1999a). In these circumstances, serologic differentiation is best accomplished by simple comparison of antibody titers, since higher titers are usually developed to the homologous microorganism. Simultaneous testing for antibodies to both agents is advised to differentiate between the two diseases,

especially in regions where both pathogens are present. The diagnosis of HGA or HME would depend on the presence of a four-fold or greater titer against *A. phagocytophilum* or *E. chaffeensis*, respectively. Although less frequent, cross-reactivity with other agents such as *B. burgdorferi* s.l., *C. burnetii*, and *Rickettsia* spp. has also been described (Comer *et al.*, 1999a; Blanco & Oteo, 2002). Moreover, patients with Q fever and bartonellosis have been described to react with *A. phagocytophilum* antigen (Brouqui *et al.*, 2001). Whether these findings represented cross-reactivity directed to common antigens, such as the heat shock proteins, or antibody induced by separate exposures to different organisms remains to be ascertained (Wong *et al.*, 1997; Ijdo *et al.*, 1998b; Unver *et al.*, 2001a). At least in some cases, *B. burgdorferi* and TBE virus serologic cross-reactions with *A. phagocytophilum* have been explained by confirmed coinfections with both agents (Nadelman *et al.*, 1997; Horowitz *et al.*, 1998a; Belongia *et al.*, 1999; Bjoersdorff *et al.*, 2002b; Moss & Dumler, 2003; Lotric-Furlan *et al.*, 2005, 2006; Grzeszczuk *et al.*, 2006b).

The problem of potential cross-reactivity of antibodies and the possibility of dual or past infections indicate that additional testing is required to confirm simultaneous HGA. Another way to distinguish cross-reactivity is by use of immunoblots demonstrating reactivity to specific antigens. As mentioned by Dumler (2003), several recombinant proteins- including members of the Msp2 (P44) major outer surface protein family, AnkaA, and GroEL - have been cloned and evaluated as potential serodiagnosis reagents with variable promise (Ijdo *et al.*, 1998a; Murphy *et al.*, 1998; Storey *et al.*, 1998; Zhi *et al.*, 1998; Caturegli *et al.*, 2000).

1.3.5.3. CASE DEFINITION

The diagnosis of HGA requires the combination of an adequate history of tick exposure, suggestive clinical and laboratory findings, such as documented fever in the absence of specific findings during physical examination, abnormal hematological/ metabolic values and diagnosis confirmation by use of one or several specific laboratory tests.

The criteria for case definition of confirmed and probable infection by *A. phagocytophilum* are showed in table 11.

TABLE 11. Proposed case definition for human granulocytic anaplasmosis (adapted from Brouqui *et al.*, 2004).

Confirmed infection
Febrile illness with a history of a tick bite or exposure to tick-infested habitats <i>and</i> Demonstration of seroconversion or \geq four-fold change in antibody titer in acute and convalescent samples ^a <i>or</i> Positive PCR result with subsequent sequencing of the amplicons demonstrating <i>Anaplasma</i> -specific DNA ^b <i>or</i> Isolation of <i>A. phagocytophilum</i> in culture
Probable infection
Febrile illness with a history of a tick bite or exposure to tick-infested habitats <i>and</i> Presence of a stable antibody titer in acute and convalescent samples if titer >four-fold above the cut-off value ^c <i>or</i> Positive PCR result without sequence confirmation ^d <i>or</i> Presence of intracytoplasmic morulae in neutrophils

^aBy indirect immunofluorescence antibody test with *A. phagocytophilum* antigen; ^bThe American Society of Microbiology's Task Force on Consensus Approach for Ehrlichiosis considers positive PCR alone (without other laboratory support) to represent probable laboratory evidence of HGA (Walker *et al.*, 2000); ^cA cut-off value of 1:80 is currently used; ^dWith *A. phagocytophilum* species-specific primers.

1.3.6. TREATMENT

Since it is difficult to predict whether patients with *A. phagocytophilum* infection will experience a mild or severe clinical course, prompt institution of antibiotic therapy is advocated for all individuals who are symptomatic and suspected of having HGA (Bakken & Dumler, 2006; Chapman *et al.*, 2006; Wormser *et al.*, 2006a). Specific laboratory tests that confirm clinical suspicion are generally not available in the acute care setting, making empiric antibiotic therapy necessary pending the results of confirmatory tests. Table 12 shows the recommended antibiotic therapy for HGA.

Tetracyclines have been traditionally considered the first-line antibiotics for treatment of HGA, based on clinical efficacy and uniform *in vitro* susceptibility of *A. phagocytophilum* strains for these compounds (Bakken *et al.*, 1994; Dumler & Bakken, 1995; Aguero-Rosenfeld *et al.*, 1996; Bakken *et al.*, 1996c; Walker & Dumler, 1996; Klein *et al.*, 1997; Dumler & Bakken, 1998; Horowitz *et al.*, 2001; Maurin *et al.*, 2003; Branger *et al.*, 2004). Doxycycline hyclate is the treatment of

choice due to its excellent pharmacokinetic properties and less frequent gastric intolerance compared with other tetracycline derivatives (Bakken & Dumler, 2006). It also has the advantage of showing additional activity against *B. burgdorferi* (Bakken & Dumler, 2006; Wormser *et al.*, 2006a), covering potential coinfections in areas where both LB and HGA are endemic. Although broad-use of tetracyclines derivatives is typically contraindicated during pregnancy, its use is advocated in life-threatening situations (Chapman *et al.*, 2006). Moreover, the American Academy of Pediatrics Committee on Infectious Diseases has revised its recommendations in 1997 and precluded limited doxycycline courses that do not pose a substantial risk for tooth staining, as the preferred antibiotic treatment for children of any age diagnosed with clinically apparent HGA, RMSF or HME (Chapman *et al.*, 2006). In fact, doxycycline therapy has been successfully used for treatment of a newborn with HGA (Horowitz *et al.*, 1998c) and a 5-year-old child, who had simultaneous LB (Moss & Dumler, 2003).

TABLE 12 – Recommended adult and pediatric antibiotic treatment for HGA (adapted from Bakken & Dumler, 2006; Wormser *et al.*, 2006a).

Antibiotic	Dose ^a		Duration (days)
	Adults	Children	
Doxycycline hyclate ^b	100 mg i.v. or p.o.q 12h ^c	2 mg/Kg p.o.q 12h (max. 100 mg/dose) ^d	5-14
Rifampin ^e	300 mg p.o.q 12h	10 mg/Kg p.o.q 12h (max. 300 mg/dose)	7

^ai.v. Intravenous administration, p.o. Oral administration; ^bIneffective for HB; ^cA treatment of 10 days is usually recommended for adults with HGA or 14 days if coinfection with *B. burgdorferi* is suspected; ^dChildren ≥ 8 years-old may be treated with a 10-day course. Children > 8 years-old are recommended to receive an abbreviated treatment of 4–5 days (i.e., for 3 additional days after resolution of fever). If concomitant LB is suspected, administration of amoxicillin (50 mg/kg per day in 3 divided doses [maximum of 500 mg per dose]) or cefuroxime axetil (30 mg/kg per day in 2 divided doses [maximum of 500 mg per dose]) is recommended at the conclusion of doxycycline treatment to complete a 14-day total course of antibiotic therapy; ^eIneffective therapy for LB and HB.

In vitro studies also showed that rifamycins have excellent activity against *Anaplasma* species (Klein *et al.*, 1997; Horowitz *et al.*, 2001; Maurin *et al.*, 2003; Branger *et al.*, 2004). This group of antibiotics is regarded as an alternative therapy for patients in whom tetracyclines use are contraindicated or limited, such as pregnant or lactating women, children younger than 8 years of age if not seriously ill, and intolerant or allergic individuals. Rifampin has already been used successfully in a small number of pediatric patients and pregnant women (Buitrago *et al.*, 1998; Dumler & Bakken, 1998; Krause *et al.*, 2003). However, the use of rifampin should be considered

with caution because of the possibility of rapid selection of resistant microbial populations, as has been demonstrated for other bacterial species [(Enright *et al.*, 1998; Heep *et al.*, 1999) in Maurin *et al.*, 2003]. Other compounds such as fluoroquinolones have also showed *in vitro* activity against *A. phagocytophilum*, although further clinical data is needed to define a safe alternative to tetracyclines (Klein *et al.*, 1997; Horowitz *et al.*, 2001; Maurin *et al.*, 2003; Branger *et al.*, 2004). For example levofloxacin, one of the most active fluoroquinolones against *A. phagocytophilum*, has been recently implicated in poor *in vivo* activity with the report of a clinical and microbiological relapse after completion of treatment (Wormser *et al.*, 2006b). Moreover, a *gyrA*-mediated resistance in the related species *E. canis* and *E. chaffeensis* that likely corresponds to a single amino acid difference in the GyrA protein in *A. phagocytophilum*, has recently been described (Maurin *et al.*, 2001).

In vitro investigations of several clinical isolates have demonstrated that *A. phagocytophilum* is resistant to the majority of broad-spectrum antimicrobials such as β -lactam compounds (ampicillin, amoxicillin, ceftriaxone), macrolides (azithromycin, clarithromycin, erythromycin, telithromycin), amikacin, sulfamethoxazole-trimethoprim and chloramphenicol (Klein *et al.*, 1997; Horowitz *et al.*, 2001; Maurin *et al.*, 2003; Branger *et al.*, 2004). The lack of a peptidoglycan layer or LPS in *A. phagocytophilum* outer membrane (Lin & Rikihisa, 2003; Hotopp *et al.*, 2006) is a possible explanation for β -lactam resistance. This situation is similar to that of mycoplasmas, which are also naturally resistant to all β -lactam compounds (McCormack, 1993 in Branger *et al.*, 2004). Macrolide resistance is probably the result of point mutations that have been observed in *A. phagocytophilum* 23S rRNA genes, and are known to confer resistance in other bacteria (Vester & Douthwaite, 2001 in Maurin *et al.*, 2003; Branger *et al.*, 2004). Amoxicillin, azithromycin, and erythromycin, as well as the cephalosporin ceftriaxone, are agents that may be used to treat *B. burgdorferi* infection (Wormser *et al.*, 2006a). Thus, persistent symptoms or slow resolution of LB after treatment with β -lactam or macrolides antibiotics may suggest underlying HGA. The same is applicable for HB that uses atovaquone in combination with azithromycin as one of the treatment options (Wormser *et al.*, 2006a).

A close clinical follow-up is recommended to ensure that patients respond as expected to therapy. Although severely ill individuals might require longer periods before clinical improvement is noted, especially if they have dysfunction of multiple organs, administration of effective HGA therapy usually results in defervescence within 24 to 48 hours (Bakken *et al.*, 1994;

Dumler & Bakken, 1995; Agüero-Rosenfeld *et al.*, 1996; Bakken *et al.*, 1996c; Walker & Dumler, 1996; Buitrago *et al.*, 1998; Dumler & Bakken, 1998; Horowitz *et al.*, 1998c; Krause *et al.*, 2003; Bakken & Dumler, 2006). Thus, patients who fail to respond to treatment within this time frame should be reevaluated for alternative diagnosis, including the possibility of coinfections. Although tetracyclines are active against *B. burgdorferi* but not *Babesia* spp., rifampin is inactive against both (Wormser *et al.*, 2006a).

1.3.7. PREVENTION

The best currently available method for preventing infection with *A. phagocytophilum*, as for other tick-borne pathogens, is to avoid tick exposure. Strategies aimed to reduce vector densities in backyards and regular application of ectoparasite control on pets help to control infestations of domestic environments. Moreover, the use of both protective clothing and tick repellents when entering tick-infested habitats are also important measures recommended to reduce the risk of infection.

Long-sleeved shirts tucked into pants, long pants tucked into socks, and closed-toe shoes are helpful in preventing ticks from reaching the skin and attaching. The selection of khaki neutral-colored clothing is preferred to allow a background contrast with any eventual crawling ticks. Various over-the-counter products containing DEET (*N,N*-diethyl-*m*-toluamide) are available for topical application on exposed skin. The optimal concentration ranges from 15%-35%, which allows high performance and a high margin of safety. There is no evidence that concentrations >50% are more efficient or provide longer protection period. The timing of reapplication depends on the specific preparation utilized. Some products may provide up to 12 hours protection from one application, but long-acting formulations are being developed (Salafsky *et al.*, 2000). Neurologic manifestations in children after excessive application of DEET-containing repellents have been reported (CDC, 1989), but the compound appears to be safe when used as directed in the product labels, even for young children 12 months old (Fradin, 1998; Qiu *et al.*, 1998; Koren *et al.*, 2003). Products containing Permethrin can be used to treat outer clothing (e.g., shirts and pants). It should be applied according to label directions in a well-ventilated area and clothing must completely dry before being worn. This chemical is nontoxic to humans although it is not licensed for direct application to the skin.

In tick-infested habitats it is also important to avoid wooded or grassy areas and walk on cleared trails. Brushing against tall grass and other vegetation is regarded as a risk factor (Lane *et al.*, 2004). This practice is particularly essential during periods of peak tick activity (i.e., late spring and summer) but should be followed throughout the year, regardless of the season. Frequent visual inspection of skin and clothes may help to identify crawling ticks preventing attachment. Limited data exist regarding the interval of *A. phagocytophilum* transmission after tick attachment, but animal studies indicate that 24-48 hours might elapse before effective pathogen transmission (Hodzic *et al.*, 1998; Katavolos *et al.*, 1998; Des Vignes *et al.*, 2001); transmission has been demonstrated under experimental circumstances in as little as 4 hours after attachment. The risk of *A. phagocytophilum* infection and other tick borne-diseases can therefore be reduced substantially by performing daily inspections of entire body and by promptly removing attached ticks after outdoor activities.

Attached ticks should be removed preferably by grasping with tweezers or fine-tipped forceps close to the skin and gently pulling in a constant and steady motion. Folk methods of removing ticks, such as using lighted cigarettes, petroleum jelly, fingernail polish, etc, should be avoided because they may increase the risk of agent transmission by increasing tick salivation or body damage and consequent fluid leaking into the wound (Needham, 1985; Boer & Van den Boggard, 1993). If a portion of the ticks mouth parts remains embedded in the skin, only topical disinfection of the site is suggested, because attempts to remove this material can cause tissue damage and are unnecessary as the risk of agent transmission is unaffected. Ticks that have been removed should not be crushed between the fingers to prevent contamination. After tick removal, the bite wound should then be disinfected and hands should be washed to avoid potential conjunctival contamination. Although there is a potential risk of infection, most tick bites are uncomplicated and result only in benign cutaneous inflammatory reactions that may be pruritic for a few days. Sometimes a granuloma may develop, supposedly as a result of mouthparts being retained at the feeding site (Parola & Raoult, 2001a).

The prophylactic potential of antimicrobials have been studied in animal model of granulocytic anaplasmosis (Blagburn *et al.*, 2004; Massung *et al.*, 2005b) but its usefulness for humans has not been demonstrated. In general, the use of antibiotics is strictly recommended for clinically ill individuals.

1.4. ANAPLASMATACEAE IN PORTUGAL

The presence of Anaplasmataceae family member species in Portugal has been long recognized starting with the 1943 description of bovine and ovine anaplasmosis due to *A. marginale* (Silva Leitão, 1943). Today the disease is still regarded as a veterinary problem that affects flocks and herds across the country, with the highest prevalence found in Alentejo region, Southern mainland Portugal (J Gomes, personal communication).

In 1990, Filipe and coworkers described an *Ehrlichia*-like organism in the hemolymph of *Rhipicephalus sanguineus* ticks parasitizing a domestic dog from Setúbal District (Filipe *et al.*, 1990). The agent was later maintained in a *R. sanguineus*-laboratory reared colony by intracelomic inoculations and found to be antigenically similar to *E. canis* (Santos, 1997). Additional studies, report that *E. canis* seroprevalence ranges from 45.4 - 54.5% in stray dogs from this same geographic area (Silveira, 1992; Bacellar *et al.*, 1995). More recently, *E. canis* DNA was detected in a dog hospital population in the Algarve region, Southern mainland, definitively confirming the association of this Anaplasmataceae family member with canine disease in Portugal (Alexandre, 2006). Due to the association of *E. canis* and *R. sanguineus*, one of the most prevalent tick species in the region (Caeiro, 1999), it is expected that canine monocytic ehrlichiosis occurs broadly across the country, especially in the Southern regions.

The existence of other Anaplasmataceae member species and their potential involvement in human disease was first suggested by David de Morais and coworkers (1991). The authors described a case of febrile illness without rash, accompanied by leucopenia, thrombocytopenia, mild anemia and increase of hepatic enzymes in a 21-year-old man from Évora District, Alentejo region. The patient worked in an office and had no regular contact with animals and no history of tick bite, although he had visited a farm two weeks before the onset of symptoms in January 1991. Serological tests for typhoid fever, brucellosis, Mediterranean spotted fever (MSF), and LB were negative. Human monocytic ehrlichiosis was suggested by a >four-fold decrease in IFA titer against *E. chaffeensis* antigen in two consecutive samples collected 15 days after the onset and two months later, showing an antibody decrease from 1024 to 128. Three months after the onset of disease, the serum titer against *E. chaffeensis* was 64. A high, stable IFA titer of 512 against *C. burnetii* phase II antigen was also observed in all three serum samples (David de Morais *et al.*, 1991, 1992b). Based on serology, another patient with a febrile illness associated with *E*

chaffeensis antibody was described by Rodrigues and coworkers (1998). However, neither agent isolation nor convincing DNA detection have been achieved in human, animal, or tick samples to reinforce these data.

Additionally, a study performed in Madeira Island designed to clarify the importance of *I. ricinus* as vector of tick-borne agents showed for the first time the presence of *A. phagocytophilum* DNA in this tick species (Núncio *et al.*, 2000). The finding was not completely unexpected since the agent was long known to occur in Europe (Gordon *et al.*, 1932) and had been previously detected in *I. ricinus* from another Mediterranean region (Cinco *et al.*, 1997) but this observation highlighted the possible role of Anaplasmtaceae in Public Health, and added to the list of *Ixodes*-borne agents in Portugal potentially involved in human diseases.

I. ricinus is described as a hygrophilic tick [(Daniels *et al.*, 1977; Gray, 1991; EUCALB) in Baptista, 2006] dispersed throughout Portugal with a patchy geographic distribution mainly influenced by environmental determinants such as climate (temperature, humidity and precipitation), landscape fragmentation, and landscape composition (open areas, mixed and deciduous forests) (Baptista, 2006). Although it has been reported from all districts of mainland Portugal (Dias *et al.*, 1994; Caeiro, 1999), when compared with other species such as *R. sanguineus* and *Dermacentor marginatus*, it has a more restricted distribution, with the highest prevalence registered in rural regions (Baptista, 2006). Moreover, *I. ricinus* is also present in the Atlantic Archipelagos of Madeira and Açores, essentially in Madeira and Pico Islands, respectively [(Dias, 1992; Vieira, 1997) in Núncio, 2001; Almeida, 1996]. In some areas with favorable ecological conditions, it is of interest that this tick is a dominant species, as in Mafra (Lisboa District, Estremadura region, mainland Portugal) and Madeira Island (Almeida, 1996; Baptista, 2006; MM Santos-Silva, personal communication). As observed in other countries, here *I. ricinus* is a permissive feeder, parasitizing a broad-range of mammalian hosts from at least six different orders, including Artiodactyla, Rodentia, Soricomorpha, Erinaceomorpha, Carnivora, and Lagomorpha (Tendeiro, 1962 in Dias *et al.*, 1994; Dias *et al.*, 1994; Bacellar, 1996; Caeiro, 1999; Estrada-Peña & Santos-Silva, 2005). Human parasitism by this species is also commonly reported and is associated with expected Public Health consequences (Dias *et al.*, 1994; Bacellar, 1996; Caeiro, 1999; MM Santos-Silva, personal communication). To date, seven species of tick-borne bacteria have either been isolated or detected in Portuguese *I. ricinus*, and some are already associated with human disease: *Borrelia lusitaniae*, *B. valaisiana*, *B. afzelii*, *B. garinii*, *B. burgdorferi* s.s., and *R. helvetica*, beside *A. phagocytophilum* (Núncio *et al.*, 1993;

Matuschka *et al.*, 1994, 1998; Bacellar *et al.*, 1999a; De Michelis *et al.*, 2000; Nuncio *et al.*, 2000; Nuncio, 2001; Baptista *et al.*, 2004; Baptista, 2006). It is worth mentioning that the first Portuguese isolation of *B. burgdorferi s.l.* from this tick vector reported by Nuncio and coworkers (1993), was later identified as a new species, *B. lusitaniae* (Le Flèche *et al.*, 1997). The first human clinical case of LB was reported in Alentejo region by David de Morais and coworkers (1989), and this was followed by several other reports from the same area and other parts of the country (David de Morais *et al.*, 1992c, 1994; Collares-Pereira & Franca, 2000; Nuncio, 2001; Baptista, 2006). The research investment in LB revealed its national importance as a tick-borne disease, and in 1999, LB was included in the list of national notifiable diseases (<http://www.dgsaude.pt>). Despite the pathogenic potential of several *B. burgdorferi s.l.* species that circulate in the country, so far only three species are linked to human disease, including *B. garinii*, *B. afzelii* and *B. lusitaniae*, the latter never before reported as human pathogen (Collares-Pereira *et al.*, 2004; Baptista, 2006). *R. helvetica* is another example of an *Ixodes*-borne bacterium that has recently been linked to human pathology after its detection in French patients with febrile illnesses (Fournier *et al.*, 2000) although it has not yet been identified as a cause of disease in our country. Moreover, another *Ixodes*-borne disease, HB caused by *Babesia divergens*, was reported in a splenectomized patient (Centeno-Lima *et al.*, 2003).

Given to i) the presence of *I. ricinus* in several regions of the country and its known role as a primary European vector of *A. phagocytophilum*, ii) the existence of the *A. phagocytophilum* itself in Portugal, and iii) the substantial opportunity for human exposure to the vector tick, proven by occurrence of *Ixodes*-borne diseases such as LB, the hypothesis that human *A. phagocytophilum* infections and HGA disease in Portugal were considered, further stimulating the investigation described in the following chapters. In order to promote a better awareness of tick-borne diseases, especially that caused by *A. phagocytophilum*, two revision articles were published and directed toward the practicing medical community (Appendix 1 and 2).

CHAPTER II

EXCHANGE TECHNOLOGY IN ANAPLASMATACEAE FIELD

2.1. DISTRIBUTION OF "*EHRlichia WALKERi*" IN *IXODES RICINUS* (ACARI: IXODIDAE) FROM THE NORTHERN PART OF ITALY*

MATSUMOTO KOUTARO, ANA SOFIA SANTOS, J STEPHEN DUMLER AND PHILIPPE BROUQUI

RESEARCH ARTICLE

JOURNAL OF MEDICAL ENTOMOLOGY 2005; 42(1):82-3

* Article published in collaboration with the Unité des Rickettsies, Faculté de Médecine, Marseille, France

SHORT COMMUNICATION

Distribution of 'Ehrlichia walkeri' in *Ixodes ricinus* (Acari: Ixodidae) from the Northern Part of Italy

MATSUMOTO KOUTARO,¹ ANA SOPHIA SANTOS,² J. STEPHEN DUMLER,³
AND PHILIPPE BROUQUI^{1,4}

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ABSTRACT The prevalence of 'Ehrlichia walkeri' in *Ixodes ricinus* in northern Italy was studied. A total of 456 ticks were collected from seven places around Belluno, and 292 living ticks were examined using polymerase chain reaction (PCR). Nineteen ticks were positive for *gltA* of 'E. walkeri', and the prevalence rate for each place ranged from 0 to 12.8%. The disparity of prevalence rates among areas examined suggests that 'E. walkeri' is not widespread in ticks and requires an animal host for its maintenance in nature.

KEY WORDS 'Ehrlichia walkeri', *gltA*, *Ixodes ricinus*, Italy

'EHRlichia WALKERi' IS A NEWLY detected ehrlichial species from *Ixodes ricinus* ticks for which the medical importance is yet unknown (Brouqui et al. 2003). Sequence analysis of 16S rRNA genes reveals that 'E. walkeri' is closely related to *E. ruminantium*, the agent of heartwater disease in ruminants, and is 99% related to an *Ehrlichia*-like agent described as Schotti variant (Brouqui et al. 2003). 'E. walkeri' (Schotti variant) was detected in the Netherlands (Schouls et al. 1999) and in the Baltic region of Russia (Aleksiev et al. 2001), with a prevalence of 6.6 and 7.1%, respectively. In the Belluno area in Italy, it was reported to be present in 10 of 357 ticks tested (Brouqui et al. 2003). Transmission of *Ehrlichia* spp. in ticks is shown to occur transstadially but not transovarially (Groves et al. 1975, Ogden et al. 1998), suggesting that a reservoir needs to be present to maintain the organism in nature. This observation predicts that these agents are not uniformly present in all ticks but are found in areas restricted by the presence of both vector and reservoir. To confirm this hypothesis, we collected ticks in seven different biotopes located around Belluno (northern Italy) where 'E. walkeri' was originally detected and studied the prevalence of the organism in ticks using polymerase chain reaction (PCR).

Materials and Methods

Collection of Ticks. Ticks were collected from seven places in and near Belluno in northern Italy, where a previous study has detected this organism

(Brouqui et al. 2003) by flagging during 2 consecutive days in April 2003 (Fig. 1). Exact locations were determined by GPS values of each place. *I. ricinus* collected from three areas (sites 1-3, Losego; sites 4-6, Farra d'Alpago; site 7, Sospirolo) were used for study. Ticks were transported alive to Marseille and tested by PCR.

DNA Extraction and PCR. Because we expected to assess isolation of the bacteria, ticks were disinfected by immersion in 70% ethanol solution for 5 min. After two rinses with sterile water, DNA was extracted using the QIAamp DNA Mini Kit (Qiagen, Courtaboeuf, France) according to the manufacturer's manual and eluted in a final volume of 50 μ l. The extracted DNA was screened by PCR specific for *gltA* of 'E. walkeri' (Inokuma et al. 2001). The primer pairs Wf319 (5'-CTAAGGTGTGCTATTTTGTGTC-3') and Wr474 (5'-CTTAGCGACAAGATCATTAC-3') were designed based on *gltA* sequences of 'E. walkeri' (Gene Bank accession number AYO98730) (Brouqui et al. 2003) and confirmed for specificity in silico by BLASTN analysis (National Center for Biotechnology Information: <http://www.ncbi.nlm.nih.gov/blast/>). PCR was performed in a total volume of 25 μ l of master mix consisting of 12.5 pmol of each primer, 0.5 μ l of Elongase Enzyme Mix (Invitrogen, Carlsbad, CA), 20 mM of each dNTP, and 1.8 mM MgCl₂, and carried out under the following conditions: 94°C for 3 min, 45 cycles of 94°C for 30 s, 55°C for 30 s, 68°C for 90 s, and 68°C for 7 min. DNA from noninfected lice was used as the control of each PCR. PCR products were applied for electrophoresis on a 1% agarose gel and visualized under UV illumination after staining with ethidium bromide.

Sequencing. Several positive samples were randomly chosen for sequencing using the method described previously (Brouqui et al. 2003) with modifications to confirm the specificity of PCR. Briefly, PCR

¹Unité des Rickettsies, Faculté de Médecine, 13385 Marseille, France.

²Centro de Estudos de Vetores e Doenças Infecciosas, Instituto Nacional de Saúde Drive Ricardo Jorge, Aguas de Moura, Portugal.

³Department of Pathology, The Johns Hopkins Medical Institutions, Baltimore, MD 21205.

⁴E-mail: philippe.brouqui@medecine.univ-mrs.fr.

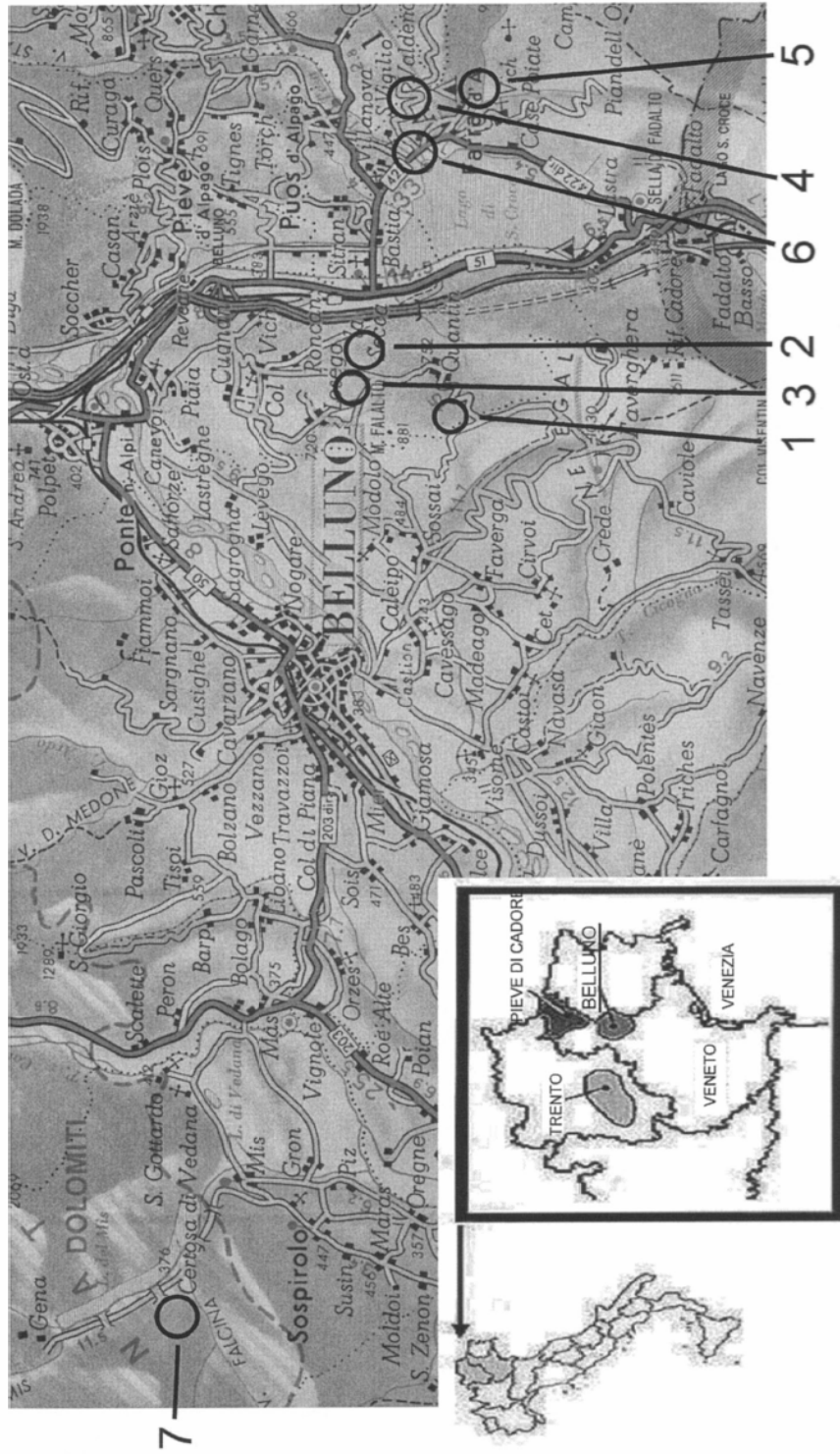


Fig. 1. Map of Belluno and suburbs in northern Italy. Numbers show the sites where ticks were collected. Sites 1-3 were in Losego, an area with wild field covered with short grasses where there were pasture and farms with sheep and goats. Sites 4-6 were in Farra d'Alpago, an area of small abandoned houses under big trees and high grass. Site 7 was in Sospirolo, a remote camping area close to a lake and distant from houses.

These facts suggest that 'E. walkeri' is not widely spread in ticks and that some reservoir animals are needed for maintenance. The identical prevalence rate in nymphs and adults suggests a stronger likelihood for a small mammal reservoir such as *Apodemus* or *Clethrionomys*. Trapping and animal surveillance are needed in these areas to obtain more information, particularly because reservoirs are likely to live in close contact with humans.

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2.2. DETECTION OF A NON-PATHOGENIC VARIANT OF *ANAPLASMA PHAGOCYTOPHILUM* IN *IXODES RICINUS* FROM LA RIOJA, SPAIN*

A. PORTILLO, A.S. SANTOS, S. SANTIBÁÑEZ, L. PÉREZ-MARTÍNEZ, J.R. BLANCO, V. IBARRA, J.A. OTEO

SHORT REPORT

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Detection of a Non-Pathogenic Variant of *Anaplasma phagocytophilum* in *Ixodes ricinus* from La Rioja, Spain

A. PORTILLO,^a A.S. SANTOS,^b S. SANTIBÁÑEZ,^a L. PÉREZ-MARTÍNEZ,^a
J.R. BLANCO,^a V. IBARRA,^a AND J.A. OTEO^a

^aÁrea de Enfermedades Infecciosas, Hospitales San Millán-San Pedro-de La Rioja, Logroño, (La Rioja), Spain

^bCentro de Estudos de Vectors e Doenças Infecciosas, Instituto Nacional de Saúde Dr. Ricardo Jorge, Aguas de Moura, Portugal

ABSTRACT: Our aim was to identify variants of *Anaplasma phagocytophilum* 16S rRNA gene sequences among products amplified from *Ixodes ricinus* collected in La Rioja, Spain. *A. phagocytophilum* AP-variant 1, reported as non-pathogenic, was detected in 12 samples (two adults and ten nymphs). This finding could justify the low incidence of human anaplasmosis in our area, despite the high prevalence of *A. phagocytophilum* in ticks.

KEYWORDS: *Anaplasma phagocytophilum*; human anaplasmosis; *Ixodes ricinus*; ticks; AP-Variant 1; Spain

INTRODUCTION

Human anaplasmosis (HA), previously designated as human granulocytic ehrlichiosis or HGE,¹ is an emerging tick-borne zoonosis transmitted by *Ixodes* ticks, specifically *Ixodes ricinus* in Europe. High prevalence of *Anaplasma* (formerly, *Ehrlichia*) *phagocytophilum* infection in *I. ricinus* from the North of Spain (La Rioja and Basque Country) has been reported.^{2,3} However, to date, only sporadic cases of HA in Spain have been reported.^{4,5} One hypothesis is that only a subset of the *A. phagocytophilum* strains that exist in nature cause human disease.^{6–8} As little information exists about the host range and pathogenicity of different strains or variants of *A. phagocytophilum* in Europe, the objective of our study was to identify possible variants of *A. phagocytophilum* in *I. ricinus* collected in La Rioja (Spain) according to the sequence of 16S rRNA gene.

Address for correspondence: José A. Oteo, Área de Enfermedades Infecciosas. Hospitales San Millán-San Pedro-de La Rioja. Avda. Viana, No. 1. 26001, Logroño (La Rioja), Spain. Voice: 34 941 297275; fax: 34 941 297267.
jaoteo@riojasalud.es

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MATERIAL AND METHODS

Two hundred and forty eight *I. ricinus* were tested for the pathogen. A total of 90 specimens (84 adults and 6 nymphs) were removed from cows (*Bos taurus*) in Villoslada de Cameros, a rural mountainous area from La Rioja, during November 2003. Since the collection from bovines (or any other potential animal reservoir) would favor the identification of *A. phagocytophilum* strains to which this host were susceptible and could not be representative of tick population, samples were also collected from vegetation. For this reason, in 2004 a total of 158 questing *I. ricinus* (54 adults and 104 nymphs) collected from six different sites of our region were also analyzed.

All ticks were classified according to standard taxonomic keys. Specimens were kept in 70% ethanol solution at room temperature and individually processed. Genomic DNA extraction for PCR was performed as described before.^{9,10} Ticks were taken from the 70% ethanol solution, washed with sterile water, air dried and boiled for 20 min in 100 μ L of 0.7 M ammonium hydroxide to free the DNA. After cooling, the vials with the lysed material were left open in a laminar airflow cabinet for 20 min at 90°C to evaporate the ammonia. The tick lysates were either used directly for PCR or stored at -20°C until used. DNA samples were pooled for initial PCR screening of 16S rRNA gene from *A. phagocytophilum* under conditions previously reported.¹¹ Individual samples corresponding to vials that yielded positive PCR results were additionally tested with the same primers. In addition, another pair of primers that targets the *msp2* gene was used to confirm all individual specimens that showed positive PCR results.¹² Quality control included both positive (*A. phagocytophilum* Webster, kindly provided by Dr. Dumler, from The Johns Hopkins University School of Medicine, Baltimore, USA) and negative controls that were extracted and PCR amplified in parallel with all specimens. Negative controls consisted of sterile water instead of template DNA. Subsequent sequence analysis of both strands of each amplicon of 16S rDNA [Universidad de Alcalá de Henares (Spain)] were carried out. Homology of nucleotide sequences was determined through the BLAST National Centre for Biotechnology Information (NCBI).¹³

RESULTS

Products of the expected sizes were amplified from DNA of one of 6 nymphs removed from cows (16.6%) when tested with 16S rRNA and *msp2* primers (919 and 550 bp, respectively). *A. phagocytophilum* was not detected in adult ticks removed from cows. For ticks collected from vegetation, 9 of 104 questing nymphs (8.6%), and 2 of 54 unfed host-seeking adult ticks (3.7%) were infected with *A. phagocytophilum*. For these 11 samples, 16S rDNA and *msp2* PCR amplifications were achieved. No products were amplified from any of the negative control samples.

Sequence homology searches of 16S rRNA gene revealed that these 12 sequences analyzed were identical, and all of them differed from that of the 16S rRNA sequence of a human *A. phagocytophilum* strain (GenBank accession no. U02521) by only two nucleotides: G and A in positions 76 and 84, respectively. These changes corresponded to the AP-variant 1 strain of *A. phagocytophilum* (GenBank accession no. AY193887) previously reported as potentially non-pathogenic in USA.^{6,8} These

specific nucleotide substitutions were not observed in our positive control (human-infective *A. phagocytophilum*).

DISCUSSION

AP-variant 1 has been previously found in *I. scapularis* ticks and deer blood in the USA but never from a confirmed human infection.^{14,15} Identical portions of 16S rRNA gene from European *A. phagocytophilum* are available in GenBank. Sequences that showed 100% of identity to AP-variant 1 were derived from *I. ricinus* ticks in Sweden and Germany, and from roe deer in Switzerland and Slovenia (GenBank accession nos. AJ242784; AF136713; AY281806; AF384212; AF481850, among others).^{16–20} The impact of *A. phagocytophilum* 16S rRNA gene variants has been a matter of debate. The sequence variability in one gene is not sufficient to determine the genetic diversity of a certain strain. It is necessary to cultivate some of the *A. phagocytophilum* strains and to compare them in animal models in order to unravel the biological significance of the observed genetic differences. The latest advances in this field were presented at the Fourth International Conference on Rickettsiae and Rickettsial Diseases held in Logroño, Spain.^{21,22}

In conclusion, AP-variant 1 strain of *A. phagocytophilum* in *I. ricinus* has been detected for the first time in Spain. To date, this variant has not been associated with human disease, and its presence may belie the few clinical cases of HA on the peninsula in contrast with the high prevalence of *A. phagocytophilum* infection found in *I. ricinus* in this region. To our knowledge, this is the first study in which *A. phagocytophilum* DNA sequences derived from ticks in Spain were compared. Further studies are needed to compare *A. phagocytophilum* DNA sequences derived from ticks and HA patients in our region.

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CHAPTER III

ANAPLASMA PHAGOCYTOPHILUM IN TICKS (ACARI:IXODIDAE)

3.1. DETECTION OF *ANAPLASMA PHAGOCYTOPHILUM* DNA IN *IXODES* TICKS (ACARI:IXODIDAE) FROM MADEIRA ISLAND AND SETÚBAL DISTRICT, MAINLAND PORTUGAL

ANA SOFIA SANTOS, MARGARIDA SANTOS-SILVA, VICTOR CARLOS ALMEIDA, FÁTIMA BACELLAR, AND JOHN STEPHEN DUMLER

RESEARCH ARTICLE

EMERGING INFECTIOUS DISEASES 2004; 10(9):1643-8

Detection of *Anaplasma phagocytophilum* DNA in *Ixodes* Ticks (Acari: Ixodidae) from Madeira Island and Setúbal District, Mainland Portugal

Ana Sofia Santos,* Maria Margarida Santos-Silva,* Victor Carlos Almeida,† Fátima Bacellar,* and John Stephen Dumler‡

A total of 278 *Ixodes* ticks, collected from Madeira Island and Setúbal District, mainland Portugal, were examined by polymerase chain reaction (PCR) for the presence of *Anaplasma phagocytophilum*. Six (4%) of 142 *Ixodes ricinus* nymphs collected in Madeira Island and 1 nymph and 1 male (2%) of 93 *I. ventraloi* collected in Setúbal District tested positive for *A. phagocytophilum* *msp2* genes or *rrs*. Infection was not detected among 43 *I. ricinus* on mainland Portugal. All PCR products were confirmed by nucleotide sequencing to be identical or to be most closely related to *A. phagocytophilum*. To our knowledge, this is the first evidence of *A. phagocytophilum* in ticks from Setúbal District, mainland Portugal, and the first documentation of *Anaplasma* infection in *I. ventraloi*. Moreover, these findings confirm the persistence of *A. phagocytophilum* in Madeira Island's *I. ricinus*.

Anaplasma phagocytophilum (formerly *Ehrlichia phagocytophila*, *E. equi*, and the human granulocytic ehrlichiosis agent [HGE agent] [1]) is well established as a worldwide tickborne agent of veterinary importance and is considered an emerging human pathogen. The initial reports of human disease caused by *A. phagocytophilum*, now called human granulocytic anaplasmosis, came from Minnesota and Wisconsin in 1994 (2,3). Human granulocytic anaplasmosis is an acute, nonspecific febrile illness characterized by headache, myalgias, malaise, and hematologic abnormalities, such as thrombocytopenia and leukopenia as well as elevated levels of hepatic transami-

nases (4). Since that first report, an increasing number of cases have been described, mostly in the upper Midwest and in the Northeast regions of the United States (5). Three years later, in 1997, acute cases of this disease were also described in Europe (6,7). Several serologic and polymerase chain reaction (PCR)-based studies described the wide distribution of *A. phagocytophilum* across Europe and in some parts of the Middle East and Asia (8–10). Nevertheless, confirmed cases of human granulocytic anaplasmosis are rare; most European cases are described in Slovenia (11), with only a few reports from other European countries (12) and China (13).

The ecology of *A. phagocytophilum* is still being defined, but the agent is thought to be maintained in nature in a tick-rodent cycle, similar to that of *Borrelia burgdorferi* (the agent of Lyme disease), with humans being involved only as incidental “dead-end” hosts (14–17). Exposure to tick bites is considered to be the most common route of human infection, although human granulocytic anaplasmosis has been reported after perinatal transmission or contact with infected animal blood (18,19). *A. phagocytophilum* is associated with *Ixodes* ticks that are known vectors, including *I. scapularis*, *I. pacificus*, and *I. spinipalpis* in the United States (15,20,21), *I. ricinus* mostly in southern, central and northern European regions (22–26), *I. trianguliceps* in the United Kingdom (27), and *Ixodes persulcatus* in eastern parts of Europe (28) and Asia (9).

In Portugal little information is available concerning the epidemiology of *A. phagocytophilum*; the agent was documented only once in *I. ricinus* ticks from Madeira Island (Núncio MS, et al, unpub data). However, the true prevalence and public health impact of *A. phagocytophilum*

*Instituto Nacional de Saúde Dr. Ricardo Jorge, Águas de Moura, Portugal; †Direcção Regional de Pecuária, Funchal, Portugal; and ‡Johns Hopkins University School of Medicine, Baltimore, Maryland, USA

RESEARCH

is likely underestimated since little research has been conducted on this bacterium in Portugal. In fact, seasonal outbreaks of enzootic abortions and unspecific febrile illness (commonly named pasture fever) in domestic ruminants, which could be attributable to *A. phagocytophilum*, have been known to breeders and veterinarians across the country for years. Thus, to expand knowledge of *A. phagocytophilum* in Portugal, a detailed investigation was initiated. The preliminary results concerning agent distribution are presented here. The purpose of this study was to investigate both the persistence of *A. phagocytophilum* on Madeira Island, where it was initially described, and the presence of the agent in *Ixodes* ticks from mainland Portugal.

Materials and Methods

Tick Sampling

During 2003 and the beginning of 2004, adults and nymphs were collected from one site on Madeira Island (site 1, Paúl da Serra–Porto Moniz) and from five different sites in the Setúbal District, mainland Portugal (site 2, Barris–Palmela; site 3, Baixa de Palmela; site 4, Picheleiros–Azeitão, site 5, Azeitão, site 6, Maça–Sesimbra) (Figure 1). Most ticks were unfed, actively questing arthropods; they were obtained by flagging vegetation on pastures and wooded areas bordering farms and country houses. In site 3, additional specimens were also collected from domestic cats (*Felis catus domesticus*). The ticks were identified by morphologic characteristics according to standard taxonomic keys (29,30).

Preparation of DNA Extracts from Ticks

Ticks were processed individually as described (25). Briefly, each tick was taken from the 70% ethanol solution used for storage, air dried, and boiled for 20 min in 100 μ L of 0.7 mol/L ammonium hydroxide to free DNA. After cooling, the vial with the lysate was left open for 20 min at 90°C to evaporate the ammonia. The tick lysate was used directly for PCR. To monitor for occurrence of false-positive samples, negative controls were included during extraction of the tick DNA (one control sample for each six tick samples, with a minimum of two controls).

PCR Amplification

DNA amplifications were performed in a Biometra T-3 thermoblock thermal cycler (Biometra GmbH, Göttingen, Germany) with two sets of primers: *msp465f* and *msp980r*, derived from the highly conserved regions of major surface protein-2 (*msp2*) paralogous genes of *A. phagocytophilum* (31), and *ge9f* and *ge10r*, which amplify a fragment of the 16S rRNA gene of *A. phagocytophilum* (3). PCR was performed in a total volume of 50 μ L that contained 1 μ mol/L of each primer, 2.5 U of Taq DNA

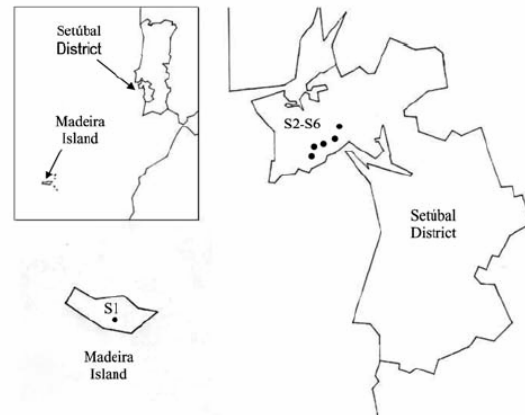


Figure 1. Collection sites in Madeira Island and Setúbal District, mainland Portugal. S, collection site.

polymerase (Roche, Mannheim, Germany), 200 μ mol/L of each deoxynucleotide triphosphate (GeneAmp PCR Reagent Kit, Perkin-Elmer, Foster City, CA), 10 mmol/L Tris HCL, 1.5 mmol/L MgCl₂, and 50 mmol/L KCl pH 8.3 (Roche), as described (3,31). Adult ticks were tested individually by using 5 μ L of DNA extract. Nymphs were pooled according to geographic site, up to a maximum of 10 different tick extracts per reaction, and 10 μ L of the pooled DNA was used for initial screening. All positive pools were confirmed in a second PCR round that used 5 μ L of original DNA extract from each nymph. PCR products were separated on 1.5% agarose by electrophoretic migration, stained with ethidium bromide, and visualized under UV light. Quality controls included both positive and negative controls that were PCR amplified in parallel with all specimens. To minimize contamination, DNA preparation with setup, PCR, and sample analysis were performed in three separate rooms.

DNA Sequencing and Data Analysis

Each positive PCR product was sequenced after DNA purification by a MiniElute PCR Purification Kit (Qiagen, Valencia, CA). For DNA sequencing, the BigDye terminator cycle sequencing Ready Reaction Kit (Applied Biosystems, Foster City, CA), was used as recommended by the manufacturer. Sample amplifications were performed with the forward and reverse primers used for PCR identification (3,31), with the following modifications: 25 cycles of 96°C for 10 s, 4°C below the melting temperature of each primer for 5 s, and 60°C for 4 min. Dye Ex 96 Kit (Qiagen) was used to remove the dye terminators. Sequences were determined with a 3100 Genetic Analyzer sequencer (Applied Biosystems). After review and editing, sequence homology searches were made by BLASTN

analysis of GenBank. Sequences were aligned by using ClustalX (32) with the neighbor-joining protocol and 1,000 bootstrap replications, and comparing with the 2 *msp2* paralogs of *A. phagocytophilum* Webster strain (AY253530 and AF443404), one *msp2* paralog of USG3 strain (AF029323), and with *A. marginale msp2* (AY138955) and *msp3* (AY127893) as outgroups. Dendrograms illustrating the similarity of *msp2*s were visualized with TreeView (33).

Results

A total of 278 *Ixodes* ticks were tested for *A. phagocytophilum* DNA, including 142 *I. ricinus* from Madeira Island and 43 *I. ricinus* and 93 *I. ventralloi* from Setúbal District. The site of collection, origin, and tick stage are shown in Table 1 and Figure 1. PCR performed with the *msp2* primers detected *A. phagocytophilum* DNA in seven pools of nymphs (six pools of 10 *I. ricinus* from site 1, Madeira Island, and one pool of 4 *I. ventralloi* from site 3, Setúbal District) and also in 1 male *I. ventralloi* from site 3, Setúbal District, as demonstrated by the characteristic 550-bp band. PCRs conducted on individual ticks that comprised positive pools confirmed the results and showed that only one nymph per positive pool contained *A. phagocytophilum* DNA (Tables 1 and 2). PCR test results were negative for all *I. ricinus* collected in the sites in Setúbal District. Overall, the infection rate was 6 (4%) of 142 for *I. ricinus* and 2 (2%) of 93 for *I. ventralloi*. Analysis based on direct amplicon sequencing showed the expected conserved 5' end followed by ambiguous sequences that corresponded to the hypervariable central region of *msp2*, as anticipated based on the presence of >52 *msp2* copies in the *A. phagocytophilum* HZ strain genome (34). Thus, for appropriate comparison and alignment, the *msp2* 5' sequences were edited from the positions where unambiguous reads could be determined and terminated 70 nt into the sequence at the approximate beginning of the hypervariable region. A similar alignment protocol for the

3' end of the *msp2* amplicons showed more ambiguous positions, which prohibited effective alignment and sequence determination. Thus, *msp2* sequence alignments depended upon approximately 70 nt 5' to the hypervariable region and were performed less for phylogenetic stratification of *A. phagocytophilum* in the ticks than to confirm that the amplified *msp2* sequences were not derived from other related *Anaplasma* or *Ehrlichia* spp. The nucleotide sequences determined for this 70-bp region amplified from all eight ticks showed 98.5%–85.7% similarity, 94.2%–86.9% similarity when compared to representative *msp2* sequences of *A. phagocytophilum* Webster and USG3 strains, and 63.7%–35.0% similarity when compared to *A. marginale msp2* and *msp3* sequences (Figure 2). Sequences obtained from the two *I. ventralloi* from mainland Portugal clustered together and separately from other *msp2* sequences obtained from *I. ricinus* on Madeira Island (Figure 2).

When amplified by using *rrs* primers ge9f and ge10r, compared to *A. phagocytophilum* U02521, sequences were 99% identical to two *I. ventralloi* (636/640 positions and 846/848 positions, respectively) on mainland Portugal and to three *I. ricinus* (836/841, 817/820, and 838/839 positions, respectively) on Madeira Island.

Discussion

This study constitutes part of a larger effort to investigate the distribution of *A. phagocytophilum* in various regions of Portugal. Our data provide supporting evidence that *A. phagocytophilum* is present in actively questing *I. ricinus* from Madeira Island and in *I. ventralloi* from Setúbal District, mainland Portugal.

We used two approaches for identifying *A. phagocytophilum* in ticks: 1) standard amplification of *rrs* that can have limited sensitivity because of a single copy in each bacterial genome, and 2) amplification of *msp2*, a gene for which as many as 52 paralogs are present in the *A. phagocytophilum* genome and for which detection sensitivity is

Table 1. Results of PCR to detect *Anaplasma phagocytophilum* DNA in ticks^a

Area	Site	Origin	<i>Ixodes ricinus</i>			<i>I. ventralloi</i>			Total ^c
			Nymphs ^b	F ^b	M ^b	Nymphs ^b	F ^b	M ^b	
Madeira Island									
Paúl da Serra–Porto Moniz	1	Vegetation	6/139	0/2	0/1	–	–	–	142
Setúbal District Portugal Mainland									
Barris–Palmela	2	Vegetation	0/1	0/5	0/7	–	–	0/1	14
Baixa de Palmela	3	Vegetation	0/2	0/2	0/2	1/15	0/6	0/7	34
		<i>Felis catus domesticus</i>	–	–	–	–	0/6	1/4	10
Picheleiros–Azeitão	4	Vegetation	–	0/2	0/2	0/12	0/9	0/18	43
Azeitão	5	Vegetation	–	–	0/1	–	–	0/1	2
Maçã–Sesimbra	6	Vegetation	–	0/10	0/9	0/1	0/4	0/9	33
Total ^c			142	21	22	28	25	40	278

^aPCR, polymerase chain reaction; F, female; M, male.

^bNumber of positives ticks/number of ticks examined.

^cTotal number of ticks examined.

RESEARCH

Table 2. PCR-positive results of ticks^a

Sites	No. positive nymphs	No. positive adults	Tick extracts codes
Madeira Island			
1	6	–	11; 60; 93; 118; 122; 137
Setúbal District Mainland Portugal			
3	1	1	160; 246 (respectively)

^aPCR, polymerase chain reaction.

enhanced (34). The pitfall of *msp2* amplification derives from targeting conserved sequences that flank a hypervariable central region, which results in amplicons with partial sequence ambiguity when cloning is not attempted before sequencing (31). These findings are highly unlikely to represent amplicon contamination since marked sequence diversity was observed, and since only a single tick from each pool was positive in each reaction. Although only limited data can be gleaned by this analysis, which interrogates only nucleic acids of small size, Casey et al. have shown that *msp2* “similarity” groups, reflecting clusters determined by a similar sequencing approach, can be useful in predicting phylogenetic relationships, particularly with reference to adaptation to specific host niches (35).

Madeira, the main island of the Madeira Archipelago, is located in the North Atlantic Ocean, about 800 km west of

the African continent and 1,000 km from the European coast. On this island, *I. ricinus* is the most abundant tick species and the only *Ixodes* tick that was found in this study. *A. phagocytophilum* was detected in 4% of *I. ricinus* collected in Paúl da Serra. Our results corroborate previous findings, although prevalence here is slightly lower than the 7.5% infection rate in ticks previously collected in similar areas (Núncio MS, et al., unpub data). These differences may be attributable to seasonal variations in *A. phagocytophilum* prevalence within reservoir hosts or ticks or to technical aspects of detection. Regardless, studies that use a greater number of samples and that are performed in different seasons, locations, and habitats will be needed to confirm the levels of infection. Nevertheless, these findings are generally similar to those described elsewhere in Europe, although prevalence rates can vary greatly with the origin of *I. ricinus* examined, ranging from a minimum of $\leq 1\%$ in the United Kingdom, France, and Sweden (23,24,36) to a maximum of 24% to 29% in northern Italy, Germany, and Spain (22,25,26). The public health importance of these findings still remains to be determined. *I. ricinus* is an exophilic, three-host tick known to bite several domestic animals and humans in Portugal (30). Therefore, we can assume that the presence of *A. phagocytophilum* on Madeira Island *I. ricinus* suggests a potential health threat to animals and humans and should be investigated.

Mainland Portugal is the most western region of Europe, with an area of 89,000 km², divided into 18 districts. Although *I. ricinus* is not the main tick species in mainland Portugal, it can be found across the country in habitats with favorable conditions. Focused in Setúbal District, to the south of the Tejo River, our study detected *I. ricinus* in all five sites chosen for field work: Barris; Baixa de Palmela; Picheleiros; Azeitão, and Maçã. In those sites, the distribution of *I. ricinus* was accompanied by another *Ixodes* species, *I. ventralloii*. Another ecologically interesting finding that should be further confirmed was that, although all of the *I. ricinus* from mainland Portugal tested negative, evidence of *A. phagocytophilum* was found in 2% of all *I. ventralloii*, including 5% collected in Baixa de Palmela. The *msp2* sequences identified in these two ticks were more closely related to each other than to any *msp2* sequence identified in ticks from Madeira Island. In contrast, *A. phagocytophilum msp2* diversity in *I. ricinus* from Madeira Island was broad and showed overlap with gene sequences identified in North American strains,

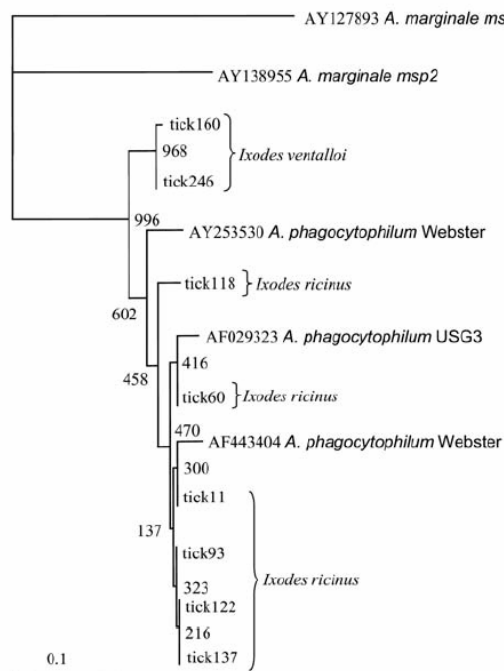


Figure 2. Dendrogram showing the phylogenetic relationships of the *msp2* sequences of the newly identified strains and other representative sequences from North American *Anaplasma phagocytophilum* strains (Webster strain–Wisconsin and USG3 strain–eastern United States), and from *A. marginale* Florida strain (*msp2* and *msp3*). Bootstrap values (out of 1,000 iterations) are shown at the nodes. Bar, substitutions/1,000 bp.

as observed for some *A. phagocytophilum* strains in the United Kingdom (35).

To our knowledge, this identification of *A. phagocytophilum* in ticks is the first from mainland Portugal and the first documentation of *Anaplasma* infection in *I. ventalloi*. This species is an endophilic, three-host tick well adapted to a broad range of habitats that vary from open, dry forest in semidesert Mediterranean areas to the mild humid conditions in the southern part of the British Isles. In Portugal, *I. ventalloi* infest a variety of small rodents, carnivores, and lizards but have not been found to feed on humans (30). *A. phagocytophilum* has already been reported in other ticks, besides the known vector species (37–41). The presence in alternate ticks is attributable to the existence of secondary maintenance cycles, in which *A. phagocytophilum* circulates between relatively host-specific, usually nonhuman-biting ticks and their hosts (38,39). Those additional cycles would buffer the agent from local extinction and help reestablish the primary cycles (38,39). Although this hypothesis might explain our results, the competency of *I. ventalloi* to act as vector for *A. phagocytophilum* has yet to be demonstrated. Moreover, the different average prevalences observed in each location suggest that *A. phagocytophilum* is not widely spread in ticks and that some reservoir animals or hosts are needed for its maintenance. Trapping and animal surveillance are needed to provide more information that could help to explain the biological importance of those findings.

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Ms. Santos works at the Centre of Vector-Borne and Infectious Diseases, National Institute of Health, Portugal. Her research has been focused on tickborne agents, mainly rickettsial agents with human health importance. She is pursuing a doctoral degree focused on human anaplasmosis and ehrlichiosis in Portugal.

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Address for correspondence: Ana Sofia Santos, Centro de Estudos de Vectores e Doenças Infecciosas, Instituto Nacional de Saúde Dr. Ricardo Jorge, Avenida da Liberdade 5, 2965-575 Águas de Moura, Portugal; fax: +351-265-912568; email: ana.santos@insa.min-saude.pt

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**3.2. TICKS PARASITIZING WILD BIRDS IN PORTUGAL: DETECTION OF
RICKETTSIA AESCHLIMANNII, *R. HELVETICA* AND *R. MASSILIAE***

MARIA MARGARIDA SANTOS-SILVA, RITA SOUSA, ANA SOFIA SANTOS, PEDRO MELO,
VICTOR ENCARNAÇÃO, FÁTIMA BACELLAR

RESEARCH ARTICLE

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Ticks parasitizing wild birds in Portugal: detection of *Rickettsia aeschlimannii*, *R. helvetica* and *R. massiliae*

Maria Margarida Santos-Silva · Rita Sousa ·
Ana Sofia Santos · Pedro Melo ·
Victor Encarnação · Fátima Bacellar

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Abstract From January 2002 to December 2004, 152 ticks were collected from 40 wild birds recovered in Santo André Natural Reserve and Monsanto Forestal Park, Portugal mainland. Five ticks species were identified from 22 species of birds, and new host record were provided for some species. In addition, 32 (21%) ticks were screened by PCR to detect infections with agents belonging to order Rickettsiales: *Anaplasma phagocytophilum*, *Ehrlichia chaffeensis*, and *Rickettsia* spp. PCR amplicons were obtained in 5 (15.6%) tick samples. *Rickettsia* DNA exhibiting *gltA* sequences similar to those of *Rickettsia aeschlimannii*, *R. helvetica* and *R. massiliae* were identified in *Hyalomma marginatum*, *Ixodes ventralloi* and in *Rhipicephalus turanicus*, respectively. This is the first report of rickettsiae infections in ticks collected from wild birds in Portugal. Giving the results presented above wild birds play an important role in the maintenance and dissemination of several tick species and associated rickettsiae.

Keywords Birds · Ticks · *Rickettsia* · Portugal

M. M. Santos-Silva (✉) · R. Sousa · A. S. Santos · F. Bacellar
Centro de Estudos de Vectors e Doenças Infecciosas, Instituto Nacional de Saúde Dr. Ricardo Jorge, Avenida da Liberdade 5, 2965-575 Águas de Moura, Portugal
e-mail: m.santos.silva@insa.min-saude.pt

P. Melo
Centro de Recuperação de Animais Silvestres/Parque Florestal Monsanto, Câmara Municipal de Lisboa, Lisboa, Portugal

V. Encarnação
Instituto da Conservação da Natureza, Lisboa, Portugal

Introduction

Wild birds are known as important reservoir of some pathogens and disseminators hosts of several arthropods, including ticks. Concerning rickettsial pathogens, birds have been described as reservoirs for *Coxiella burnetii* (Syruczek and Raska 1956) and as hosts for ticks infected with *Rickettsia sibirica* (Somov and Soldatov 1964 in Hubalek 2004) and *Anaplasma phagocytophilum* (Alekseev et al. 2001; Bjoersdorf et al. 2001; Daniels et al. 2002). In Portugal, wild birds were found parasitized by several tick species, namely *Hyalomma lusitanicum*, *H. marginatum*, *Ixodes canisuga*, *I. frontalis*, *Rhipicephalus pusillus*, *R. sanguineus*, *R. turanicus* and *Ornithodoros maritimus* (Dias 1994; Silva et al. 2001). However, there are no references about the occurrence of rickettsial infections neither on birds nor in the ticks they harbour. The aim of this work was to collect more data about tick species that parasitize wild birds in Portugal and to study the occurrence of rickettsial infections in those arthropods.

Material and methods

Between January 2002 and December 2004, wild birds were captured in mist nets at Santo André Natural Reserve, SANR (38°1'N, 8°49'W) and in the Bird Rehabilitation Centers of Monsanto Forest Park, MFP (38°44'N, 9°8'W) and Quercus Santo André, QSA (38°1'N, 8°49'W). Bird identification and tick collection were done according to Nature Preservation Institute (ICN) methodologies (CEMPA/ICN 1995; Silva et al. 2001). Ticks were identified by morphological characters using standard taxonomic keys (Cordas et al. 1993; Dias 1994) and separated by species, instars and sex. Ticks that were collected alive and/or in good conditions were preserved at -80°C and processed individually for DNA extraction, as previously described (Schouls et al. 1999). Briefly, each tick was washed in 70% ethanol solution, dried and boiled for 20 min in 100µl of 0.7 M ammonium hydroxide to free the DNA. After cooling, ammonia was evaporated for 20 min at 90°C. To monitor the occurrence of false-positive samples, laboratory ticks not infected were included during DNA extraction. As positive controls we have used *A. phagocytophilum* Webster strain, *E. chaffeensis* Arkansas strain, *R. conorii*. Tick lysate was used directly for PCR. DNA amplifications were performed in a Biometra T-3 thermoblock thermal cycler employing TaqPCR master mix kit (Qiagen) according to manufacturer recommendations. Five sets of primers were used for rickettsial DNA detection according to previous descriptions: (1) Msp465f/Msp980r derived from the highly conserved regions of major surface protein-2 (*mSP2*) paralogous genes of *Anaplasma phagocytophilum* (Caspersen et al. 2002); (2) ECC/ECB associated with HE1/HE3 for the amplification of *Ehrlichia chaffeensis* 16S rRNA fragment (Dawson et al. 1996); (3) RpCs.877p/RpCs.1258n and Rr190.70p/Rr190.602n, targeting the rickettsial genes for citrate synthase (*gltA*) and outer membrane protein A (*ompA*), respectively (Regnery et al. 1991). Positive PCR products were sequenced, after DNA purification by a MiniElute PCR Purification Kit (Qiagen), using an ABI automated sequencer (Applied Biosystems) according to manufacturer's instructions. Sequencing was performed with the forward and reverse primers used for PCR identification. Sequences were identified using the BLAST software (Altschul et al. 1990, 1997).

Nucleotide sequence accession numbers

The GenBank nucleotide sequence accession numbers for partial sequences of *gltA* a gene generated in this study are for PoTiRAv3:DQ459392. For partial sequences of *gltA* and *ompA* gene generated for PoTiRAv26 are DQ459393 and DQ4459388, respectively. For PoTiRAv20 are: DQ459394 and DQ459389, respectively. For PoTiRAv25 are: DQ459395 and DQ459390, respectively. For PoTiRAv27 are: DQ459396 and DQ459391, respectively.

Results

One hundred fifty two ticks were collected from 40 birds, belonging to 22 species. Five species of ticks were found: *Hyalomma marginatum* (111 nymphs, 7 larvae), *Ixodes ventalloi* (11 adults, 3 nymphs), *Ixodes frontalis* (3 adults, 1 nymph), *Rhipicephalus turanicus* (4 adults) and *Haemaphysalis punctata* (3 nymphs). Six ticks (3 adults, 2 nymphs, 1 larva) were grouped as *Ixodes* spp. due to the lack of body parts essential for specific identification. The instars ratio of collected ticks was 22 (14.5%) adults, 122 (80.2%) nymphs, 8 (5.3%) larvae. *H. marginatum* was the most abundant tick, infesting 77.5% (31/40) wild birds, mainly as nymphal stage. Regarding host preferences, this species also showed the widest host range, parasitizing 15 birds species. All these data are summarized in Table 1.

Of thirty-two ticks (21%) screened by PCR we were able to detect rickettsial DNA in 5 (15.6%) specimens (Table 2). Three ticks, identified as *Hyalomma marginatum* contained a rickettsia exhibiting nucleotide sequence of *gltA* 100% (347/347 bp) similar to *R. aeschlimannii* (U59722) and also the same similarity for *ompA* 100% (378/378 bp) (DQ379982). One *Rhipicephalus turanicus* was detected with rickettsial DNA exhibiting nucleotide sequence 100% similar to *R. massiliae* to both *gltA* (347/347 bp) (U59722) and *ompA* (334/334) (U43799). In one *Ixodes ventalloi* was identified a nucleotide sequence of *gltA* 100% (347/347) similar to *R. helvetica* (U59723). All ticks tested negative for the presence of DNA for *Anaplasma phagocytophilum* and *Ehrlichia chaffeensis*.

Discussion

This study is the first report of the presence of *Haemaphysalis punctata* and *Ixodes ventalloi* parasitizing wild birds in Portugal. Additionally, is documented for the first time the occurrence of *Haemaphysalis punctata* in *Acrocephalus scirpaceus*, *Emberiza cirulus* and *Turdus merula*; *Hyalomma marginatum* in *Athene noctua*, *Carduelis chloris*, *Hirundo rustica*, *Lanius meridionalis*, *Milvus migrans*, *Milvus milvus*, *Parus caeruleus*, *Parus major*, *Passer montanus*, *Tyto alba* and *Turdus merula*; *I. frontalis* in *Asio otus*; *Ixodes ventalloi* in *Asio flammeus*; *Rhipicephalus turanicus* in *Aquila nipalensis* and *Buteo buteo*.

Most of the tick species and instars described here are commonly associated to birds. Immatures of *Hyalomma marginatum*, well known as vectors of pathogens to man and animals, are frequently transported both northward and southward by birds being one of the most recorded ticks on these host (Hoogstraal 1956, 1961; Hoogstraal and Kaiser 1961; Hoogstraal et al. 1961, 1963; Hoogstraal and

Table 1 List of wild birds parasitized by ticks

Bird Species	No of infested birds	Site	Tick species (number and stage)					
			<i>Hyalomma marginatum</i>	<i>Haemaphysalis punctata</i>	<i>Ixodes frontalis</i> spp. ^a	<i>Ixodes ventralloi</i>	<i>Rhipicephalus turanicus</i>	
<i>Asio otus</i> (Long-eared owl)	1	MFP/QSA			3F; 1N			
<i>Asio flammeus</i> (Short-eared owl)	2	MFP/QSA			1F; 2N; 1L	5M; 7F; 5N		
<i>Alcedo atthis</i> (Kingfisher)	2	MFP/QSA	15N					
<i>Athene noctua</i> (Little owl)	2	MFP/QSA	3N					
<i>Acrocephalus scirpaceus</i> (Reed warbler)	3	SANR	2N	1N				
<i>Aquila nipalensis</i> (Steppe eagle)	1	MFP/QSA	4N				1F	
<i>Bubo bubo</i> (Eagle owl)	1	MFP/QSA					3F	
<i>Buteo buteo</i> (Common buzzard)	1	MFP/QSA						
<i>Carduelis carduelis</i> (Goldfinch)	1	MFP/QSA						
<i>Carduelis chloris</i> (Greenfinch)	1	SANR	1N		1F			
<i>Emberiza citrulus</i> (Cirl bunting)	1	SANR		1N				
<i>Hirundo rustica</i> (Barn swallow)	1	SANR	1N					
<i>Lanius meridionalis</i> (Iberian great grey shrike)	2	SANR	19N					
<i>Milvus migrans</i> (Black kite)	1	SANR	7N					
<i>Milvus milvus</i> (Red kite)	1	MFP/QSA	4L					
<i>Parus caeruleus</i> (Blue tit)	2	SANR	3N					
<i>Parus major</i> (Great tit)	1	SANR	3N					
<i>Passer montanus</i> (Tree sparrow)	2	SANR	2N					
<i>Saxicola communis</i> (Common whitethroat)	1	SANR			1F			
<i>Saxicola torquata</i> (Common stonechat)	6	SANR	28N					
<i>Turdus merula</i> (Black bird)	5	SANR	20N	1N				
<i>Tyto alba</i> (Barn owl)	2	SANR	3N; 3L					
Total (no. ticks/no. birds)	40		118/31	3/9	4/1	17/2	6/4	4/2

M—male; F—female; N—nymph; L—larvae

^a All the *Ixodes* spp could not be attributed to any species as they were lacking parts necessary for identification

Table 2 List of wild birds parasitized with ticks infected with rickettsial agents

Bird species ^a	Origin	Species of tick	No. positive ticks/ no. tested	Rickettsial detection/tick instars		
				<i>Ehrlichia chaffeensis</i>	<i>Anaplasma phagocytophilum</i>	<i>Rickettsia</i> spp.
<i>Alcedo atthis</i> (OM/S)	MFP/QSA	<i>Hyalomma marginatum</i>	1/7	–	–	<i>R. aeschlimannii</i> /1N
<i>Athene noctua</i> (R/F)	MFP/QSA	<i>Hyalomma marginatum</i>	1/1	–	–	<i>R. aeschlimannii</i> /1N
<i>Asio flammeus</i> (M/F)	MFP/QSA	<i>Ixodes ventralis</i>	1/17	–	–	<i>R. helvetica</i> /1M
<i>Buteo buteo</i> (OM/S)	MFP/QSA	<i>Rhipicephalus turanicus</i>	1/3	–	–	<i>R. massiliae</i> /1F
<i>Bubo bubo</i> (R/S)	MFP/QSA	<i>Hyalomma marginatum</i>	1/4	–	–	<i>R. aeschlimannii</i> /1N
Total			5/32			

^a (Bird status: M—migrant, OM—occasional migrant, R—resident; M—male; F—female; N—nymph/season of capture: S—Spring; F—Fall)

Aeschlimann 1982). This study corroborates that finding since *H. marginatum* was the most abundant tick and the species that showed the widest host range. In addition, these tick species might play a role in public health in Portugal, regarding rickettsial diseases. PCR testing has shown that *H. marginatum* was infected with *Rickettsia aeschlimannii*, an agent that has been recently implicated in human disease (Raoult et al. 2002). The genus *Ixodes* includes several species that are commonly or even exclusively associated with birds in Europe (Papadopoulos et al. 2001). *I. frontalis* is known to be exclusively associated with birds, which is in accordance to what we have been observing in our country. Regarding *I. ventalloi*, the bird association is not strict, although we found it on two birds. In fact, the original description of *I. ventalloi* was based on the observation of specimens collected on birds (Gil Collado 1936). The present work also describes *I. ventalloi* infection by *R. helvetica*, associated with human cases of chronic perimyocarditis (Nielsson et al. 1999). *R. helvetica* is commonly associated with *I. ricinus* ticks, which is considered the main vector implicated in human cases. The presence of this rickettsiae in alternative ticks could be attributable to the existence of secondary maintenance cycles, where agents circulate between relatively host-specific, usually non-human biting ticks and their hosts, as described for other tick-borne Rickettsiales in places where *I. ricinus* and other *Ixodes* species co-exist (Bown et al. 2003). Those additional cycles would buffer the agent from local extinction and help to re-establish the primary cycles. This hypothesis might explain our results since it has been observed that the distribution of *I. ricinus* is followed by *I. ventalloi*, in part of the country (Santos et al. 2004). In addition, the potential role of this species in public health might be considered since there are reports of human parasitism by *I. ventalloi* (Gilot and Marjolet 1982). In the literature, immatures of *Haemaphysalis punctata* are also frequently detected on Passeriformes birds, preferentially *Emberiza cirrus* (Osacar-Jimenez et al. 1998). Although rarely collected in Portugal, the presence of *H. punctata* nymphs in wild birds seems to corroborate that finding, but more birds need to be studied (especially *Emberiza cirrus*). It is worth mentioning that we have also found *Rhipicephalus turanicus* that is not commonly associated with birds. This finding could be attributable to bird's health conditions since both birds parasitized by this tick were wounded. This fact could have allowed an unusual contact with the ground which might have favoured their parasitism by *R. turanicus*. PCR assays have shown the infection of this tick species by *Rickettsia massiliae* recently shown to be pathogenic (Giustina et al. 2006).

This is the first report of rickettsiae detection in ticks collected from wild birds in Portugal, although the tick species reported here have been already described in other hosts in different regions of Portugal (Caeiro 1999; Estrada-Peña and Santos-Silva 2005). In a study conducted by Bacellar (1999), the prevalence of infection of Rickettsia like organisms (positive by hemolymph test) in different tick species was: 11.2% (33/294) in *H. marginatum*, 3.6% (13/361) in *R. turanicus*, and 100% (4/4) in *I. ventalloi*. Moreover the successful isolation of rickettsia by shell-vial was achieved in 2 (3.6%) *H. marginatum*, 1 (1.8%) *I. ventalloi* and in 6 (11%) *R. turanicus*. The strain isolates were characterized as *Rickettsia aeschlimannii*, *R. helvetica* and *R. massiliae*, respectively (Bacellar 1999). Here were found similar rates of rickettsial infection in the same tick species (Table 2). Nevertheless, previous studies were based only on haemocyte test and isolation, comparing with our study that only reports the detection of rickettsial pathogens by PCR. Regarding the migratory

status of birds, the occurrence of *R. helvetica* in *I. ventalloi* collected on migrating *Asio flammeus* potentially reflects the long-distance dispersion of tick-borne pathogens and the settlement of new focus. *Asio flammeus* was captured during fall migration to the south, which means that ticks and their pathogens could have originated in areas of Eastern Europe, where *R. helvetica* is commonly found. Moreover, occasional migrating *Alcedo atthis*, and *Buteo buteo* and resident *Athene noctua* and *Bubo bubo* are more likely to contribute to the maintenance and amplification of local endemic rickettsiae focus. In conclusion, this study corroborates the important role of birds in tick's dissemination and their influence on epidemiology of tick-borne rickettsiae agents in Portugal. Improvement of our knowledge about avian migration patterns and the agents that bird ticks harbour might be useful in helping to predict future outbreaks of infection due to emerging zoonotic tick-borne pathogens.

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3.3. TICKS AND TICK-BORNE RICKETTSIAE SURVEILLANCE IN MONTESINHO NATURAL PARK, PORTUGAL

M. SANTOS-SILVA, R. SOUSA, A.S. SANTOS, D. LOPES, E. QUEIJO, A. DORETA, L. VITORINO, AND F. BACELLAR

SHORT REPORT

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Ticks and Tick-Borne Rickettsiae Surveillance in Montesinho Natural Park, Portugal

M. SANTOS-SILVA,^a R. SOUSA,^a A.S. SANTOS,^a D. LOPES,^b E. QUEIJO,^c A. DORETA,^b L. VITORINO,^d AND F. BACELLAR^a

^a*Centro de Estudos de Vectores e Doenças Infecciosas, Instituto Nacional de Saúde Dr. Ricardo Jorge, 2965 Águas de Moura, Portugal*

^b*Camãra Municipal de Vinhais, Portugal*

^c*Organização de Produtores Pecuários de Vinhais, Vinhais, Portugal*

^d*Departamento de Biologia Vegetal/Centro de Genética e Biologia Molecular, Faculdade de Ciências, Universidade de Lisboa, Lisboa, Portugal*

ABSTRACT: This study constitutes the first contribution to the knowledge of tick dynamics and its implication in the epidemiology of rickettsial diseases in Montesinho Natural Park (MNP), Bragança district of Portugal. Of 76 ticks collected, 12 (15.8%) were *Dermacentor (D.) marginatus*, 36 (47.4%) *D. reticulatus*, and 28 (36.8%) *Rhipicephalus (R.) sanguineus*. Isolation assays were performed by shell-vial technique on 41 ticks. Israeli spotted fever strain was an isolate from *R. sanguineus*, and three isolates of *Rickettsia slovaca* were obtained from *D. reticulatus*. All 76 ticks were screened by PCR for *Rickettsia* sp., *Ehrlichia (E.) chaffeensis*, and *Anaplasma (A.) phagocytophilum*. *Rickettsia* Rpa4 strain DNA was detected in 10 *D. marginatus* and 2 *D. reticulatus*, and Israeli spotted fever strain in 1 *R. sanguineus*. No *E. chaffeensis* or *A. phagocytophilum* infection was detected. New host records are provided for *D. reticulatus*. Also described for the first time in Portugal is the isolation of *R. slovaca* from *D. reticulatus* and the isolation of Israeli spotted fever strain from *R. sanguineus*. This confirms the association of the last rickettsiae strain with the same vector tick as previously described in Israel and Sicily.

KEYWORDS: ticks; *Dermacentor marginatus*; *Dermacentor reticulatus*; *Rhipicephalus sanguineus*; Rickettsiae; *Rickettsia slovaca*; Israeli spotted fever; Rpa4; Portugal

Address for correspondence: Margarida Santos-Silva, Center for Vectors and Infectious Diseases Research, National Institute of Health, Av. Liberdade 5, 2965-575 Águas de Moura, Portugal. Voice: +351-265-912-222; fax: +351-265-912-568.
e-mail: m.santos.silva@insa.min-saude.pt

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INTRODUCTION

Ticks are important parasites present in almost every geographic zone in the world. Several tick species are involved in the transmission of a wide range of pathogens with medical significance. In Portugal different rickettsial agents have been isolated and detected from different tick species in boutonneuse fever (BF), caused by *R. conorii*, the tick-borne disease with major implication on public health.¹ Bragança, a northeastern district of Portugal, presents the highest incidence rate of BF,² but no studies have been done on the prevalence of rickettsial agents in ticks from this region. As the importance of this geographical area in BF cases contrasts with the lack of information about ticks and tick-borne rickettsiae, the aim of the study was to assess tick species and pathogen interactions present in this area.

MATERIALS AND METHODS

Ticks were collected in Montesinho Natural Park (41°47'N–42°N, 6°30'W–7°12'W), Bragança district, from September to November 2004 by dragging vegetation or directly removed from hosts. All specimens were identified by morphological characters using standard taxonomic keys^{3,4} and kept alive until being processed for hemolymph test as previously described.⁵ Suspected ticks were directly used to rickettsiae isolation by shell-vial technique.⁶ Additionally, all ticks were processed individually for DNA extraction as described.⁷ PCR approaches to detect DNA from *Rickettsia* (*R.*) spp., *Ehrlichia* (*E.*) *chaffeensis*, and *Anaplasma* (*A.*) *phagocytophilum* were performed using five primer sets. Rickettsiae DNA detection was achieved by amplification of *gltA* fragment gene (RpCs.877p–RpCs.1258n) and *ompA* fragment gene (Rr190.70p–Rr190.602n).⁸ The amplification of *E. chaffeensis* DNA was assayed by a nested PCR using ECC-ECB and HE1-HE3 primers, which amplify a fragment of the 16S rRNA gene.⁹ *A. phagocytophilum* DNA was amplified by *msp465f* and *msp980r* primers, derived from the highly conserved regions of major surface protein-2 (*msp2*) paralogous genes.¹⁰ Positive PCR products were sequenced directly using an ABI automated sequencer (Applied Biosystems USA) according to the manufacturer's instructions. Sample amplifications were performed with the forward and reverse primers used for PCR identification. Sequences were identified using the BLAST software.¹¹

RESULTS

From a total of 76 ticks collected in Montesinho Natural Park (MNP), 12 (15.8%) were *Dermacentor marginatus*, 36 (47.4%) *D. reticulatus*, and

TABLE 1. Number of ticks by species and stage collected in MNP and the detection assay results

Month	Origin	Site	Dermacentor		<i>Rhipicephalus</i> <i>sanguineus</i> (n)	Rickettsial detection/Tick instar					
			<i>marginatus</i> (n)	<i>reticulatus</i> (n)		<i>Anaplasma</i> <i>phagocytophilum</i>	<i>Ehrlichia</i> <i>chaffeensis</i>	<i>Rickettsia</i>			
September	Vegetation	Cerdeira	5M; 2F							RpA4/ 5M; 2F	
		Trincheira	3F							RpA4/ 1F	
	<i>Canis familiaris</i>	Gondosende		1M; 1F							
		Paradinha		1M; 1F	1F; 3 N						
		Paramio			3 N						
		Fontes de			1N						
		Transbaceiro									
		Lagarelhos			18N						ISF/1N
		Tuizelo			2 N						
October	<i>Canis familiaris</i>	Moimenta		1F							
		Quintanilha									
	<i>Canis lupus</i>	Quintanilha		1F						RpA4/ 1F	
November	<i>Canis familiaris</i>	Lagarelhos		1M; 3F							
		Moimenta		3 M							
	Paramio		1M								
	Travanca		14 M; 7 F								
	Sobreiró de Baixo		1 F								
TOTAL				12	36					28	

M = male; F = female; N = nymph.

TABLE 2. *Rickettsia* isolation results

Origin	Site	Tick species	No positive ticks/ no tested	<i>Rickettsia</i> isolates
<i>Canis familiaris</i>	Moimenta	<i>D. marginatus</i>	0/1	
	Quintanilha		0/1	
<i>Canis familiaris</i>	Lagarelhos	<i>D. reticulatus</i>	1/2	<i>R. slovacca</i>
	Moimenta		0/3	
	Paramio		0/3	
	Sobreiró de Baixo		0/1	
	Travanca		2/15	
<i>Canis lupus</i>	Quintanilha	<i>D. reticulatus</i>	0/1	
<i>Canis familiaris</i>	Fontes de Transbaceiro	<i>R. sanguineus</i>	0/1	
	Lagarelhos		1/7	ISF
	Paramio		0/1	
	Paradinha		0/3	
	Tuízelo		0/2	
Total		4/41		

28 (36.8%) *Rhipicephalus sanguineus*. Seasonal distribution of ticks regarding origin, site of collection, and arthropod instars are provide in TABLE 1 and FIGURE 1. Four *Rickettsia* strains were isolated. Israeli spotted fever strain (ISF) was obtained from one *R. sanguineus* (1/14), after nymph molting, and three isolates of *Rickettsia slovacca*, from adult *D. reticulatus* (3/24) as shown in TABLE 2. Of the 76 ticks tested by PCR, 83.3% *D. marginatus* (10/12), 5.6% *D. reticulatus* (2/36), and 3.6% *R. sanguineus* (1/28) were positive for the presence of rickettsial DNA using *gltA* and *OmpA* primers. Rickettsiae detected in the *Dermacentor* ticks were identified as *Rickettsia* RpA4 (similarity values between 98% and 100% for *OmpA* gene sequence; GenBank, AF120022). ISF was detected in one *R. sanguineus* tick (similarity values 99% for *gltA* gene sequence; GenBank, U59727), the same specimen with positive isolate, referred to above. All *D. reticulatus* positive by shell-vial for *R. slovacca* were PCR-negative, which may be on account of PCR inhibition. No *E. chaffeensis* or *A. phagocytophilum* infection was detected on ticks (TABLE 1).

DISCUSSION

This is the first report of *D. marginatus* and *D. reticulatus* in MNP, although other studies have already documented the same species in other regions.¹² In Portugal *D. reticulatus* has a patchy distribution associated with continental climate inlands in the northeast region, with only one host known—*Canis lupus*. Here is also report the first association of *D. reticulatus* to *Canis familiaris*. In MNP the domestic dog appears to contribute not only to the maintenance of

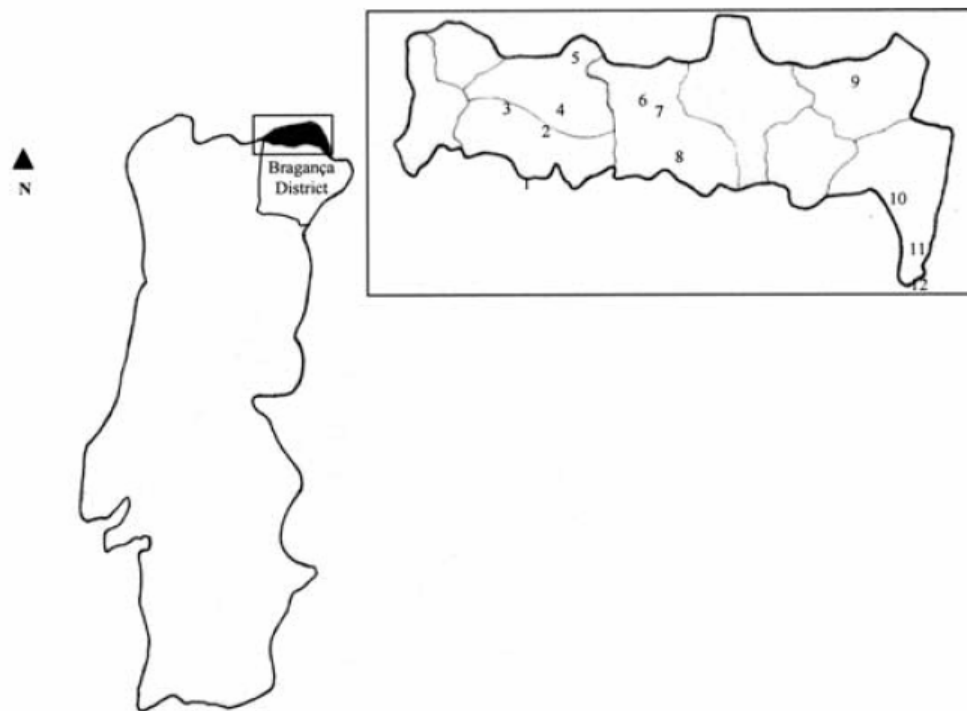


FIGURE 1. Monteseinho Natural Park. Site of tick collection: Sobreiró de Baixo (1); Lagarelhos (2); Tuízelo (3); Travanca (4); Moimenta (5); Fontes de Transbaceiro (6); Paramio (7); Gondosende (8); Trincheira (9); Cerdeira (10); Quintanilha (11); Paradinha (12). Site of rickettsiae isolation/detection: Lagarelhos (2); Travanca (4); Moimenta (5); Trincheira (9); Cerdeira (10); Quintanilha (11).

R. sanguineus but represents an important host for *D. reticulatus*. This fact largely contrasts with all data recovered from other parts of the country, particularly in the south, where dogs are not involved in *D. reticulatus* cycle (Santos-Silva, unpublished data). This is the first isolation of *R. slovaca* from *D. reticulatus* and ISF strain from *R. sanguineus* in Portugal, confirming the association of this rickettsiae strain with the same vector tick as previously described in Israel and Sicily.¹³ ISF isolate done after nymph molting reinforces the importance of transstadial transmission in rickettsial infectious maintenance. In Portugal *Rickettsia* RpA4 genotype has been already described in *D. marginatus* collected in the south (Vitorino *et al.* unpublished data). This study shows that *Rickettsia* RpA4 is also present in *D. reticulatus*, the same species in which it has been described for the first time in Russia.¹⁴ The pathogenic role of this rickettsia has not yet been proven. In conclusion, the results obtained will be an important tool to develop strategies of control and prevention against ticks and tick-borne rickettsiae pathogens in Monteseinho Natural Park.

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3.4. DETECTION OF *RICKETTSIA HELVETICA* AND OTHER SPOTTED FEVER GROUP RICKETTSIAE IN *IXODES RICINUS* FROM TAPADA NACIONAL DE MAFRA, PORTUGAL

SANTOS AS, SANTOS-SILVA MM, DE SOUSA R, FORMOSINHO P, NÚNCIO MS, BACELLAR F

SHORT REPORT

IN SUBMISSION

Detection of *Rickettsia helvetica* and other spotted fever group rickettsiae in *Ixodes ricinus* from Tapada Nacional de Mafra, Portugal

Santos AS¹, Santos-Silva MM¹, De Sousa R¹, Formosinho P², Nuncio MS¹, Bacellar F¹

¹Centro de Estudos de Vectores e Doenças Infecciosas, Instituto Nacional de Saúde Dr. Ricardo Jorge, Lisboa, Portugal;

²Laboratório Privado de Análises Clínicas, Lisboa, Portugal.

Corresponding author: Ana Sofia Pereira dos Santos. Centro de Estudos de Vectores e Doenças Infecciosas, Instituto Nacional de Saúde Dr. Ricardo Jorge, Edifício LEMES, Avenida Padre Cruz, 1649-016 Lisboa, Portugal;

Tel: +351 217 508 125; Fax: +351 217 508 521

e-mail: ana.santos@insa.min-saude.pt

ABSTRACT:

The presence of tick-borne rickettsial agents in *Ixodes ricinus* ticks was investigated in a densely infested Portuguese recreational park, Tapada Nacional de Mafra. A total of 998 *Ixodes ricinus* were tested by PCR, individually or in pools, for detection of *Rickettsia* spp., *Ehrlichia chaffeensis* and *Anaplasma phagocytophilum*. *Rickettsia* DNA exhibiting sequences similar to those of *Rickettsia helvetica*, and *R. monacensis* strains IRS3 and IRS4 were identified. This is the first report of *I. ricinus* infection by other spotted fever rickettsiae beside *R. helvetica* in Portugal. Further consideration should be given to *I. ricinus* as vector of several rickettsiae whose pathogenicity to humans is still unknown.

RUNNING TITLE

Rickettsia spp. in *Ixodes ricinus*, Portugal

KEY WORDS: *Ixodes ricinus*; Spotted fever group rickettsiae; *Rickettsia helvetica*; IRS3; IRS4; *gltA*; *OmpA*; *OmpB*; Portugal.

INTRODUCTION:

Ixodes ricinus are among the most important European ticks regarding Public Health concerns. It is a well-known vector of several agents causing diseases in humans, such as tick-borne encephalitis virus (TBE), *Borrelia burgdorferi* s.l. (Lyme borreliosis), *Anaplasma phagocytophilum* (human granulocytic anaplasmosis), *Babesia divergens* and *B. microti* (human babesiosis) (Estrada-Pena & Jongejan, 1999). It is also responsible for the transmission of *Rickettsia helvetica* recently associated to cases of febrile illness (Fournier *et al.*, 2000). *I. ricinus* is regarded as a hygrophilic species presenting in Portugal a patchy distribution influenced mainly by environmental determinants, such as climate, landscape fragmentation and composition (Baptista, 2006). Regardless, in some areas of the country with adequate conditions this tick species can be

abundant as in the case of *Tapada Nacional de Mafra (TNM)*. This national park with more than 800 ha is a densely wooded territory located in the Central Western Coast of Portugal (38° 56'N 9° 17'W). It was originally created as a hunting area, but it is also used as a recreational and educational park. *TNM* supports a diverse wildlife population composed of birds, reptiles, and small to large mammals, including rodents, insectivores, carnivores, lagomorphs, and artiodactyls (wild boars, fallow deer and elks). The availability of such diverse vertebrate hosts helps to maintain an abundant tick's population, dominated by *I. ricinus* but also including other *Ixodes*, *Dermacentor*, *Haemaphysalis*, and *Rhipicephalus* species (MM Santos-Silva, unpublished data). Given the repeated contact between humans and ticks in *TNM*, the occurrence of tick-borne agents with potential Public Health importance has been a matter of concern for the park's administration which has promoted the realization of several studies to increase knowledge regarding this subject. The occurrence of a great variety of *B. burgdorferi s.l.* in ticks, including *B. afzelii*, *B. garinii*, *B. lusitaniae*, and *B. valaisiana* has already been documented (Baptista *et al.*, 2004, 2006). However, no studies have yet addressed the occurrence of other tick-borne agents, such as those belonging to the Order Rickettsiales. In this study, the presence of *Anaplasma phagocytophilum*, *Ehrlichia chaffeensis*, and *Rickettsia* spp. was investigated in *I. ricinus* ticks from *TNM*.

MATERIALS AND METHODS:

Tick sampling. During 4 day-trials in February 2002, a total of 1064 ticks were collected from *TNM*, including: 998 *I. ricinus*, 29 *Haemaphysalis inermis*, 28 *H. punctata* and 9 *Dermacentor marginatus*. This work details only the study regarding *I. ricinus* ticks. The majority of *I. ricinus* (132 males, 130 females and 710 nymphs) was collected when questing for hosts, by means of flagging vegetation in 4 sampling areas. These areas are designated feeding places for the large animal population, and were selected for hosting a large number of animals daily. Additional specimens were collected from *Dama dama*, captured during the hunting season (9 males and 17 females). Most arthropods were processed in groups pooled by sex, stage, and sampling area comprising 36 pools of adult ticks (ranging from 2 to 20 arthropods) and 6 pools of immatures (ranging from 55 to 200 arthropods). Approximately 9% of the questing adults collected in each sampling area were processed individually, representing a total of 24 ticks (12 males and 12 females). The ticks were

washed in alcohol 70%, passed through distillate water and dried in filter paper. Using a sterile pestle per sample, ticks were homogenized in 400µl PBS supplemented with 10% fetal calf serum (Gibco, Invitrogen, UK). Half sample homogenate was used for DNA extraction and the other 200µl was stored at -80°C.

Polymerase chain reaction (PCR). Genomic DNA was extracted using DNeasy Tissue Kit, according to the manufacture's instructions (Qiagen GmbH, Germany). To monitor the occurrence of false-positive samples, homogenates of laboratory-reared ticks were included during extraction as negative controls (one control per each extraction run containing 5 tick samples). Several sets of primers were used for Rickettsiales detection, including: i) GE9f/GE10r for the amplification of *A. phagocytophilum* 16S rRNA (*rrs*) gene (Chen *et al.*, 2004) and MSP465f/MSP980r, for the amplification of a hypervariable region of *A. phagocytophilum* surface protein genes (Caspersen *et al.*, 2002); ii) ECC/ECB followed by HE1/HE3, outer and inner primer pair, respectively, targeting *E. chaffeensis* *rrs* (Dawson *et al.*, 1996); iii) RpCs415/RpCs1220 and Rr190.70p/Rr190.602n, which target a fragment of *Rickettsia* spp. genes encoding for citrate synthase (*gltA*) and outer membrane protein A (*ompA*), respectively (Regnery *et al.*, 1991). Due to the lack of *ompA* gene in some *Rickettsia* spp., to complement these later screening all *gltA* positive samples that were not amplified with *ompA* primers were re-tested with OF/OR pair, for the amplification of the alternative outer membrane protein B (*ompB*) gene (Choi *et al.*, 2005). Primer sequences and amplification conditions have been previously described (Regnery *et al.*, 1991; Chen *et al.*, 1994; Dawson *et al.*, 1996; Choi *et al.*, 2005; Caspersen *et al.*, 2002). PCR were performed in Biometra T3 thermoblock thermal cycler (Biometra GmbH, Germany) using a total volume of 50µl master mix containing 1 µM of each primer, 2.5 U of Taq DNA polymerase, 20mM of each dNTP, 10 mM Tris-HCL, 1.5 mM MgCl₂, 50 mM KCl and 10µl DNA extract (1µl in nested reactions). As PCR negative controls we have used DNA extracted from arthropods reared in a laboratory tick colony and as positive controls *R. conorii* Malish strain, *A. phagocytophilum* Webster strain and *E. chaffeensis* Arkansas strain.

Sequencing. DNA amplicons from positive samples were purified (Jetquick PCR Purification Kit; Genomed GmbH, Germany) and sequenced using an ABI automated sequencer (Applied Biosystems). After manual review and editing, sequence homology searches were performed using BLASTn and the NCBI nr nucleotide database.

Nucleotide sequence accession numbers: The GenBank nucleotide sequence accession numbers for partial sequences generated in this study are: DQ910783 (PoTiR1dt), DQ910784

(PoTiR2dt), DQ910785 (PoTiR3dt), and EF051167 (PoTiR4dt) for *gltA* gene; DQ910781 (PoTiR1dt), DQ910782 (PoTiR2dt) and EF053275 (PoTiR4dt) for *ompA* gene; EU126928 (PoTiR3dt) for *ompB*.

RESULTS:

Seven out of 42 pools and 1 out of 24 individually processed *I. ricinus*, tested positive for rickettsiae. Positive amplicons were obtained only from questing ticks and the sequencing results are presented in table 1. DNA from female I-7 (named PoTiR1dt) and pool 26 (named PoTiR2dt) exhibited nucleotide sequence 99% similar to spotted fever *Rickettsia* strain IRS3 to both *gltA* (372/373 bp) (AF140706) and *ompA* (497/499) (AF141909) genes. Pool 1 (named PoTiR3dt) contained rickettsial DNA exhibiting nucleotide sequences 99% similar in both *gltA* and *ompB* (positions 361/363 bp and 495/499 bp, respectively) when compared to *R. helvetica* sequences available in GenBank (U59723 and AF123725, respectively). The tick pool 4 (named, PoTiR4dt) presented DNA with a 100% homology to *R. monacensis* (IRS4) in both *gltA* (373/373) (DQ100163) and *ompA* (499/499) (DQ100169) sequences. Additionally, 4 other pools (P31-33) revealed appropriate amplicons with *gltA* and *ompA* fragments of 376-bp and 534-bp, respectively. However, DNA sequencing of these PCR products showed ambiguous bases in the sequence, probably resulting from pooling samples and they were excluded from further analysis. Neither *A. phagocytophilum* nor *E. chaffeensis* DNA was detected in this study.

DISCUSSION:

In Europe several agents belonging to the order Rickettsiales have been associated to *I. ricinus*. *A. phagocytophilum* is now reported in several countries and cases of human disease associated to this agent are especially documented in Northern and Central Europe (Strle, 2004). *Rickettsia helvetica*, initially described in Switzerland as the Swiss agent, was the first rickettsia to be isolated from this tick species (Beati *et al.*, 1994). More recently, *R. monacensis* (previous known as IRS4) was isolated from ticks collected in a public park in Munich, Germany (Simser *et al.*, 2002). Other yet-to-be-cultured rickettsiae have also been detected by PCR testing, such as the Cadiz agent in southwestern Spain and IRS3 in Slovakia (Márquez *et al.*, 1998; Sekeyova *et*

al., 2000), probably representing variant genotypes of the *R. monacensis*. So far *R. helvetica* is the only rickettsiae species transmitted by *I. ricinus* that has been associated to human disease after its detection in French patients with febrile illness (Fournier *et al.*, 2000).

In Portugal, both *A. phagocytophilum* and *R. helvetica* has been already identified in *I. ricinus* (Bacellar, 1999; Santos *et al.*, 2004), but no cases of human infection by these Rickettsiales have been definitely proven. Additionally, the description of a case fulfilling the serological criteria for *E. chaffeensis* infection (David de Morais *et al.*, 1991), suggested the occurrence of this agent in our country. Since the vector of *E. chaffeensis* is largely unknown in Europe, it was considered of interest to include this agent's screening in the present study. The results presented herein evidenced the occurrence of *R. helvetica*, IRS3 and IRS4 in *TMM*. The detection of *R. helvetica* in an area such as *TMM*, where the exposure to tick infested habitats is highly promoted, could have direct implication in Public Health and thus deserves further investigation. Moreover, the association of IRS3 and IRS4 to *I. ricinus*, a tick species that frequently bites humans, should also merit attention. Regarding the other Rickettsiales in study, no active infections could be identified in the analysed ticks. Given the presence of *A. phagocytophilum* in other Portuguese areas where *Ixodes* spp. are known to occur, the present results may be justified by the patchy seasonal and spatial distribution that usually characterizes this agent.

Further investigation should be planed in *TMM* to investigate aspects such as the absence of *A. phagocytophilum*, rickettsiae prevalence, occurrence of co-infection in ticks and the rickettsiae species involved in human diseases in the area.

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TABLE 1 – Tick samples detected with *Rickettsia* DNA

Sample ^a	Tested ticks stage ^b (origin) ^c	PCR results					<i>Rickettsia</i> homology (genotype designation)
		<i>A. phagocytophilum</i>		<i>E. chaffeensis</i>	<i>Rickettsia</i> spp.		
		<i>rrs</i>	<i>msp2</i>	<i>rrs</i>	<i>gltA</i>	<i>OmpA (OmpB)</i>	
I-7	1F(V)	-	-	-	+	+	IRS3 (PoTiR1dt)
P1	10M(V)	-	-	-	+	(+)	<i>R. helvetica</i> (PoTiR3dt)
P4	10M(V)	-	-	-	+	+	<i>R. monacensis</i> IRS4 (PoTiR4dt)
P26	20F(V)	-	-	-	+	+	IRS3 (PoTiR2dt)
P30	100N(V)	-	-	-	+	+	
P31	100N(V)	-	-	-	+	+	
P32	200N(V)	-	-	-	+	+	
P33	200N(V)	-	-	-	+	+	

^aI individually processed arthropods, P pool of ticks; ^bM male, F female, N nymph; ^cV ticks collected in vegetation (questing ticks).

3.5. PCR-BASED SURVEY OF *ANAPLASMA PHAGOCYTOPHILUM* IN PORTUGUESE TICKS (ACARI: IXODIDAE)

SANTOS AS, SANTOS-SILVA MM, SOUSA R, BACELLAR F, DUMLER JS

RESEARCH ARTICLE

IN SUBMISSION

PCR-based survey of *Anaplasma phagocytophilum* in Portuguese ticks (Acari: Ixodidae)

Santos AS¹, Santos-Silva MM¹, Sousa R¹, Bacellar F¹, Dumler JS²

¹Centro de Estudos de Vectores e Doenças Infecciosas, Instituto Nacional de Saúde Dr. Ricardo Jorge, Lisboa, Portugal;

²Division of Medical Microbiology, Department of Pathology, The Johns Hopkins University School of Medicine, Baltimore, Maryland, USA.

Corresponding author: Ana Sofia Pereira dos Santos. Centro de Estudos de Vectores e Doenças Infecciosas, Instituto Nacional de Saúde Dr. Ricardo Jorge, Edifício LEMES, Avenida Padre Cruz, 1649-016 Lisboa, Portugal;

Tel: +351 217 508 125; Fax: +351 217 508 521

e-mail: ana.santos@insa.min-saude.pt

ABSTRACT

A total of 2006 ticks, collected in Madeira Island and seven districts of Mainland Portugal, were examined by polymerase chain reaction (PCR) for the presence of *Anaplasma phagocytophilum*. Active infections were detected exclusively in *Ixodes* species, including six questing *I. ricinus* nymphs from Madeira Island, one questing *I. ventalloi* nymph from Setúbal District, and two *I. ventalloi* adults found parasitizing domestic cats in both Setúbal and Santarém District. These findings confirm prior observations and suggest the persistence of *A. phagocytophilum* on Madeira Island, where its presence was first documented in 2000. Moreover, it adds *I. ventalloi* and domestic cats to the list of potential elements of the agent's enzootic cycles in Portugal. Molecular analysis of PCR amplicons suggests the existence of two *A. phagocytophilum* genotypes in Portugal, one of which is identical or very similar to North American strains implicated in human disease.

RUNNING TITLE

Anaplasma phagocytophilum in Portuguese ticks

KEYWORDS

Ticks; Tick-borne agent; *Anaplasma phagocytophilum*; Polymerase chain reaction (PCR); Portugal;

INTRODUCTION

Anaplasma phagocytophilum (formerly *Ehrlichia phagocytophila*, *E. equi* and the human granulocytic ehrlichiosis agent [HGE agent]) (Dumler *et al.*, 2001) is an obligate intracellular bacterium that is well established as a worldwide tick-borne agent of veterinary importance and is also currently considered an emerging human pathogen in both US and Europe (Strle, 2004; Dumler, 2005; Lotric-Furland *et al.*, 2006). The disease in humans is known as human granulocytic anaplasmosis (HGA), formerly human granulocytic ehrlichiosis, and presents clinically as a non-

specific febrile illness accompanied by hematological abnormalities and hepatic injury. Severe and fatal infections have been occasionally reported, especially in US (Bakken *et al.*, 1994, 1996; Hardalo *et al.*, 1995; Jahangir *et al.*, 1998). The main route of *A. phagocytophilum* transmission is via infected tick salivary secretions during a tick-bite. Several ticks species in the *Ixodes persulcatus/ricinus* complex are considered primary vectors for this agent, including *I. scapularis* and *I. pacificus*, respectively in Eastern and Western parts of North America, *I. ricinus* in Western, Central and Northern Europe (Macleod & Gordon, 1933; Richter *et al.*, 1996; Telford *et al.*, 1996) and *I. persulcatus* in Western Europe and Asia (Cao *et al.*, 2000, 2006; Morozova *et al.*, 2002; Kim *et al.*, 2003; Wen *et al.*, 2003; Rar *et al.*, 2005).

When this study was initiated in 2002, limited information was available regarding the presence of *A. phagocytophilum* in Portugal, except for Madeira Island that described its presence in *I. ricinus* (Núncio *et al.*, 2000). Thus a broader study was undertaken to investigate the occurrence of *A. phagocytophilum* in Portuguese ticks and to further characterize the agent by molecular approaches. It was integrated with other research activities of Center for Vector and Infectious Diseases Research, National Institute of Health Dr. Ricardo Jorge (CEVII/INSA), in a joint effort to promote improved knowledge of tick-borne agents potentially involved in human disease in the country. The present report summarizes all available data regarding *A. phagocytophilum* detection in ticks collected by active surveillance in Portugal during 2002-2006.

MATERIAL AND METHODS

Ticks sampling. During 2002 to 2006, ticks were collected in several areas of Bragança, Braga, Leiria, Lisboa, Portalegre, Santarém, and Setúbal Districts, mainland Portugal and on Madeira Island, Madeira Archipelago. The areas were selected for the field-trials, either because *Ixodes* species were known to be present, or because specific interest in a given tick-borne disease was expressed for integration with ongoing projects. Detailed information regarding 1,384 ticks was previously described (Santos *et al.*, 2004; Santos-Silva *et al.*, 2006a, 2006b; Santos *et al.*, in submission). The remaining 622 ticks included in this study were obtained either from additional field work or collected during the above mentioned surveys (Santos *et al.*, 2004; Santos *et al.*, in submission). Ticks were obtained by flagging vegetation or were directly removed from wild and domestic animals. Some additional specimens found parasitizing humans and sent to our

laboratory by medical institutions or directly removed from persons who presented at CEVDI/INSA were also included in this study. All specimens were identified to the species level by standard taxonomic keys (Cordas *et al.*, 1993; Dias, 1994), and either immediately processed or frozen at -80°C until used.

DNA extraction and polymerase chain reaction (PCR). Ticks were processed individually, or in some samples obtained from Lisboa District, pooled according to feeding condition, stage, sex, and site of collection, as described elsewhere (Santos *et al.*, in submission). Genomic DNA was extracted from individual ticks by crude digestion of tissues in 0.7 mol/L ammonium hydroxide at 100°C, as described by Schouls and coworkers (1999). DNA from pooled samples was extracted from 200 µl of tick homogenates prepared in PBS using the DNeasy Tissue Kit, according to the manufacturer's instructions (Qiagen GmbH, Germany). To monitor the occurrence of cross-contamination, laboratory-reared ticks were included during extraction as negative controls (one control per each extraction run containing 6 to 23 tick samples). The presence of *A. phagocytophilum* DNA in tick samples was screened by PCR or nested PCR using different sets of primers: i) MSP465f/MSP980r derived from the highly conserved 5' region of major surface protein-2 (*mSP2*) paralogous genes (Caspersen *et al.*, 2002); ii) GE9f/GE10r which amplify a 919 bp fragment of the 16S rRNA gene (*rrs*) (Chen *et al.*, 1994); iii) HS1/HS6 followed by HS43/HS45 for the amplification of a 442-bp sequence of heat-shock operon, *groESL* (Sumner *et al.*, 1997). Both *mSP2* and *rrs* primers were used for the initial screening of part of the samples, as described elsewhere (Santos *et al.*, 2004; Santos *et al.*, in submission). The rest of the ticks presented here were screened using *mSP2* testing alone. All samples that tested positive with the *mSP2* and *rrs* screening during 2002-2006 were further analysed using *groESL* primers. PCR was performed in a total 50 µl volume containing 1 µM of each primer, 2.5 U of Taq DNA polymerase, 200 mM of each dNTP, 10 mM Tris-HCl, 1.5 mM MgCl₂, 50 mM KCl and 5 to 10 µl of DNA template (1 µl in nested reactions). Primer sequences and PCR conditions were previously described (Chen *et al.*, 1994; Sumner *et al.*, 1997; Caspersen *et al.*, 2002). In each PCR run, known positive and negative samples (extraction controls and water) were included as controls. DNA amplicons from positive samples were purified (Jetquick PCR Purification Kit; Genomed GmbH, Germany) and sequenced using an ABI automated sequencer (Applied Biosystems). After manual review and editing, sequence homology searches were performed using BLASTn using the NCBI nr nucleotide database.

GenBank accession numbers. The accession numbers of *A. phagocytophilum* 16S rRNA partial gene (*rrs*) sequences obtained in this study are: EU098006 for ticks nos. 118 and 122; EU098007 for ticks nos. 160 and 246. The *A. phagocytophilum groESL* partial sequences are: EU004826 for ticks nos. 93 and 118; EU004827 for ticks nos. 160 and 246.

RESULTS

A total of 2006 ticks belonging to 14 species were collected, including 117 *Dermacentor marginatus*, 76 *D. reticulatus*, 6 *Hyalomma lusitanicum*, 12 *H. marginatum*, 29 *Haemaphysalis inermis*, 34 *H. punctata*, 2 *Ixodes acuminatus*, 1 *I. bivari*, 5 *I. hexagonus*, 1202 *I. ricinus*, 144 *I. ventalloi*, 49 *Rhipicephalus bursa*, 77 *R. pusillus* and 252 *R. sanguineus group* (Figure 1, Table 1-2). PCR testing was performed either on individually processed ticks (n=1032) or using pooled ticks (n=974, divided in 42 tick samples), representing a total of 1074 DNA samples. Of the 320 samples initially screened by both *msp2* and *rrs* primers, *A. phagocytophilum* DNA was detected in 8 samples, corresponding to 6 questing *I. ricinus* nymphs collected from Madeira Island, previously referred as nos. 11, 60, 118, 122, and 137 (Santos *et al.*, 2004) and 1 questing *I. ventalloi* nymph and 1 male *I. ventalloi* collected from a domestic cat, both obtained from Setúbal District and referred as nos. 160 and 246, respectively (Santos *et al.*, 2004). All 8 positive samples were identified by *msp2* primers, although *rrs* PCR failed to amplify DNA in 3 of these ticks. The standard amplification of *rrs* can be limited by low sensitivity owing to the presence of a single copy in each bacterial genome. In contrast *msp2* is a member of a multigene family composed as many as 105 paralogs per genome, which enhances detection sensitivity (Scorpio *et al.*, 2004). Because of the higher sensitivity of PCR for *msp2* compared to *rrs*, the remaining study samples (712 DNA samples) were screened only using *msp2* DNA testing. Of these, one additional sample was found positive for *A. phagocytophilum*, corresponding to an *I. ventalloi* female collected from a domestic cat in Santarém District (no. 348). Additional amplifications with the *groESL* primers were performed in 4 *A. phagocytophilum msp2* and *rrs* positive samples (nos. 93, 118, 160, 246).

Partial sequences of *msp2* obtained from all 9 ticks showed between 85.7% to 98.5% similarity, between 86.9% and 94.2% similarity when compared to representative *msp2* sequences from North American *A. phagocytophilum* strains isolated from humans (Webster strain - Wisconsin and USG3 strain - eastern US), and between 35.0% and 63.7% similarity compared to outgroup *A.*

marginale msp2 and *msp3* sequences, respectively (Figure 1A). Of interest, the sequences obtained from *I. ventalloi* from mainland Portugal clustered together and separate from other *msp2* sequences obtained from *I. ricinus* on Madeira Island (Figure 1A). When amplified using *rrs* primers, compared to other US *A. phagocytophilum* strains obtained from humans (U02521, Wisconsin strain and CAHU-HGE1 and CAHU-HGE2, California strains), sequences were 100% (783/783) identical for the *I. ventalloi* nos. 160 and 246 and *I. ricinus* no. 118 and 100% (645/645) identical for *I. ricinus* no 93 (Figure 1B). Moreover, the *groESL* partial sequences were also identical for the two *I. ricinus* (nos. 93 and 118) and two *I. ventalloi* (nos. 160 and 246) showing 100% (463/463) and 97.8% (453/463) similarity to the Californian strains, CAHU-HGE1 and CAHU-HGE2. Although the *rrs* failed to provide any evidence of differences between the mainland and Madeira Island strains, the *groESL* analysis reinforced the differences observed in *msp2* sequences of *A. phagocytophilum* strains derived from *I. ricinus* and *I. ventalloi* ticks (Figure 1C).

DISCUSSION

These data confirm, in actively questing *I. ricinus* collected from Madeira Island, the presence of *A. phagocytophilum* that is closely related to the North American strains involved in human disease. *I. ricinus* is regarded as a hygrophilic tick that presents a patchy distribution in Portugal mainly influenced by environmental determinants, such as climate, landscape composition and fragmentation (Baptista, 2006). Regardless, in areas with favorable conditions, as is the case for Madeira Island and Mafra (Lisboa District, mainland), it can be the dominant tick species (Almeida, 1996; Baptista, 2006). Moreover, *I. ricinus* is also frequently found parasitizing humans in Portugal (MM Santos-Silva, unpublished data) and their potential for transmitting pathogenic agents is illustrated by the occurrence of at least one *Ixodes*-borne disease, Lyme borreliosis caused by the bacteria *Borrelia burgdorferi* s.l., which has been included in the list of national notifiable diseases since 1999 (Lopes de Carvalho & Nuncio, 2006). Thus, one can assume that the presence of *A. phagocytophilum* in *I. ricinus* on Madeira Island presents a potential health threat to both humans and animals that needs further investigation.

These data also illustrate that *A. phagocytophilum* might not be uniformly distributed in our country. For example in Mafra (Lisboa District), an area where *I. ricinus* are abundant no infected

ticks were found. In contrast, on Madeira Island, *A. phagocytophilum* seems to be endemic given the detection of infected *I. ricinus* in surveys conducted at two different times (Núncio *et al.*, 2000; Santos *et al.*, 2004). This reflects either continuous introduction of the agent by migrating birds and/or the existence of vertebrate hosts that sustain the agent's active cycles, again likely rewarding subjects for further investigation.

Another ecologically interesting finding was the identification of *A. phagocytophilum* in *I. ventalloi* ticks either collected from vegetation in Setúbal District or parasitizing cats in both Setúbal and Santarém District. Besides the major vectors of the *I. persulcatus/ricinus* complex species, the involvement of other *Ixodes* ticks in natural enzootic cycles of *A. phagocytophilum* is already reported, such as with *I. spinipalpis* in Colorado (Zeidner *et al.*, 2000), *I. dentatus* on the New England Coast (Goethert & Telford, 2003) and possibly *I. trianguliceps* in England (Bown *et al.*, 2003). Although the direct role of these ticks in human and domestic animal diseases still needs to be evaluated, it seems to be limited due to their relative host specificity and restricted questing potential. When compared with members of the *I. persulcatus/ricinus* complex, *I. spinipalpis*, *I. dentatus*, and *I. trianguliceps* are regarded as important bridge-elements, maintaining parallel transmission cycles that could provide support for primary vectored infectious agents (Zeidner *et al.*, 2000; Bown *et al.*, 2003; Goethert & Telford, 2003). This is a possible explanation for the results obtained here, although the vector competency of *I. ventalloi* for *A. phagocytophilum* transmission has yet to be demonstrated.

Of interest is the fact that *msp2* and *groESL* sequences of *A. phagocytophilum* derived from *I. ventalloi* were closely related to each other and divergent from those obtained in *I. ricinus*. The *A. phagocytophilum* HZ strain genome has at least 105 copies of the *msp2* (or *p44*) gene multifamily and *msp2* primers were designed to target the highly conserved 5' flanking sequences detected in a sample of about 30 of these copies (Caspersen *et al.*, 2002). The *msp2* possesses 5' and 3' conserved sequences that flank a hypervariable region that recombines to generate antigenically diverse bacterial populations. Thus, *msp2* is best known for diversity and not for its potential application as a molecular phylogenetic or epidemiological tool. Yet, given the high degree of nucleotide conservation surrounding the *msp2* hypervariable region, its application for molecular phylogeny is likely valid, and the agreement with *groESL* results supports the hypothesis that distinct *A. phagocytophilum* lineages exist in Portugal.

Since 2 of the 3 infected *I. ventalloi* ticks were obtained from domestic cats, a potential role is suggested for these animals in agent's maintenance cycles. In fact, domestic cats are on the list

of vertebrate hosts affected by *A. phagocytophilum* infections in both US and Europe (Bjoerdorff *et al.*, 1999; Lappin *et al.*, 2004; Shaw *et al.*, 2005). Additionally, a study performed by Levin and coworkers (2002) also describes the presence of active infection in feral cats captured in Connecticut, US. Although no clinical evaluation was undertaken in the current study, the cat that harboured the infected ticks in Setúbal District was apparently healthy but free-roaming; no information was available regarding the Santarém District cat. Additionally, *I. ventalloi* has also been found parasitizing wild birds and several orders of mammals, such as Carnivora, Erinaceomorpha, Lagomorpha, Rodentia, and Soricomorpha (Dias *et al.*, 1994; Santos-Silva *et al.*, 2006b). So far, no cases of human parasitism by this species are reported in Portugal, although *I. ventalloi* has been found on humans in France (Gilot & Marjolet, 1982). Thus, the enzootic cycles of this *A. phagocytophilum* strain may involve several wild animals and the pathogenic potential for both humans and domestic animals should be evaluated.

It is also worth mentioning the lack of *A. phagocytophilum* detection in non-*Ixodes* ticks, such as in a 500 m² site in Baixa de Palmela, Setubal District where positive *Ixodes* ticks were found, and the analysis of several other tick species revealed no *A. phagocytophilum*. In this site during the morning flagging performed on April 2003, 1 positive *I. ventalloi* was collected with 13 *R. pusillus* and 5 *R. sanguineus* group (data not detailed). These results are in accordance with several other studies that link *A. phagocytophilum* to the genus *Ixodes* and only sporadically to other arthropods, such as *Dermacentor variabilis*, *Dermacentor occidentalis* and *Haemaphysalis leporispalutris* in US (Goethert & Telford, 2003; Holden *et al.*, 2003), *Haemaphysalis longicornis* in Korea (Kim *et al.*, 2003), *Hyalomma detritum* in Tunisia (Sarih *et al.*, 2005), *Dermacentor silvarum* in China (Cao *et al.*, 2006), the Trombiculidae mite *Neotrombicula autumnalis* in Spain (Fernandez-Soto *et al.*, 2001), Syringophilidae quill mites *Torotroglia merulae* and *Syringophilopsis sturni* in Poland (Skoracki *et al.*, 2006). The majority of these arthropods were collected while feeding on vertebrate hosts. Thus, it is possible that these reports represent the passive acquisition of *A. phagocytophilum* infected blood and not the capacity for reproduction or transmission. Regarding *H. leporispalutris* and *D. variabilis*, experimental studies demonstrate that although these ticks are susceptible to infection, they are unable to maintain the agent transstadially and to successfully transmit it to a vertebrate host, respectively, and are therefore considered incompetent vectors (Des Vignes *et al.*, 1999; Goethert & Telford, 2003).

In summary, the results of this 4-year study of Portuguese ticks show that *A. phagocytophilum* occurs in *Ixodes* species from both mainland and Madeira Island and as such,

the potential exists for both human and animal infections. Moreover, these molecular analyses document the existence of two *A. phagocytophilum* genotypes in Portugal, one of which is identical or very similar to North American strains implicated in human cases of disease.

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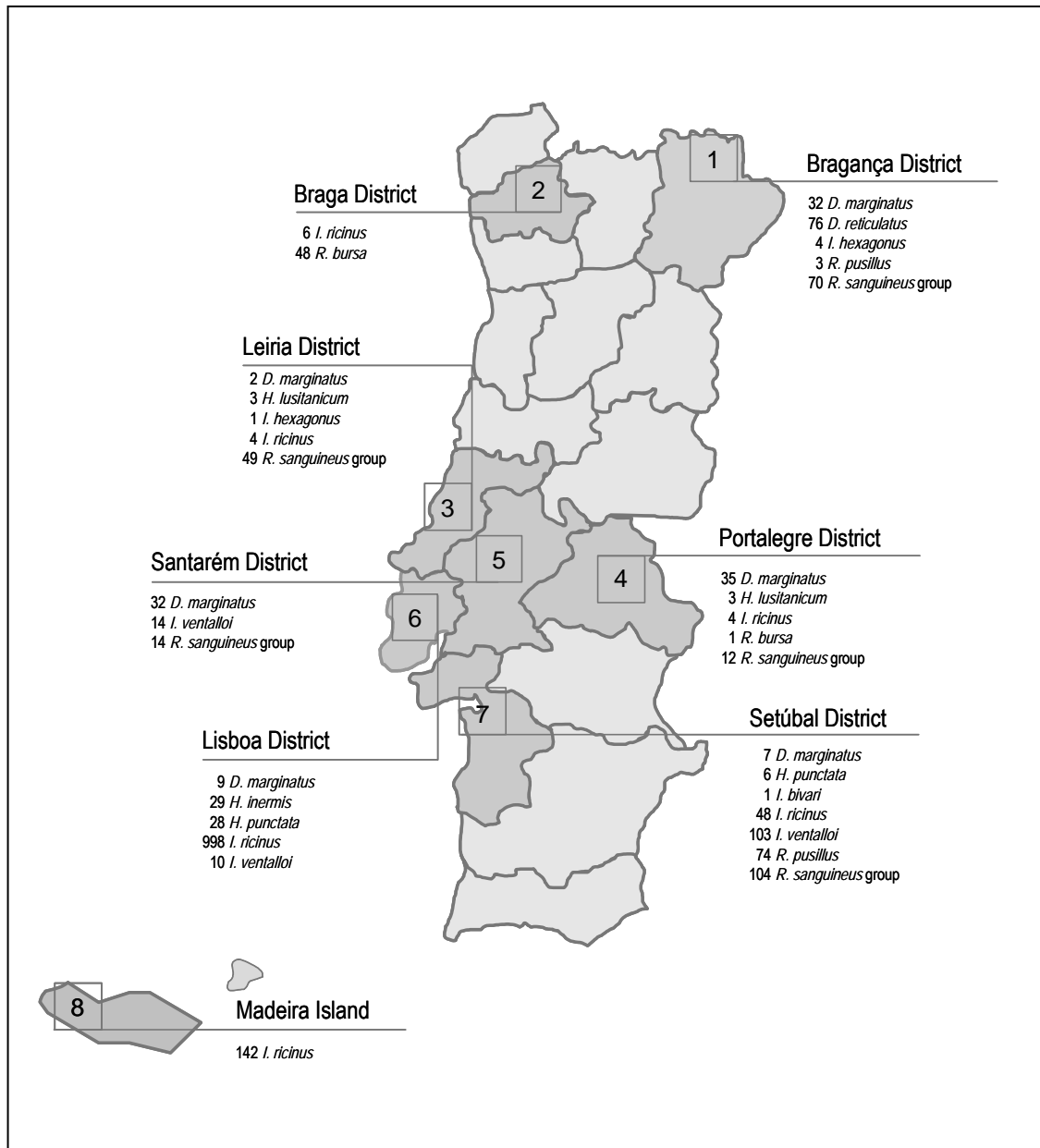
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FIGURE 1. Tick species* and collection areas on the mainland Portugal and in the Madeira Archipelago (2002-2006).



*Ticks species in study: *Dermacentor marginatus*, *D. reticulatus*, *Haemaphysalis inermis*, *H. punctata*, *Hyalomma lusitanicum*, *Ixodes bivari*, *I. hexagonus*, *I. ricinus*, *I. ventraloi*, *Rhipicephalus bursa*, *R. pusillus*, *R. sanguineus* group;
From a total of 2006 ticks, 34 could not be ascribed to any specific collection area.

TABLE 1. *A. phagocytophilum* PCR results from ticks collected in vegetation, according to sampling area, species and gender.

Area	Ticks species*	No tested†‡	No of positives†‡	Sample code
1	<i>D. marginatus</i>	(5M, 5F) ^a 1M, 1F	-	
	<i>D. reticulatus</i>	(1M, 1F) ^a 2M, 1F	-	
	<i>R. sanguineus</i> group	8M, 8F	-	
2	<i>I. ricinus</i>	3N	-	
3	<i>D. marginatus</i>	2F	-	
	<i>H. lusitanicum</i>	2M, 1F	-	
	<i>I. ricinus</i>	3F, 1M	-	
	<i>R. sanguineus</i> group	24M, 21F	-	
4	<i>D. marginatus</i>	14M, 21F	-	
	<i>H. lusitanicum</i>	2M, 1F	-	
	<i>R. bursa</i>	1F	-	
	<i>R. sanguineus</i> group	5M, 7F	-	
	<i>I. ricinus</i>	2M, 1F	-	
5	<i>D. marginatus</i>	14M, 18F	-	
	<i>R. sanguineus</i> group	7M, 7F	-	
6	<i>D. marginatus</i>	3M, 6F	-	
	<i>H. inermis</i>	26M, 3F	-	
	<i>H. punctata</i>	9M, 19F	-	
	<i>I. ricinus</i>	(12M, 12F) ^b (120M, 118F, 710N) ^b , pool	-	
7	<i>D. marginatus</i>	6M, 1F	-	
	<i>H. punctata</i>	2M, 1F, 3N	-	
	<i>I. ricinus</i>	(21M, 19F, 3N) ^c	-	
	<i>I. ventalloi</i>	(36M, 19F, 28N) ^c	(1N) ^c	160
	<i>R. pusillus</i>	27M, 47F	-	
<i>R. sanguineus</i> group	56M, 44F	-		
8	<i>I. ricinus</i>	(1M, 2F, 139N) ^c	(6N) ^c	11; 60; 93; 118; 122; 137

*Ticks species in study: *Dermacentor marginatus*, *D. reticulatus*, *Haemaphysalis inermis*, *H. punctata*, *Hyalomma lusitanicum*, *Ixodes ricinus*, *I. ventalloi*, *Rhipicephalus bursa*, *R. pusillus*, *R. sanguineus* group;

†M male, F female, N nymph;

‡Ticks in parentheses were previously processed for *A. phagocytophilum* testing and described elsewhere: ^aSantos-Silva *et al.*, 2006a; ^bSantos *et al.*, in submission; ^cSantos *et al.*, 2004;

^{pool}ticks were processed in pools according to sampling area, stage and gender, comprising 30 pools of adult ticks (ranging from 2 to 20 arthropods) and 6 pools of immatures (ranging from 55 to 200 arthropods).

TABLE 2. *A. phagocytophilum* PCR results from ticks collected parasitizing vertebrate hosts, according to sampling area, species and gender.

Host	Ticks Species*	No tested per area†‡	No of positives†‡	Sample code
Wild birdsΨ				
<i>Alcedo athis</i>	<i>H. marginatum</i>	<u>Area NA</u> - (7N) ^a	-	
<i>Athene noctua</i>	<i>H. marginatum</i>	<u>Area NA</u> - (1N) ^a	-	
<i>Asio flammeus</i>	<i>I. ventalloi</i>	<u>Area NA</u> - (5M, 7F, 5N) ^a	-	
<i>Bubo bubo</i>	<i>H. marginatum</i>	<u>Area NA</u> - (4N) ^a	-	
<i>Buteo buteo</i>	<i>R. sanguineus</i> group	<u>Area NA</u> - (3F) ^a	-	
Feral mammals				
<i>Canis lupus</i>	<i>D. reticulatus</i>	<u>Area 1</u> - (1F) ^b	-	
	<i>I. ricinus</i>	<u>Area 2</u> - 1N	-	
<i>Capreolus Capreolus</i>	<i>I. ricinus</i>	<u>Area 2</u> - 1F	-	
<i>Dama dama</i>	<i>I. ricinus</i>	<u>Area 6</u> - (9M, 17F) ^{c, pool}	-	
<i>Meles meles</i>	<i>I. hexagonus</i>	<u>Area 3</u> - 1F	-	
<i>Mustela putoris</i>	<i>I. acuminatus</i>	<u>Area NA</u> - 2F	-	
Domestic mammals/ Men				
<i>Canis familiaris</i>	<i>D. marginatus</i>	<u>Area 1</u> - (2F) ^b 5M, 6F	-	
	<i>D. reticulatus</i>	<u>Area 1</u> - (20M, 13F) ^b 19M, 15F	-	
	<i>I. hexagonus</i>	<u>Area 1</u> - 1F, 3N	-	
	<i>R. sanguineus</i> group	<u>Area 1</u> - (1F, 27N) ^b 4M, 4F	-	
	<i>R. pusillus</i>	<u>Area 1</u> - 1M, 2F	-	
<i>Capra hircus</i>	<i>D. marginatus</i>	<u>Area 1</u> - 1M, 1F	-	
	<i>R. sanguineus</i> group	<u>Area 1</u> 1M, 1F <u>Area 3</u> 1M, 3F	-	
<i>Equus caballus</i>	<i>R. bursa</i>	<u>Area 2</u> - 29M, 19F	-	
<i>Felis catus</i>	<i>I. bivari</i>	<u>Area 7</u> - 1F	-	
	<i>I. ventalloi</i>	<u>Area 5</u> 14F; <u>Area 6</u> 4M, 6F; <u>Area 7</u> (4M, 6F) ^d 2M, 8F	<u>Area 5</u> 1F <u>Area 7</u> (1M) ^d	348 246
<i>Ovis aires</i>	<i>D. marginatus</i>	<u>Area 1</u> - 2M, 3F	-	
	<i>D. reticulatus</i>	<u>Area 1</u> - 1M, 2F	-	
	<i>R. sanguineus</i> group	<u>Area 1</u> - 8M, 8F	-	
<i>Homo sapiens</i>	<i>I. ricinus</i>	<u>Area 2</u> 1N; <u>Area 4</u> 1F; <u>Area 7</u> 5F		
	<i>R. sanguineus</i> group	<u>Area 7</u> - 1F, 3N		

*Ticks species in study: *Dermacentor marginatus*, *D. reticulatus*, *Hyalomma marginatum*, *Ixodes acuminatus*, *I. bivari*, *I. hexagonus*, *I. ricinus*, *I. ventalloi*, *Rhipicephalus sanguineus* group;

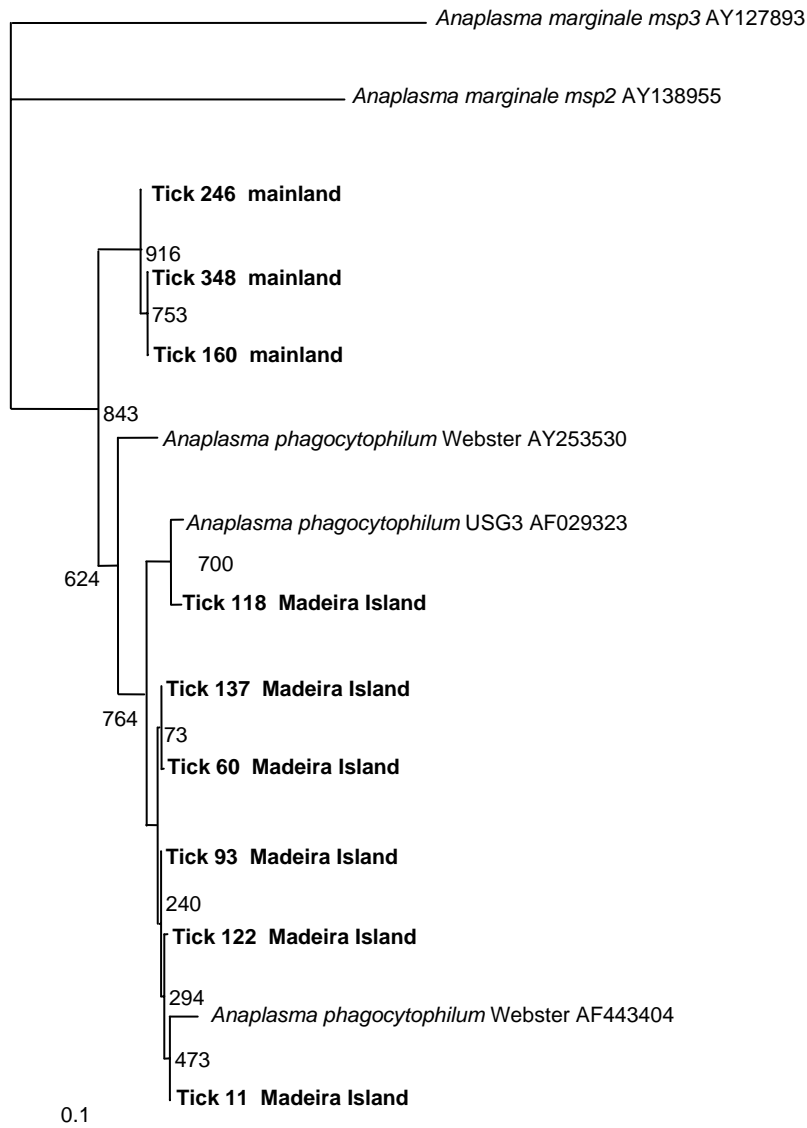
†M male, F female, N nymph;

‡Ticks in parentheses were previously processed for *A. phagocytophilum* testing and described elsewhere: ^aSantos-Silva *et al.*, 2006b; ^bSantos-Silva *et al.*, 2006a; ^cSantos *et al.*, in submission; ^dSantos *et al.*, 2004; NA Ticks that could not be ascribed to any specific collection area;

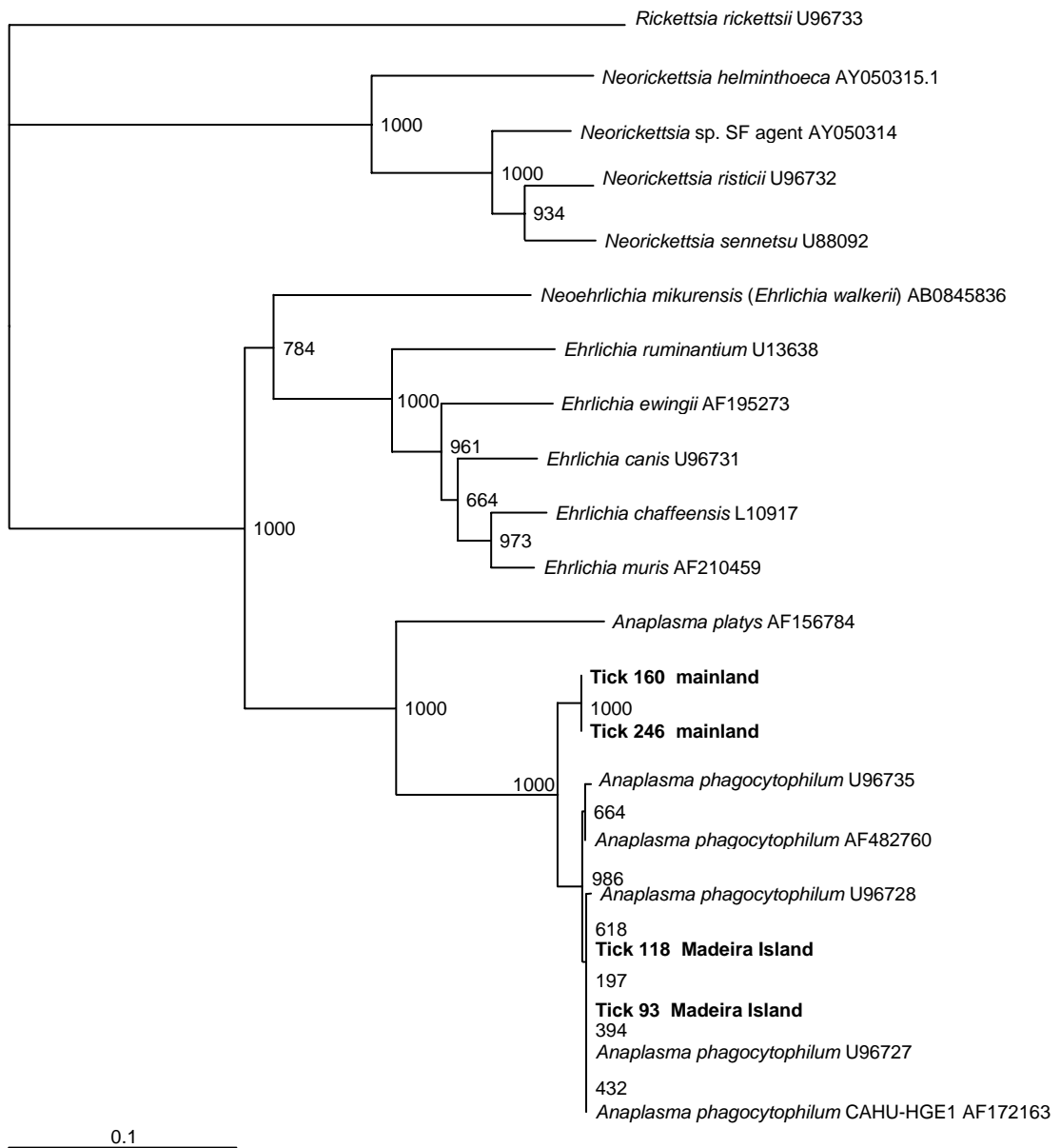
ΨBirds in study were found wounded and sent to 2 rehabilitation centres located in Setúbal and Lisboa District, respectively. The geographic area of capturing was missing for all animals.

^{pool}Ticks were processed in pools comprising 6 pools of adult ticks (ranging from 2 to 10 arthropods), according to the animal sampled and ticks gender.

FIGURE 2- Dendrograms showing the phylogenetic relationships between *A. phagocytophilum* sequences presented in this study and other Anaplasmataceae based on partial nucleotide sequences of the *msp2* (A), *rrs* (B), and *groESL* (C). Bootstrap values (out of 1000 iterations) are shown at the nodes. Bar = substitutions/1000 bp.

A) *msp2*

C) *groESL*



CHAPTER IV

ANAPLASMA PHAGOCYTOPHILUM IN NON-HUMAN VERTEBRATE HOSTS

4.1. DETECTION OF ANTIBODIES AGAINST *ANAPLASMA PHAGOCYTOPHILUM* IN WILD-RODENTS, PORTUGAL

SANTOS AS, AMARO F, SANTOS-SILVA MM, DE SOUSA R, MATHIAS ML, RAMALHINHO MG,
NUNCIO MS, ALVES MJ, BACELLAR F; DUMLER JS

RESEARCH ARTICLE

IN SUBMISSION

Detection of antibodies against *Anaplasma phagocytophilum* in wild-rodents, Portugal

Santos AS¹, Amaro F¹, Santos-Silva MM¹, De Sousa R¹, Mathias ML², Ramalhinho MG^{2,3}, Nuncio MS¹, Alves MJ¹, Bacellar F¹; Dumler JS⁴

¹Centro de Estudos de Vectores e Doenças Infecciosas, Instituto Nacional de Saúde Dr. Ricardo Jorge, Lisboa, Portugal;

²Centro de Biologia Ambiental, Faculdade de Ciências de Lisboa, Lisboa;

³Museu de História Natural, Lisboa;

⁴Division of Medical Microbiology, Department of Pathology, The Johns Hopkins University School of Medicine, Baltimore, Maryland, USA.

Corresponding author: Ana Sofia Pereira dos Santos. Centro de Estudos de Vectores e Doenças Infecciosas, Instituto Nacional de Saúde Dr. Ricardo Jorge, Edifício LEMES, Avenida Padre Cruz, 1649-016 Lisboa, Portugal;

Tel: +351 217 508 125; Fax: +351 217 508 521

e-mail: ana.santos@insa.min-saude.pt

ABSTRACT

The recent detection of *Anaplasma phagocytophilum* in Portugal stimulated further research on the agent's enzootic cycle, which usually involves rodents. Thus a total 322 rodents belonging to five species, including *Apodemus sylvaticus*, *Mus musculus*, *M. spretus*, *Rattus norvegicus* and *R. rattus*, were studied by indirect immunofluorescent assay (IFA) and/or polymerase chain reaction (PCR) for *A. phagocytophilum* exposure in four sampling areas of mainland and two areas of Madeira Island, Portugal. Overall, 3% (6/194) of *M. spretus* presented with IFA-positive results. Seropositive mice were detected in all three sampling areas of mainland where this species was captured, with prevalence of 5.2% (5/96) and 5.0% (1/20) for the *Ixodes*-areas of Arrábida and Mafra, and 1.3% (1/78) for Mértola, a difference that was not statistically significant. Regardless neither the seropositive mice nor the additional sample of 23 *M. musculus* and 5 *R. norvegicus* collected in Madeira Island showed evidence of *A. phagocytophilum* active infections when spleen and/or lung samples were tested by PCR. Either the *M. spretus* results represents residual antibodies from past *A. phagocytophilum* infections, present infections with limited bacteremia, or cross-reactions with closely related agents deserves more investigation.

RUNNING TITLE

Anaplasma phagocytophilum antibodies in wild-rodents, Portugal

KEYWORDS

Anaplasma phagocytophilum; *Apodemus sylvaticus*; *Mus musculus*; *Mus spretus*; *Rattus norvegicus*; *Rattus rattus*; Indirect immunofluorescent assay (IFA); Polymerase chain reaction (PCR); Portugal;

INTRODUCTION

Rodents are important hosts for several *Ixodes* spp. ticks (Acari:Ixodidae), especially for larvae, to some extent also for nymphs, and in the case of host-specific species, for adults as well (Zeidner *et al.*, 2000; Brown *et al.*, 2003, 2006). Thus, it is not surprising that rodents play a role in enzootic cycles of some *Ixodes*-borne agents, such as the human pathogens *Borrelia burgdorferi* s.l., *Babesia* spp. and tick-borne encephalitis (TBE) viruses (Labuda & Randolph, 1999; Kjemtrup & Conrad, 2000; EUCALB).

Anaplasma phagocytophilum [formerly *Ehrlichia phagocytophilum*, *E. equi* and human granulocytic ehrlichiosis (HGE) agent] is another example of an agent transmitted by *Ixodes* species (Dumler *et al.*, 2001). This bacterium is distributed worldwide and has long been known in the veterinary field as a cause of disease in ruminants and horses, more recently also in dogs and cats, and it is additionally considered an emerging human pathogen that is increasingly being diagnosed in both North America and Europe (Dumler *et al.*, 2001; Strle, 2004; Dumler, 2005; Lotric-Furland *et al.*, 2006). Despite the broad-range of susceptible hosts, the occurrence of *A. phagocytophilum* variant strains with distinct pathogenicity and enzootic cycles has been suggested. Both molecular and experimental cross-infection studies has demonstrated that *A. phagocytophilum* strains associated to human, equine, and canine disease are identical or highly similar but distinct from those associated with ruminants (Chae *et al.*, 2000; Pusterla *et al.*, 2001; Stuen *et al.*, 2003). Variant strains have been detected in ticks but the apparent lack of *A. phagocytophilum* transovarial transmission in these arthropods indicates that competent vertebrates, especially those that represent a feeding support for larvae and nymphs, play potential roles in the maintenance of agent's active cycles. Although the natural history of *A. phagocytophilum* is still unfolding, variant strains causing disease in cows and sheep are especially found in wild ruminants such as cervids (Massung *et al.*, 2005, 2006). In contrast, the maintenance of variant strains involved in non-ruminant disease is believed to be dependent on tick-rodent cycles (Massung *et al.*, 2003), with humans and possibly domestic animals being involved as incidental "dead-end" hosts. In the United States *Peromyscus leucopus* (white footed mouse) and *Neotoma fuscipes* (dusky footed woodrat) are competent reservoirs in Eastern and Western regions, respectively (Telford *et al.*, 1996; Castro *et al.*, 2001; Foley *et al.*, 2002). Moreover, PCR-based studies show *A. phagocytophilum* DNA in several other rodent species, including *Myodes* (formerly *Clethrionomys*) *gapperi*, *Neotoma mexicana*, *Microtus orchogaster*, *Peromyscus*

maniculatus, *P. truei*, *Sciurus griseus*, *Spermophilus lateralis*, *Tamias minimus* and *T. striatus* in North America (Walls *et al.*, 1997; Nicholson *et al.*, 1999; Zeidner *et al.*, 2000; DeNatale *et al.*, 2002; Lane *et al.*, 2005), *Apodemus agrarius*, *A. flavicollis*, *A. sylvaticus*, *Myodes* (formerly *Cletrionomys*) *glareolus*, *Microtus agrestis*, *M. oeconomus* and *Rattus rattus* in Europe (Liz *et al.*, 2000; Brown *et al.*, 2003, 2006; Christova & Gladnishka, 2005; Grzeszczuk *et al.*, 2006), and *Apodemus agrarius*, *A. peninsulae* and *Tamias sibiricus* in Asia (Cao *et al.*, 2006).

In Portugal, *A. phagocytophilum* DNA has been detected in two *Ixodes* species, *Ixodes ricinus* collected from Madeira Island and *I. ventalloi* on the mainland (Núncio *et al.*, 2000; Santos *et al.*, 2004). Moreover, the Public Health importance of Portuguese strains of *A. phagocytophilum* is under study given the recent detection of active infection in a horse (Santos *et al.*, in submission b) and given the presence of antibodies against this agent in *Ixodes*-exposed patients (Santos *et al.*, 2006). Although no information is available regarding the natural history of *A. phagocytophilum* in Portugal, several rodents might be involved in agent's maintenance as they are known hosts for *Ixodes* species that can sustain active infection, including *Apodemus sylvaticus*, *Elyomys quercinus*, *Mus spretus*, *Rattus norvegicus* for both *I. ricinus* and *I. ventalloi*, and also *Rattus rattus* and *Sciurus vulgaris* for *I. ricinus* (Dias *et al.*, 1994; MM Santos-Silva, unpublished data). Based on serological and molecular analyses of archived rodent sera and organ samples available from Center for Vector and Infectious Diseases Research, National Institute of Health Dr. Ricardo Jorge (CEVII/INSA), the present study investigates the potential role of Portuguese rodent species in the maintenance *A. phagocytophilum* enzootic cycles.

MATERIAL AND METHODS

Sample collection. The rodents in this study were captured from 1998 through 2004 in three littoral areas (Arrábida, Gerês, Mafra) and one inland area (Mértola) of mainland Portugal and from 1998 through 1999 on Madeira Island (Santana, Seixal). In all the mainland littoral areas and Madeira Island the existence of *Ixodes* species was previously documented (further designated as *Ixodes*-areas). The animals were captured as part of ongoing projects to study rodent population dynamics and rodent-borne diseases by using baited Sherman and Tomahawk live-traps (H. B. Sherman Traps, Inc., Tallahassee, Florida; Tomahawk Live Traps Company, Tomahawk, Wisconsin). One trapping session was performed per season on the mainland, and only in spring

on Madeira Island, each conducted over 3 consecutive nights. Trapping and handling procedures were approved by the Institute for Conservation of Nature and Biodiversity (*ICNB*). Once in the laboratory, rodents were anesthetized with ethyl ether and biometric measurements were recorded to aid in identification to the species level. The presence of ectoparasites was investigated (no ectoparasite specimens were available for *A. phagocytophilum* testing) and whole-blood samples were collected in serum-gel microtainers (Microtainer; Becton Dickinson, New Jersey) by submandibular venous plexus puncture. Sera were recovered from blood either by gravity sedimentation or by centrifugation at 1000 x g for 10 min, and saved for serology. After euthanasia by cervical dislocation, organs were aseptically harvested, in most cases including spleen and lung samples (mainland specimens) or only lung samples (Madeira Island specimens); samples were individually cryopreserved in liquid nitrogen until use.

Serology. For detection of *A. phagocytophilum* antibodies, an indirect immunofluorescent assay (IFA) was used to screen all the available rodent sera. This included only mainland specimens, since no sera were available from Madeira Island rodents. IFA was performed according to *CEVDI/INSA* procedure using *A. phagocytophilum* Webster strain as a source of antigen. Briefly, uninfected HL-60 human promyelocytic leukaemia cells (ATCC CCL-240), at a concentration of 2×10^5 cells/ml, were inoculated at a 3:1 ratio with *A. phagocytophilum*-infected HL-60 cells, and maintained in antibiotic-free RPMI-1640 medium (Gibco-BRL, UK), supplemented with 2 mM L-glutamine (Gibco-BRL, UK), 1% heat-inactivated fetal bovine serum (FBS; Gibco-BRL, UK) at 37°C in 5% CO₂ atmosphere. When cultures reached an infection rate of 85-95%, cells were harvested by a low speed centrifugation (400 x g for 10 min) and resuspended in 0.1M phosphate buffered saline (PBS; Sigma-Aldrich, Germany) containing 2% FBS and 0.05% sodium azide. The optimal cell concentration was empirically determined by microscopic inspections of Diff-Quik (Medion Diagnostics GmbH, Germany) -stained preparations. Diluted antigen was applied to the wells of teflon-covered slides, allowed to air dry, fixed in cold acetone for 10 min and stored at -20°C until use. For detection of *A. phagocytophilum* antibodies, sera were initially diluted at 1:40 in PBS and applied to antigen-coated wells. Serum obtained from laboratory-reared mice after *A. phagocytophilum* infection (positive control) and PBS (negative control) were included on each antigen slide. After incubation for 30 min at 37°C in a humidified chamber, slides were washed twice in PBS for 5 min, passed through distilled water and air dried. Bound antibodies were detected after an additional incubation of antigen wells with fluorescein isothiocyanate (FITC)-labelled rabbit anti-mouse immunoglobulin G (IgG) (Dako Cytomation, Denmark) or anti-rat IgG

(Serotec, UK) in an optimal dilution of 1:40 in PBS containing 1:6000 Evans blue. The slides were washed as above, mounted with 0.3 M 1,4-diazabicyclo[2.2.2]octane (DABCO; Sigma-Aldrich, Germany) in glycerol-PBS (9:1) buffer at pH 9.0 and examined by fluorescence microscopy. Reactions were assessed for distribution, quality, morphology and intensity of fluorescent staining. Specimens were considered reactive when homogeneous fluorescence of *A. phagocytophilum* morulae or individual organisms were observed in the cytoplasm of HL-60 cells in a distribution similar to that observed using positive control sera. For the purpose of this study an IFA titer ≥ 40 was interpreted as seroreactive, and was subsequently serially diluted to determine the end-point titer, which was reported as the reciprocal of the highest dilution at which specific fluorescence is observed. The independence of proportions of rodent reactive sera was compared using Fisher's exact test. An alpha level of 0.05 was selected to indicate statistical significance.

Molecular analysis. Organ samples from all seropositive rodents captured on mainland Portugal and from 16% of rodents obtained from Madeira Island were tested for *A. phagocytophilum* DNA by polymerase chain reaction (PCR). Genomic DNA was extracted from available spleen (10 mg) and lung (20 mg) samples following the Qiamp Tissue Kit procedure (Qiagen GmbH, Germany). Samples from naïve laboratory-reared mice *A. phagocytophilum* were included as extraction controls. Molecular analysis was performed using nested or single tube PCR reactions target three *A. phagocytophilum* genes with several sets of primers: GE3a/GE10r followed by GE9f/GE2 for the amplification of a 546-bp sequence of *rrs* (16S rRNA gene) (Massung *et al.*, 1998); HS1/HS6 followed by HS43/HS45 for the amplification of a 442-bp sequence of the *groESL* heat-shock operon, (Sumner *et al.*, 1997); and the species-specific MSP465f/MSP980r for the amplification of a 550-bp region including the central hypervariable domain of the major surface protein-2 (*mSP2* or *p44*) genes (Caspersen *et al.*, 2002). Primer sequences and amplification conditions were previously described (Sumner *et al.*, 1997; Massung *et al.*, 1998; Caspersen *et al.*, 2002). PCR was performed in a total volume of 50 μ l, containing 1 μ M of each primer, 2.5 U of Taq DNA polymerase and 200 μ M of each deoxynucleotide triphosphate and 50 mM KCl 10 mM Tris-HCL pH 8.3, and 1.5 mM Mg²⁺ (Eppendorf MasterTaq Kit, Germany), and 10 μ l DNA extract (or 1 μ l of amplicon in nested reactions). Water and DNA from known negative samples and *A. phagocytophilum* Webster strain genomic DNA were tested in each PCR run as controls. Prevention of cross-contamination was managed by using barrier

pipette tips and by performing PCR in a separate room from that used for DNA extraction.

RESULTS

A total of 322 rodents belonging to five species in four genera were included in this study, comprising 30 *Apodemus sylvaticus* (wood mouse), 65 *Mus musculus* (house mouse), 194 *M. spretus* (algerian mouse), 5 *Rattus norvegicus* (brown rat) and 28 *R. rattus* (black rat). The distribution of rodent species per sampling area in mainland Portugal and Madeira Island are presented in figure 1.

The 294 rodents captured on the mainland, including 30 *A. sylvaticus*, 42 *M. musculus*, 194 *M. spretus* and 28 *R. rattus*, were initially screened by IFA for the presence of *A. phagocytophilum* antibodies. Overall, 7 mice identified as *M. spretus* were found to be seroreactive, presenting with IFA titers ranging from 80 to 320 (Table 1). The IFA-reactive *M. spretus* were detected in all three sampling areas where this species was captured, including Arrábida, Mafra and Mértola. The highest seroprevalences were observed in the *Ixodes*-areas of Arrábida and Mafra (n=5 [5.2%] and n=1 [5%], respectively), although the difference was not statistically significant when compared to Mértola (n=1 [1.3%]; $P>0.22$). Moreover, *M. spretus* were not more likely to have *A. phagocytophilum* antibodies ($P=0.09$) than the other species. Seroreactive mice were captured in all seasons: August 2002 (n=1), March 2003 (n=2), January 2004 (n=1) and April 2004 (n=1) in Arrábida; Jun 2000 (n=1) in Mafra; October 2003 (n=1) in Mértola. Analysis of proportions showed that spring was the season when seroreactive mice were more likely to be found when considering either Arrábida alone ($P=0.026$) or all *M. spretus* sampling areas together ($P=0.021$). Spleen and lung samples from all IFA-positive mice were additionally tested by PCR for the presence of *A. phagocytophilum* DNA but no positive results were detected (Table 1).

The 28 rodents captured in Madeira Island, including 23 *M. musculus* and 5 *R. norvegicus*, were tested only by PCR, since no sera samples were available at CEVDI/INSA for serology. PCRs performed on lung samples were negative for the three *A. phagocytophilum* genes analysed (Table 1).

DISCUSSION

This study provides evidence for exposure of *M. spretus* to *A. phagocytophilum* or a closely related agent in Portugal. Seropositive mice were detected in all sampling areas where this species was captured, including the *Ixodes*-areas of Arrábida and Mafra, as well as Mértola. Of interest is that collection sites in Arrábida were located in the same valley and nearby the area defined as Baixa de Palmela (Setúbal District) where a previous PCR-based study detected *A. phagocytophilum* infections in *I. ventalloi* ticks (Santos *et al.*, 2004). Moreover, *M. spretus* is a known vertebrate host for both *I. ventalloi* and *I. ricinus* ticks (Dias *et al.*, 1994); the latter tick species is regarded as the major vector of *A. phagocytophilum* in Southern, Central and Northern Europe (Dumler *et al.*, 2001; Strle, 2004). Thus these mice could be involved both in *A. phagocytophilum* primary infection cycles, promoting agent circulation between the exophylic *I. ricinus*, and in parallel cycles between endophylic species, or ticks with a more limited questing behaviour, such as *I. ventalloi*. This double involvement in *A. phagocytophilum* cycles occurs with other rodents, as with *Neotoma* sp. parasitized by *I. pacificus* and *I. spinipalpis* ticks in Colorado (Zeidner *et al.*, 2000; Burkot *et al.*, 2001), and with *M. glareolus*, and *M. agrestis* parasitized by *I. ricinus* and *I. trianguliceps* ticks in United Kingdom (Bown *et al.*, 2003, 2006).

In general, *M. spretus* mice can be found across the country especially in grassland, arable land, and rural gardens, selecting for humid biotypes. This mouse is usually crepuscular to nocturnal and is maximally active during spring through summer. The period from spring to early summer is also regarded as the time when most of *A. phagocytophilum* infections or reinfections occur in rodents, a seasonality that possibly results from the abundance of *Ixodes* spp. nymphs, and has been demonstrated in multicapture studies by examining PCR and/or by examining increase in specific antibody titers of rodent populations (Stafford *et al.*, 1999; Castro *et al.*, 2001). In our study, spring was indeed the season in which the most significant number of *A. phagocytophilum* reactive mice were detected. However, no other statistically significant difference was found in the proportion that were seropositive, even between rodent species or sampling areas, probably due to the limited number of animals studied in each location.

In areas where *A. phagocytophilum* cycles are known to occur, a proportion of rodents are simultaneously PCR and IFA-positive, varying from 20-68% for *P. leucopus* (Walls *et al.*, 1997; Yeh *et al.*, 1997; Stafford *et al.*, 1999; Levin *et al.*, 2002), 58-100% for *N. fuscipes* (Nicholson *et al.*, 1999; Castro *et al.*, 2001; Foley *et al.*, 2002) and 20-33% for *P. truei* (Nicholson *et al.*, 1999; Castro

et al., 2001). These findings seem to reflect either the occurrence of persistent infections or the interval during which immunity is strengthening before the elimination or suppression of bacteremia. Most of the studies regarding seasonal dynamics of *A. phagocytophilum* showed that although the majority of infections appeared to be transient, in a limited number of rodents, the agent can persist. Active infections of *A. phagocytophilum* can last at least 1 month in naturally-infected *M. glareolus* in United Kingdom (Brown *et al.*, 2003), 60 days-14 months in naturally and experimentally infected *N. fuscipes* in Western US (Castro *et al.*, 2001; Foley *et al.*, 2002), and 1-10 months in naturally and experimentally infected *P. leucopus* (Stafford *et al.*, 1999; Levin *et al.*, 2002; Massung *et al.*, 2004). Additionally, Levin and Fish (2000) showed that seropositive *P. leucopus* are only partially protected from reinfection. Regardless, in our case no *A. phagocytophilum* IFA-reactive *M. spretus* had an active infection, even using a cut-off criteria of 1:16-1:80 as the referenced studies (Walls *et al.*, 1997; Yeh *et al.*, 1997; Stafford *et al.*, 1999; Castro *et al.*, 2001; Nicholson *et al.*, 2001; Foley *et al.*, 2002; Levin *et al.*, 2002). Since the range, distribution, and magnitude of antibody titers produced by most wildlife species for *A. phagocytophilum* infection are largely unknown, it is prudent to avoid setting an arbitrary cut-off. Analysis of low titers is essential, particularly when little is known and clinical signs of illness cannot be discerned (as often the case in wildlife), although the risk is false positive serological reactions that could bias seroprevalence results. As a compromise for sensitivity and specificity, all sera were screened at 1:40, a dilution below the cut-off value currently used in our laboratory for human serology that is broadly accepted as the minimal definition of seropositivity against *A. phagocytophilum* (Dumler *et al.*, 1995). In fact, all samples that were found reactive in the initial dilution also had detectable antibody at a dilutions equal to or above 1:80. Moreover, molecular analyses were performed using PCR protocols generally considered to be highly sensitive (Sumner *et al.*, 1997; Massung *et al.*, 1998; Caspersen *et al.*, 2002) and using organ samples that are widely accepted as adequate for detection of *A. phagocytophilum* infection in both natural and experimentally-infected rodents (Liz *et al.*, 2000; Martin *et al.*, 2000).

The presence of residual antibodies could result from past infections or active *A. phagocytophilum* infection with low level bacteremia that is undetectable by current methods. In fact, inefficient transient infections in mice were described in an experimental study using Ap-variant 1, a dominant *A. phagocytophilum* genotype that seems important in ruminant disease (Massung *et al.*, 2003). *A. phagocytophilum* identified in Portuguese ticks seems distinct from Ap-variant 1, and at least for those detected in *I. ricinus*, similar sequences as those in non-ruminant

disease strains were observed. These data imply that infection of mice and other small mammals is likely important in natural maintenance of *A. phagocytophilum* in Portugal. Besides rodents, both *I. ricinus* and *I. ventraloi* may parasitize several other small and medium size mammalian hosts that could be potential reservoirs for *A. phagocytophilum*, including members of the orders Soricomorpha, Lagomorpha, Erinaceomorpha, and Carnivora (Dias *et al.*, 1994; MM Santos-Silva unpublished data). Moreover, the potential presence of *A. phagocytophilum* ruminant strains in our country can not be excluded because no study has yet addressed this animal population. A Spanish study performed on *I. ricinus* collected from bovines identified the presence of Ap-variant 1, and this proximity is motivation for further study (Portillo *et al.*, 2005). Apart from the economic relevance of *A. phagocytophilum* ruminant strains, a new and interesting epidemiological context for these strains has been recently suggested. This concept argues that *A. phagocytophilum* ruminant strains could interfere or compete with the non-ruminant strains for tick niches, perhaps influencing the incidence or prevalence of human and non-ruminant animal infections (Massung *et al.*, 2002, 2003). Finally, it is also important to consider the possibility of cross-reactions with agents that share antigenic similarities with *A. phagocytophilum*. For example the closely related *A. platys* recently detected in Portugal among dogs with active infections stimulated serologic reactions against *A. phagocytophilum* (Santos *et al.*, in submission a); although, other details regarding the enzootic cycle of *A. platys* are largely unknown active infections in rodents have been already documented in other countries (Chae *et al.*, 2003; Kim *et al.*, 2006).

Rodents from the other *Ixodes*-area on Madeira Island were also studied by PCR for the presence of *A. phagocytophilum* infections, but no positive results were obtained in the 16% of the captured animals available for analysis. *R. norvegicus* and *M. musculus* were the only species captured in the two sampling areas of Santana and Seixal, despite the fact that the rodent fauna of this Island also includes *R. rattus* (Almeida, 1996). To date, no report has yet described *R. norvegicus* as a potential reservoir for *A. phagocytophilum*. In contrast, the peridomestic *M. musculus* is known to be susceptible to infection by this agent, and several inbred strains derived from this species are frequently used in experimental infections with *A. phagocytophilum* (Borjesson & Barthold, 2002). Other studies have demonstrated the persistence of *A. phagocytophilum* in Madeira Island, since infected *I. ricinus* were detected at different periods of time (Núncio *et al.*, 2000; Santos *et al.*, 2004). Yet whether the agent's cycles are supported by rodents or other vertebrate animals remains unknown. This Island presents a great variety of fauna that could serve as hosts for *I. ricinus*, including several bird species, bats, ferrets, goats, sheep,

cows, horses, dogs and cats (domestic and feral). The amphibian *Rana peresi* and the lizard, *Teira dugesii* (formerly referred to as *Lacerta dugesii*) are also described (Almeida, 1996). The presence of an *A. phagocytophilum* strain closely related to human disease strains in North America (Santos *et al.*, 2004, in submission c), argues for a more detailed and directed study to investigate the agent's enzootic cycles and the potential vertebrate reservoir hosts in this Portuguese Island.

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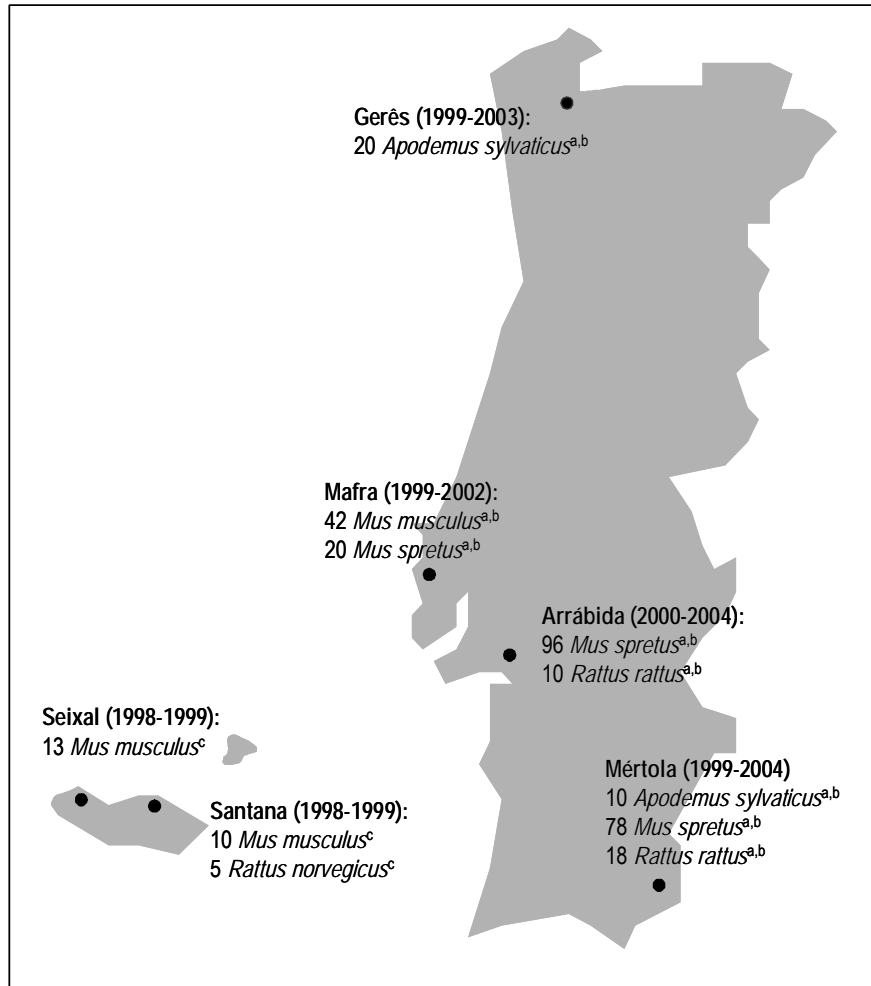
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FIGURE 1. Total number of rodent studied by IFA and/or PCR, according to sampling area (trapping period).



^aStudied by IFA; ^bIFA-seropositives studied by PCR (lung and spleen samples were available for testing); ^cStudied by PCR (only lung samples were available for testing)

TABLE 1. *A. phagocytophilum* results obtained from mainland mice tested by both IFA and PCR and Madeira Island rodents tested by PCR.

Sampling area	Rodent species	IFA results			PCR results			
		No. tested	No. (%) positive	IFA titer	No. tested	No. (%) positive		
						<i>rrs</i>	<i>groESL</i>	<i>msp2</i>
Mainland Portugal:								
Arrábida	<i>Mus spretus</i>	96	5 (5.2)	80	5	-	-	-
Mafra	<i>Mus spretus</i>	20	1 (5.0)	320	1	-	-	-
Mértola	<i>Mus spretus</i>	78	1 (1.3)	80	1	-	-	-
Madeira Island:								
Santana	<i>Mus musculus</i>	Na	Na	Na	10	-	-	-
	<i>Rattus norvegicus</i>	Na	Na	Na	5	-	-	-
Seixal	<i>Mus musculus</i>	Na	Na	Na	13	-	-	-

4.2. SEROLOGICAL SURVEY AND MOLECULAR DETECTION OF *ANAPLASMA PHAGOCYTOPHILUM* INFECTION IN PORTUGUESE HORSES

SANTOS AS, GOMES J, NUNES T, FORMOSINHO P, AGRÍCOLA R, PORTAS M, BACELLAR F;
DUMLER JS

SHORT REPORT

IN SUBMISSION

Serological survey and molecular detection of *Anaplasma phagocytophilum* infection in Portuguese horses

Santos AS¹, Gomes J², Nunes T³, Formosinho P⁴, Agrícola R⁵, Portas M⁶, Bacellar F¹; Dumler JS⁷

¹Centro de Estudos de Vectores e Doenças Infecciosas, Instituto Nacional de Saúde Dr. Ricardo Jorge, Lisboa, Portugal;

²Laboratório Nacional de Investigação Veterinária, Lisboa;

³Centro de Investigação Interdisciplinar em Sanidade Animal - Faculdade de Medicina Veterinária (CIISA-FMV), Lisboa, Portugal;

⁴Laboratório Privado de Análises Clínicas, Lisboa, Portugal;

⁵Centro de Biotecnologia da Universidade dos Açores - Angra do Heroísmo, Açores, Portugal;

⁶Direcção Geral de Veterinária, Lisboa, Portugal;

⁷Division of Medical Microbiology, Department of Pathology, The Johns Hopkins University School of Medicine, Baltimore, Maryland, USA.

Corresponding author: Ana Sofia Pereira dos Santos. Centro de Estudos de Vectores e Doenças Infecciosas, Instituto Nacional de Saúde Dr. Ricardo Jorge, Edifício LEMES, Avenida Padre Cruz, 1649-016 Lisboa, Portugal;

Tel: +351 217 508 125; Fax: +351 217 508 521

e-mail: ana.santos@insa.min-saude.pt

ABSTRACT

Three hundred and two horses from 10 districts of mainland Portugal were tested for serum antibodies against *Anaplasma phagocytophilum* by indirect fluorescent antibody test (IFA). The results demonstrated a seroprevalence of 3% (9/302) with titers ranging from 80 to 640. Moreover, DNA exhibiting nucleotide sequence similarities of 98.9% (*rrs*) and 99.7% (*groESL*) to *A. phagocytophilum* HZ strain were found in an IFA-positive serum sample from Faro District, Algarve region - Southern mainland. This is first definitive evidence of *A. phagocytophilum* active infection in Portuguese mammals and the zoonotic potential of this agent supports the continuing surveillance effort in the country.

RUNNING TITLE

Anaplasma phagocytophilum in horses, Portugal

KEYWORDS

Tick-borne disease; *Anaplasma phagocytophilum*; Horses; Indirect Immunofluorescent Assay (IFA); Polymerase chain reaction (PCR); Portugal;

INTRODUCTION

Anaplasma phagocytophilum (formerly *Ehrlichia phagocytophila*, *E. equi* and HGE agent) is a worldwide, *Ixodes* tick-borne bacterium that affects several domestic animals, including ruminants, horses, dogs and cats, but is also regarded as an emerging human pathogen (Dumler *et al.*, 2001). It causes a disease generically known as granulocytic anaplasmosis, formerly granulocytic ehrlichiosis, a designation that reflects the agent's tropism for polymorphonuclear leucocytes, especially neutrophils. In horses, the disease is usually mild, characterized by fever,

anorexia, depression, limb oedema, petechiae, icterus, ataxia and hematologic abnormalities, such as leukopenia, thrombocytopenia, and anemia (Madigan & Pusterla, 2000). Mortality is low, although complications from opportunistic secondary infection and injury due to ataxia can occur (Madigan & Pusterla, 2000). Equine granulocytic anaplasmosis (EGA) was initially described in 1969, in horses raised in the foothills of the Sacramento Valley, California (Gribble, 1969; Stannard *et al.*, 1969). Since then, it has been chiefly observed in California but sporadic cases of EGA have also been reported in other parts of US and Europe (Johansson *et al.*, 1995; Madigan *et al.*, 1996; Pusterla *et al.*, 1998; Shaw *et al.*, 2001; Bermann *et al.*, 2002; Von Loewenich *et al.*, 2003; Alberti *et al.*, 2005).

The geographic distribution of EGA, as well as other non-ruminant cases of granulocytic anaplasmosis, commonly overlaps those regions where human infection occurs. In fact, several studies demonstrate that *A. phagocytophilum* strains able to cause equine, canine or human disease are genetically identical or highly similar (Johansson *et al.*, 1995; Madigan *et al.*, 1996; Pusterla *et al.*, 1998; Bullock *et al.*, 2000; Chae *et al.*, 2000; Von Loewenich *et al.*, 2003). This relation has also been suggested by experimental cross-infections (Barlough *et al.*, 1995; Madigan *et al.*, 1995; Pusterla *et al.*, 2001). Thus, the study of *A. phagocytophilum* infections in horses or other non-ruminants is important not only for veterinary management, but also to predict human disease risk. In Portugal *A. phagocytophilum* is present in *Ixodes ricinus* and *I. ventralloi* ticks, but its Public Health potential is still incompletely appreciated (Santos *et al.*, 2004). Using serological and molecular surveys, we studied the possibility of *A. phagocytophilum* infection in horses as part of an integrated effort to define the medical importance of this agent in Portugal.

MATERIAL AND METHODS

Sera used in this study were obtained between 2002 and 2006 in collaboration with several Institutions, including *Serviço Nacional Coudélico* (now, *Fundação Alter-Real*), *Faculdade de Medicina Veterinária* and *Instituto Nacional de Investigação Veterinária*. The samples were collected either for routine evaluation or for serosurveillance of infectious diseases such as babesiosis, brucellosis, leptospirosis, herpes virus, contagious metritis, viral arteritis and West Nile virus. Clinical histories were not obtained, although limited information was available for some

animals. Sera were frozen at - 20°C until assayed.

For detection of antibodies against *A. phagocytophilum*, an indirect immunofluorescent assay (IFA) was performed as previously described (Santos *et al.*, in submission). Briefly, sera were diluted at 1:40 and incubated on antigen slides prepared with *A. phagocytophilum* Webster strain-infected HL-60 cells. A second incubation with fluorescein isothiocyanate (FITC)-labelled rabbit anti-horse immunoglobulin G (Sigma-Aldrich, Germany), was used to identify bound antibodies resulting in homogeneous fluorescence of *A. phagocytophilum* morulae. All reactive samples were serial diluted to determine the end-point titer, which was expressed as the reciprocal of the serum dilution. An IFA titer ≥ 80 was interpreted as positive. Univariate statistical analysis for verification of the association between infection, gender, origin, and age class was performed using Fisher's exact test. Statistical analysis was performed using SAS version 9.1 (SAS Institute, Inc., 2002-2003, Cary, NC). An alpha level of 0.05 was selected to indicate statistical significance.

All IFA-positive samples were also tested for the presence of *A. phagocytophilum* DNA by polymerase chain reaction (PCR). Genomic DNA was extracted from 200 μ l of horse serum using the Qiamp Blood Kit procedure (Qiagen GmbH, Germany). A known negative sample was included in every group of three sera extractions as quality control. Nested or single tube PCR reactions targeting *rrs* (16S rRNA gene), *groESL*, and *msp2* (*p44*) genes were performed as previously described (Sumner *et al.*, 1997; Massung *et al.*, 1998; Caspersen *et al.*, 2002), in a total volume of 50 μ l, containing 1 μ M of each primer, 2.5 U of Taq DNA polymerase, 200 μ M of each deoxynucleotide triphosphate, 50 mM KCl 10 mM Tris-HCL pH 8.3, 1.5 mM Mg²⁺ (Eppendorf MasterTaq Kit, Germany), and 10 μ l DNA extract (or 1 μ l of amplicon in nested PCR reactions). In each run, in addition to known negatives (three extraction controls and water), known positive samples were used as controls. Prevention of cross-contamination was managed by using pipette tips with filter barrier, and performing PCR in a three separate room (extraction, master mix preparation, and amplification/electrophoresis). DNA amplicons from positive samples were purified (Jetquick PCR Purification Kit; Genomed GmbH, Germany) and sequenced using an ABI automated sequencer (Applied Biosystems). After manual review and editing, sequence homology searches were performed using BLASTn.

Nucleotide sequence accession numbers: Partial gene sequences generated for *rrs* and *groESL* were deposited in GenBank under the accession numbers EF693890, and EF693889, respectively.

RESULTS

A total of 302 serum samples from 10 districts of Mainland Portugal were studied by IFA (Figure 1). From the limited information provided, horse age and breed were available for 38.4% and 30.8% of the cases, respectively. Individuals represented at least 6 different breeds, including Arabian (n=3), Garrano (n=33), Lusitano (n=47), Quarter (n=1), Sorraia (n=3) and Thoroughbred horses (n=6). Antibodies against *A. phagocytophilum* were detected in 3% (9/302) of sera with titers ranging from 80 to 640 (Table 1). No association was found between *A. phagocytophilum* seroprevalence and the origin of the horses. There was no consistent pattern of seropositivity among age groups or when gender was examined (Table 2). Molecular analysis of IFA-positive sera showed the presence of *A. phagocytophilum* DNA in 1 mare (Seara) from Faro District. The nucleotide sequences obtained exhibited a high degree of similarity with the human *A. phagocytophilum* HZ strain (CP000235), with values of 98.9% (459/464) and 99.7% (466/467) for partial sequences of both *rrs* and *groEL*, respectively.

DISCUSSION

Indirect immunofluorescent antibody test (IFA) is the gold standard for routine *A. phagocytophilum* diagnosis and has been also widely applied in seroprevalence studies. Here, antibodies against *A. phagocytophilum* or another antigenically similar agent were detected in 3% of the horses studied, which is in accordance with the wide range of seroprevalence (0-17.6%) reported in other countries (Madigan *et al.*, 1990; Bullock *et al.*, 2000; Magnarelli *et al.*, 2000; Engevall *et al.*, 2001; Teglas *et al.*, 2005; Amusatequi *et al.*, 2006; Levi *et al.*, 2006). Nevertheless, our seroprevalence is somewhat lower than that obtained in other parts of Europe (Engevall *et al.*, 2001; Amusatequi *et al.*, 2006), but is similar to that reported from *A. phagocytophilum* non-endemic regions in the US (Madigan *et al.*, 1990; Bullock *et al.*, 2000).

In Europe, *Ixodes ricinus* has long been known as a competent vector for *A. phagocytophilum* (Macleod & Gordon, 1933). This tick species present in Portugal a patchy distribution mainly influenced by climate (temperature, humidity and precipitation), landscape fragmentation, and landscape composition (open areas, mixed and deciduous forests) (Baptista,

2006). Although, it has been reported from all districts of mainland Portugal (Caeiro, 1999), the highest prevalence is registered in the littoral of the country (Baptista, 2006). An example of an *I. ricinus*-area is Gerês (in Braga District, Northern littoral) (Caeiro, 1999), from where the 33 Garrano horses studied in this work came from. These are feral horses, traditionally raised freely in the hills; thus, contact with *I. ricinus* is highly likely. Nevertheless, only *Rhiphicephalus bursa* and *Hyalomma marginatum* were found parasitizing these horses at the time of blood collection (data not shown) and none of the animals had *A. phagocytophilum* antibodies. Whether the serological results indicate absence of *A. phagocytophilum* in this region, the inability of any *A. phagocytophilum* variant strains present in *I. ricinus* in this region to establish infection in horses, or simply limited contact between horses and tick species linked to the agent's transmission is a matter deserving further investigation.

An important limitation of IFA testing is the potential for false positive reactions. Several studies demonstrate *A. phagocytophilum* cross-reactivity with phylogenetically-related agents, such as *A. marginale*, *A. platys*, *Ehrlichia chaffeensis* and *E. canis* (Comer *et al.*, 1999; Hinokuma *et al.*, 2001; Waner *et al.*, 2001; Dreher *et al.*, 2005). Although these microorganisms are not known to infect horses, cross-reactions with heat-shock proteins or surface proteins from other non-related agents should not be ruled out. In fact, one horse from Braga District (named Shuma) that presented an IFA titer of 320 against *A. phagocytophilum* also had positive serologic results for both *Leptospira grippityphosa* and equine rhinopneumonitis EHV 1 and EHV 4.

Another issue of serology is the difficulty in differentiating active infection from residual antibodies when only one serum sample is available. Follow-up studies on naturally infected horses have shown the presence of high antibody titers detectable by IFA several months after infection (Van Andel *et al.*, 1998; Artursson *et al.*, 1999). To overcome these limitations, serology is occasionally coupled with molecular testing to detect active *A. phagocytophilum* infections (Bullock *et al.*, 2000; Teglas *et al.*, 2005). In this study, the molecular analysis of all IFA-positive sera revealed *A. phagocytophilum* DNA in one animal from Faro District (named Seara). Confirmation of active *A. phagocytophilum* infection was achieved only by nested PCR, but using 2 separate assays that targeted *rrs* and *groESL* that are much more likely to reflect infection than amplicon contamination. Nested reactions are regarded as highly sensitive and are able to detect very small amounts of DNA, even in serum (Massung *et al.*, 1998). However, it is important to note that negative results obtained from the other IFA-positive horses could be falsely negative because of the inavailability of more reliable samples for molecular testing, such as whole-blood or buffy coat.

The results presented herein are the first definitive evidence of active *A. phagocytophilum* infection in Portuguese mammals, but due to inavailability of complete clinical records, a relationship between infection and disease could not be effectively analyzed. The partial nucleotide sequences of both *rrs* and *groESL* obtained from 1 horse were highly similar to those of *A. phagocytophilum* HZ strain, an isolate obtained from a New York human patient in 1995 (Rikihisa *et al.*, 1997; Hottop *et al.*, 2006); thus, the possibility of human infections by this agent in Portugal cannot be excluded. Algarve is an international tourist destination which receives visitors and their pets from all over the world. In addition, Algarve is in the migratory route of several bird species which could promote the introduction or spread of ticks and tick-borne pathogens. These data coupled with the zoonotic potential of *A. phagocytophilum* supports a continuous surveillance for *A. phagocytophilum* and granulocytic anaplasmosis in Portugal.

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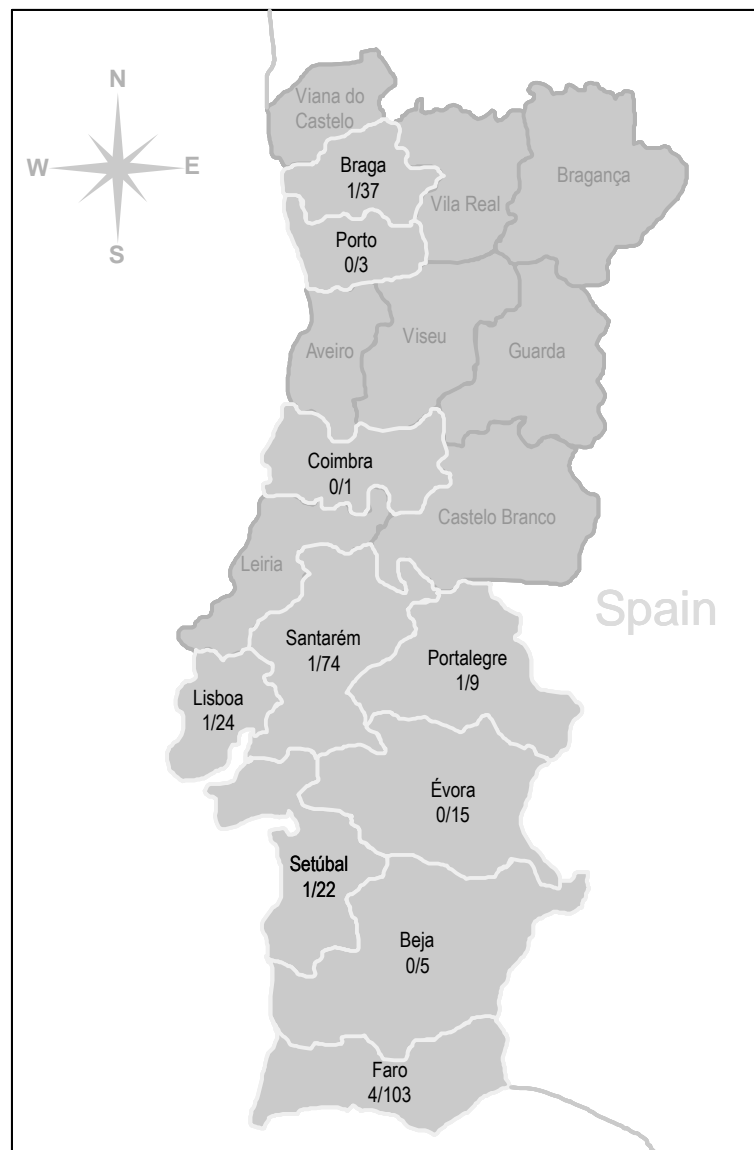


FIGURE 1. Number of *A. phagocytophilum* seropositive cases per total horses studied in each district (origin information was not available for nine animals).

TABLE 1. *A. phagocytophilum* results obtained from mainland mice tested by both IFA and PCR and Madeira Island rodents tested by PCR.

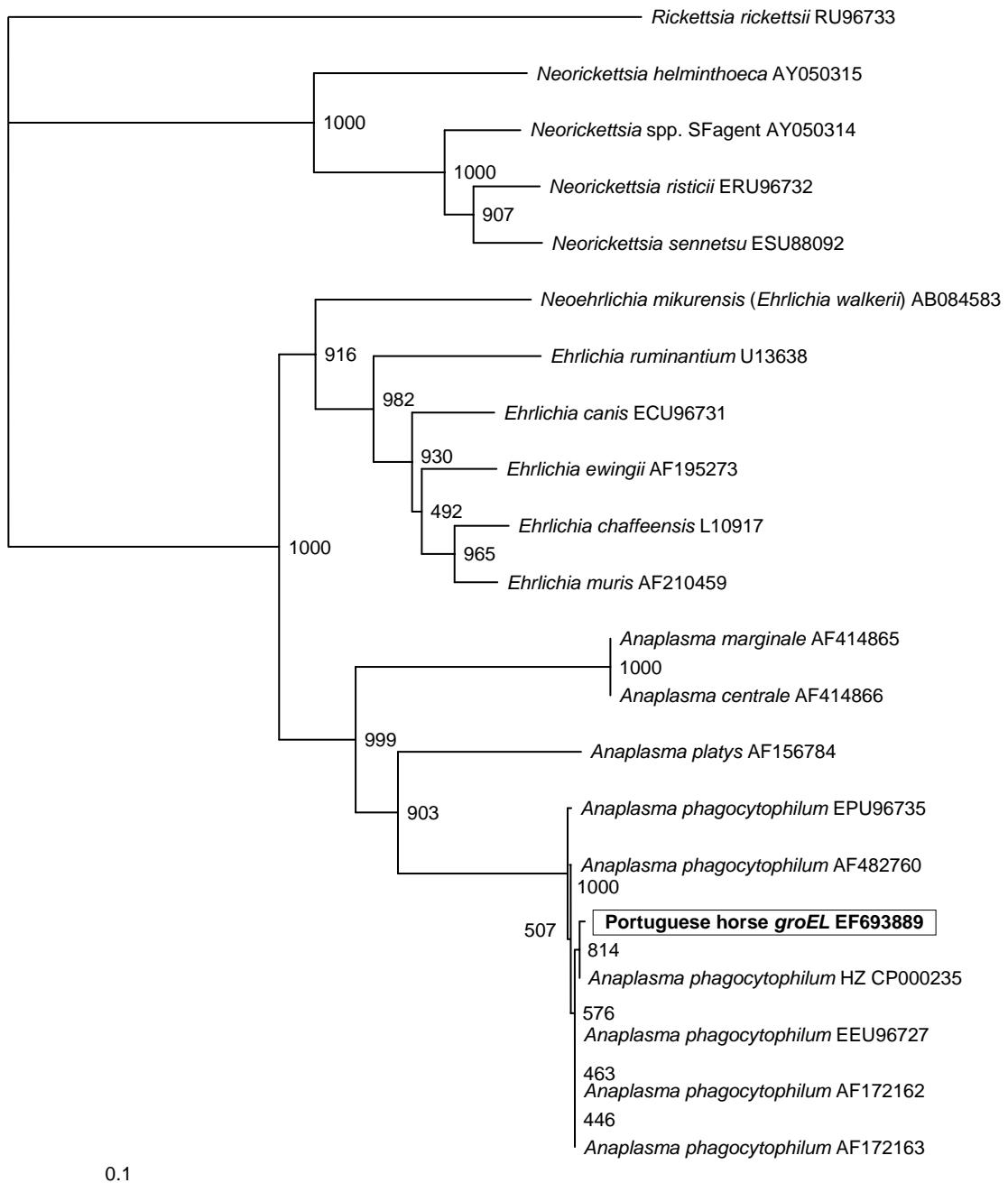
Sampling area	Rodent species	IFA results			PCR results			
		No. tested	No. (%) positive	IFA titer	No. tested	No. (%) positive		
						<i>rrs</i>	<i>groESL</i>	<i>msp2</i>
Mainland Portugal:								
Arrábida	<i>Mus spretus</i>	96	5 (5.2)	80	5	-	-	-
Mafra	<i>Mus spretus</i>	20	1 (5.0)	320	1	-	-	-
Mértola	<i>Mus spretus</i>	78	1 (1.3)	80	1	-	-	-
Madeira Island:								
Santana	<i>Mus musculus</i>	Na	Na	Na	10	-	-	-
	<i>Rattus norvegicus</i>	Na	Na	Na	5	-	-	-
Seixal	<i>Mus musculus</i>	Na	Na	Na	13	-	-	-

TABLE 2. Univariate statistical analysis of *A. phagocytophilum* seropositive horses according to age, gender and origin.

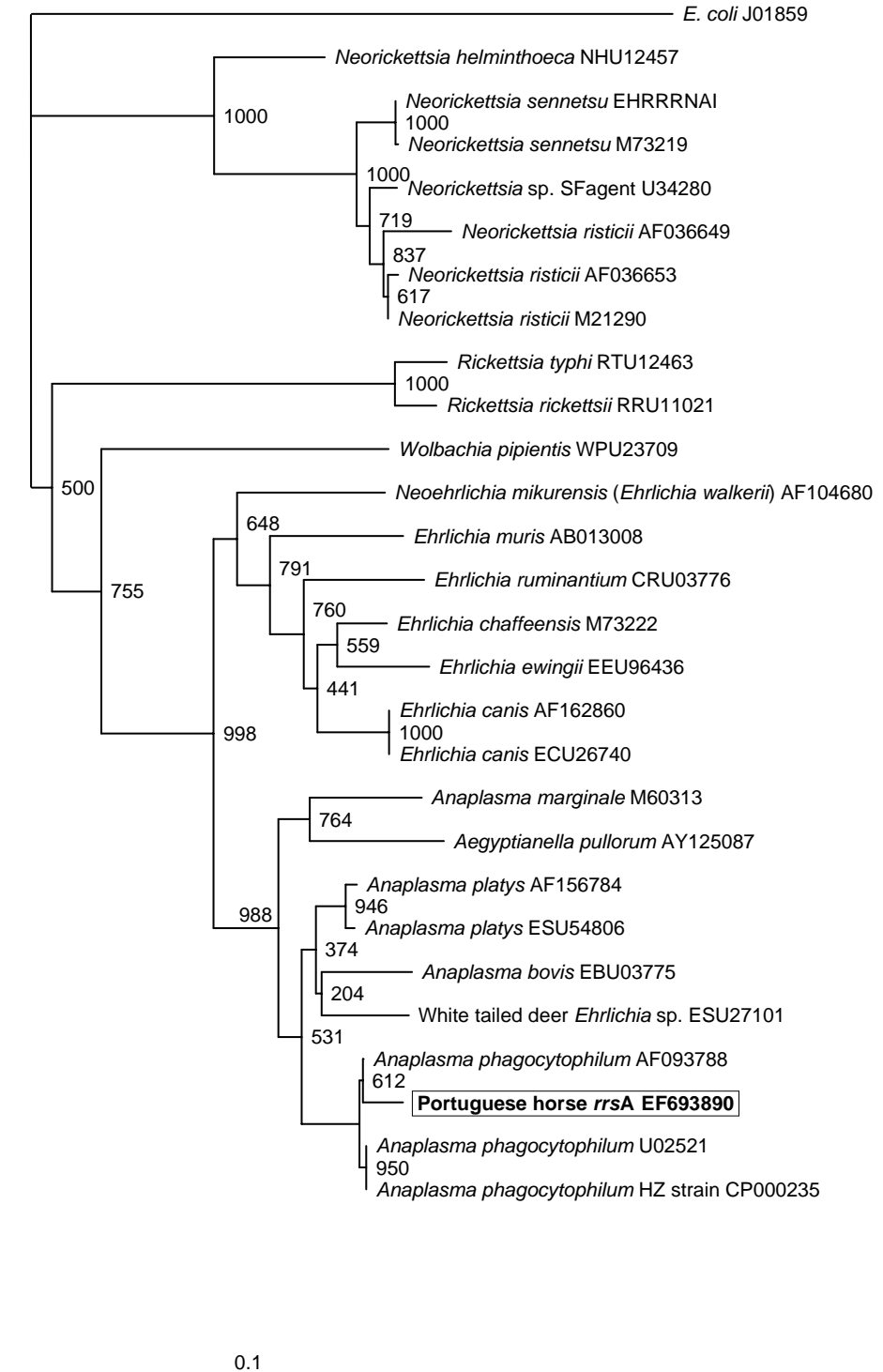
Variable	No of tested horses†	No of seropositive (%)	<i>p</i> value
Age (years)			
0-4	6	0	0.14
5-9	42	4 (9.5)	
>9	68	1(1.5)	
Gender			
Male	80	4(5.0)	1
Female	81	5(6.2)	
Origin			
Bragança	37	1(2.7)	0.64
Beja	5	0	
Coimbra	1	0	
Évora	15	0	
Faro	103	4(3.9)	
Lisboa	24	1(4.2)	
Portalegre	9	1(11.1)	
Porto	3	0	
Santarém	74	1(1.4)	
Setúbal	22	1(4.5)	

†includes only animals with available information.

FIGURE 2. Phylogenetic relationships between *A. phagocytophilum* sequences detected in this study and other Anaplasmataceae based on partial nucleotide sequences of the *groESL* (A) and *rrs* (B). The scale bar represents substitutions per 1,000 base pairs; numbers at nodes represent bootstrap values out of 1,000 iterations. The nucleotide sequences of the index horse are shown in a box; accession numbers for each sequence are also included after the genus and species designations.

A) *groESL*

B) *rrs*



4.3. ANAPLASMATACEAE AS ETIOLOGIC AGENTS OF CANINE TICK-BORNE DISEASE IN PORTUGAL

SANTOS AS, ALEXANDRE N, DE SOUSA R, NÚNCIO MS, BACELLAR F; DUMLER JS

RESEARCH ARTICLE

IN SUBMISSION

Anaplasmataceae as etiologic agents of canine tick-borne disease in Portugal

Ana Sofia Santos¹, Nuno Alexandre², Rita Sousa¹, Maria Sofia Nuncio¹, Fátima Bacellar¹; J. Stephen Dumler³

¹Centro de Estudos de Vectores e Doenças Infecciosas, Instituto Nacional de Saúde Dr. Ricardo Jorge, Lisboa, Portugal;

²Departamento de Zootecnia, Universidade de Évora, Pólo da Mitra, Évora;

³Division of Medical Microbiology, Department of Pathology, The Johns Hopkins University School of Medicine, Baltimore, Maryland, USA.

Corresponding author: Ana Sofia Pereira dos Santos. Centro de Estudos de Vectores e Doenças Infecciosas, Instituto Nacional de Saúde Dr. Ricardo Jorge, Edifício LEMES, Avenida Padre Cruz, 1649-016 Lisboa, Portugal;

Tel: +351 217 508 125; Fax: +351 217 508 521

e-mail: ana.santos@insa.min-saude.pt

ABSTRACT

Fifty five dogs with clinical signs of suspected tick-borne disease were tested by both immunofluorescence assay (IFA) and polymerase chain reaction (PCR) for *A. phagocytophilum*. Overall, 30 (54.5%) dogs presented with IFA positive results, 5 of which fulfilled the serologic criteria for active infection presenting either seroconversion or four-fold increase in antibody titers. PCR analysis failed to detect active *A. phagocytophilum* infections, but *A. platys* DNA was found in 2 seropositive and 3 seronegative animals. This provides the first definitive evidence of *A. platys* infection in Portuguese dogs and emphasizes the importance of considering infectious cyclic thrombocytopenia in the differential diagnosis of canine tick-borne disease in Portugal.

RUNNING TITLE

Anaplasmatataceae infections in dogs, Portugal

KEYWORDS

Tick-borne disease; dogs; *Anaplasma phagocytophilum*; *Anaplasma platys*; IFA; PCR; Portugal.

INTRODUCTION

Five members of the Family Anaplasmatataceae are currently implicated in canine tick-borne disease, including *Anaplasma phagocytophilum*, *A. platys*, *Ehrlichia canis*, *E. chaffeensis*, and *E. ewingii* (Dumler *et al.*, 2001; Shaw *et al.*, 2001). These Gram-negative obligate intracellular bacteria present a marked tropism for myeloid derivatives, multiplying within a membrane-bound cytoplasmic vacuole of the host cell and forming characteristic mulberry shaped microcolonies (morulae). Depending on the bacterial species, monocytes/macrophages (*E. canis*, *E. chaffeensis*), granulocytes (*A. phagocytophilum*, *E. ewingii*), or platelets (*A. platys*) are infected by these microorganisms. Acute Anaplasmatataceae infections are multisystemic disorders generically characterized by a non-specific febrile illness with depression, lethargy, anorexia, splenomegaly,

hepatomegaly, lymphadenopathy and hematological abnormalities (Shaw *et al.*, 2001). Persistent infection is a common feature of many of these organisms in canines, which in some cases may evolve into chronic disease. Canine monocytic ehrlichiosis, caused by *E. canis*, was the first canine Anaplasmataceae infection to be documented and is also one of the most important due to the number of deaths that occur with chronic disease (Donatien & Lestoquard, 1935; Huxsol, 1970; Milonasky *et al.*, 2004; Gal *et al.*, 2007).

In European dogs, only *A. phagocytophilum*, *A. platys* and *E. canis* have been isolated or detected by molecular tests (Johansson *et al.*, 1995; Sparagano *et al.*, 2003; Aguirre *et al.*, 2004). In Portugal, serology has long provided evidence for *E. canis* infection in both stray and clinically ill dogs (Silveira, 1992; Bacellar *et al.*, 1995). Additionally, *E. canis* DNA was recently identified in a case study of 55 dogs with suspected tick-borne disease, confirming canine monocytic ehrlichiosis in approximately one third of the cases (Alexandre, 2006). In the Alexandre study, a number of other tick-borne diseases such as babesiosis, hepatozoonosis, Lyme borreliosis and *Rickettsia conorii* infections were also identified in some cases (Alexandre, 2006). However, the majority of dogs remain undiagnosed. Knowing that *A. phagocytophilum* is present in Portuguese ticks (Santos *et al.*, 2004) the objective of this work was to retest the available samples from those animals in order to investigate the possible role of *A. phagocytophilum* in canine disease.

MATERIAL AND METHODS

The dogs included in this study presented with clinical signs between February and October 2004 among one hospital and seven veterinary clinics located in the Algarve region, in the South of Portugal. During the clinical evaluation, an EDTA-anticoagulated blood sample was collected from each animal for laboratory testing that included complete blood cell count, buffy coat smear examination after Diff-Quik staining (Medion Diagnostics GmbH, Germany), detection of specific antibodies by immunofluorescence assay (IFA), and DNA analysis by polymerase chain reactions (PCR). Whenever possible, a convalescent blood sample was taken to compare the evolution of IFA titers. The procedure adopted for laboratory diagnosis of *Babesia canis*, *Borrelia burgdorferi* s.l., *Hepatozoon canis*, *E. canis*, and *Rickettsia* spp. is described elsewhere (Alexandre, 2006). For *A. phagocytophilum* testing, plasma samples were screened by IFA at an initial dilution of 1:80. Sera were incubated on antigen slides prepared with *A. phagocytophilum*

Webster strain, as described elsewhere (Santos *et al.*, in submission). Fluorescein isothiocyanate (FITC)-conjugated rabbit anti-dog immunoglobulin G (IgG) and M (IgM) (Sigma-Aldrich, Germany) was used to identify bound antibodies that resulted in homogeneous fluorescence of *A. phagocytophilum* morulae. All positive samples were serially diluted to determine the endpoint titer. Serum from a naturally infected dog in the US and phosphate-buffered saline (PBS) were used as controls. Genomic DNA was extracted from the buffy coat following the Flexigene DNA Kit procedure (Qiagen GmbH, Germany). Molecular analysis was performed as nested or single tube PCR reactions using several sets of primers that target three *A. phagocytophilum* genes: GE3a/GE10r followed by GE9f/GE2 for the amplification of a 546-bp sequence of *rrs* (16S rRNA gene) (Massung *et al.*, 1998), HS1/HD6 followed by HS43/HS45 for the amplification of a 442-bp sequence of heat-shock operon, *groESL* (Sumner *et al.*, 1997), and the species-specific MSP465f/MSP980r for the amplification of a 550-bp hypervariable region of surface protein genes, *msp2* (Caspersen *et al.*, 2002). PCR was performed in a total volume of 50 μ l, containing 1 μ M of each primer, 2.5 U of Taq DNA polymerase and 200 μ M of each deoxynucleotide triphosphate and 50 mM KCl 10 mM Tris-HCl pH 8.3, and 1.5 mM Mg²⁺ (Eppendorf MasterTaq Kit, Germany), and 10 μ l DNA extract (or 1 μ l of amplicon in nested reactions). Primer sequences and amplification conditions have been previously described (Sumner *et al.*, 1997; Massung *et al.*, 1998; Caspersen *et al.*, 2002). DNA extracts obtained from the buffy coat of a healthy dog and *A. phagocytophilum* Webster strain propagated in HL-60 cells were used as controls. Since *rrs* and *groESL* primers are able to amplify DNA from other related bacteria besides *A. phagocytophilum*, PCR results from all positive reactions were confirmed by sequence analysis after DNA purification (Jetquick PCR Purification Kit; Genomed GmbH, Germany). Sequencing was performed with the forward and reverse primers used for PCR identification (internal primers in nested reactions) in an ABI automated sequencer (Applied Biosystems), according to manufacturer's instructions. After review and editing, sequence homology searches were made by BLASTN analysis. Sequences derived from this approach were aligned using the neighbor joining protocol with other Anaplasmataceae sequences for *rrs* and *groESL* using ClustalX. After trimming sequences to compare those of similar length, the sequences were re-aligned with ClustalX using the neighbor joining method, with 1000 replicate bootstraps. The resulting trees were produced using TreeView, rooting with *E. coli* as an outgroup for *rrs* and *R. rickettsii* as an outgroup for *groESL*. Partial gene sequences generated in this work are deposited in GenBank under the accession numbers EU004823 (*rrs*), EU004824 and EU004825 (*groESL*). Partial nucleotide sequences determined for *groEL* were

translated into amino acid sequences to determine whether the low level nucleotide heterogeneity identified had an impact on protein structure. To do this, the translated amino acid sequences were aligned (using ClustalX), and truncated so that each began with the initial methionine; dendrograms were constructed using TreeView.

RESULTS

Of 55 dogs with suspected tick-borne disease, 30 (54.5%) had at least one plasma sample with detectable IgG antibodies against *A. phagocytophilum*. The endpoint titers were 80 for 12 samples, 320 for 11 samples, 640 for 4 samples, 1280 for 5 samples, 2560 for 2 samples, 5120 and 10240 for 1 sample each, altogether 36 positive samples. No IgM antibodies against *A. phagocytophilum* were detected in studied animals. In dogs with more than one available sample, 25% (5/20) fulfilled the serologic criteria for active infection, presenting seroconversion (No. 1, 3, 5 and 8) or four-fold increase in antibody titer (No. 6) (Table 1). PCR amplification with *rrs* and *groESL* primers generated products of the expected size in buffy coat samples from 5 dogs, including 3 seronegative animals (No. 4, 7 and 9), 1 which seroconverted (No. 5) and 1 that had a single positive IFA titer (No. 2). No sample was found PCR positive when tested with *A. phagocytophilum* species-specific *msp2* primers. Nucleotide analysis of *rrs* and *groESL* amplicons confirmed this latter result and identified the etiologic agent to be the closely related species *A. platys*. Partial sequences of *rrs* (GenBank accession no. EU004823), excluding the primers regions were identical in all dogs and were 100% (496/496 bp) homologous with previously reported *A. platys* sequences, such as GenBank accession number AY530806 that was identified in a Spanish dog (Figure 1A). Sequence polymorphisms were observed in *groEL* and resulted in 2 different genotypes. DNA nucleotide sequences 99.3% (438/441) and 100% (441/441) similar to *A. platys* described in Venezuela (AF399916) were detected in dogs 2 and 9 (GenBank accession no. EU004825) and in dogs 4, 5 and 7 (GenBank accession no. EU004824), respectively (Figure 1B). Thus, despite the minimal heterogeneity observed at the nucleotide level, the GroEL proteins produced by each of the *A. platys* infecting these Portuguese dogs were identical in the regions examined (Figure 2). Although the *A. platys* positive PCR results, no morulae were found within platelets on blood smear examination. Moreover, the results from other tick-borne agents molecular tests also revealed coinfections. Dog 7 that was previously identified actively infected

with *R. conorii* was also found infected with *A. platys*. Additionally, three dogs (No. 1, 6 and 8) with either *R. conorii* or *E. canis* DNA also fulfilled IFA criteria for active *A. phagocytophilum* infection, although all were *A. platys* PCR negative. Clinical examination revealed that all dogs with molecular confirmation of *A. platys* infection had lymphadenopathy accompanied in the majority of cases by fever (except in dog 9). The most frequent haematological abnormality was thrombocytopenia (5/5 dogs) and anaemia (4/5 dogs). Clinical and laboratory data of dogs fulfilling serodiagnostic criteria for active infection or positive PCR results are summarized in table I.

DISCUSSION

Anaplasma phagocytophilum (formerly *Ehrlichia phagocytophila*, *E. equi* and HGE agent) is the etiologic agent of worldwide veterinary tick-borne disease that affects several domestic animals including ruminants, horses, dogs and cats, but it is also regarded as an emerging human pathogen with increasing importance (Gordon *et al.*, 1932; Gribble, 1969; Madewell & Gribble, 1982; Bakken *et al.*, 1994; Chen *et al.*, 1994; Bjoerdorf *et al.*, 1999). The disease is generically known as granulocytic anaplasmosis (GA) and in dogs it was first recognized by Madewell and Gribble (1982). The geographic distribution of GA in dogs correlates with the endemic areas of the vector ticks, members of the *Ixodes persulcatus/ricinus* complex. The disease is frequently reported in the Northeastern and Upper Midwest parts of United States and in Central and Northern Europe, but there are also some references to its presence in the Mediterranean Region (Manna *et al.*, 2004; Alberti *et al.*, 2005). The recent description of *A. phagocytophilum* in Portuguese *Ixodes* ticks (Santos *et al.*, 2004) suggested a possible role for human and animal infection in Portugal, stimulating further examination of populations with suspected tick-borne disease. In this report we present the cytological, serological and molecular screening of *A. phagocytophilum* infections in a population of dogs with clinical signs who resided in the Algarve region, South of Portugal.

Serological data obtained by IFA testing demonstrated the presence of antibodies against *A. phagocytophilum* in 40% of animals studied, 25% of which fulfilled case criteria for active infection, either by seroconversion or four-fold increase in titer. Despite these findings, the molecular analysis of buffy coat samples failed to identify *A. phagocytophilum* but instead revealed sequences that were highly homologous with the closely related *A. platys*. Serologic cross-

reactivity is common among phylogenetically-related agents that often share antigenic determinants. In fact, at least some of the *A. phagocytophilum* IFA-positive sera detected here were derived from dogs with active *A. platys* infections, a finding also documented by others (Inokuma *et al.*, 2001). Thus it seems likely that *A. platys* rather than *A. phagocytophilum* is the agent responsible for these serologic reactions, although prior infections can not be conclusively excluded. The possibility of cross-reactions with heterologous, Anaplasmataceae, such as *E. canis*, should also be considered. Cross-reactivity between the *E. canis* and *A. phagocytophilum* has been experimentally demonstrated in dogs with canine monocytic ehrlichiosis by the detection of antibodies against *A. phagocytophilum* about 90 days post-infection (Waner *et al.*, 1998). It was proposed that the development of the cross-reacting antibodies was dependent on persistence of *E. canis* infection (Waner *et al.*, 1998). In our study both dogs no. 1 and no. 8 seroconverted for *A. phagocytophilum* but had only *E. canis* DNA in the peripheral blood.

A. platys (formerly *Ehrlichia platys*) was first recognized in the US by Harvey and coworkers (1978) as a cause of canine infectious cyclic thrombocytopenia (CICT). This member of the family Anaplasmataceae is distributed worldwide, particularly associated with the brown dog tick *Rhipicephalus sanguineus*, one of the most prevalent species in Portugal (Caeiro, 1999). In fact, *A. platys* infections were previously suggested by the occasional observation of intra-platelet inclusions on dog peripheral blood smears (Simões & Puente, 1997), but its presence was never definitively proved. This study represents the first documentation of active *A. platys* infections in Portuguese dogs, although in our case no morulae were observed in blood smear examinations. The cyclical nature of CICT, with intermittent bacteremia may increase the difficulty in detection of the agent in peripheral blood (Woodly *et al.*, 1991; Martin *et al.*, 2005). This could explain not only the inability to directly visualize the bacteria in PCR-confirmed cases, but could also explain negative molecular results in dogs with positive *A. phagocytophilum* serology.

CICT is usually described as an asymptomatic or mild disease without obvious clinical signs in spite of the occasional presence of lymphadenopathy and thrombocytopenia (Harvey *et al.*, 1978; Woodly *et al.*, 1991). In our case series, both these hematological findings were present in all confirmed *A. platys*-infected dogs, although the health condition of the animals was sufficiently deteriorated to motivated a visit to the veterinarian. A few other reports also linked CICT to clinical illness, either as a result of *A. platys* infection alone or as a coinfection with other tick-borne agents such as *E. canis* (Mylonakis *et al.*, 2004; Gal *et al.*, 2007). Although most of the present cases apparently represent single infections, DNA from both *A. platys* and *R. conorii* was,

detected in one animal. To our knowledge this study represents the first molecular evidence that *A. platys* infects and causes disease in Portuguese dogs. It further supports the hypothesis that coinfections with multiple tick-borne agents are not uncommon for those that share tick vectors such as *R. sanguineus*. The extent to which coinfections potentiate disease manifestations or complicate the diagnosis and management of sick dogs will require further study.

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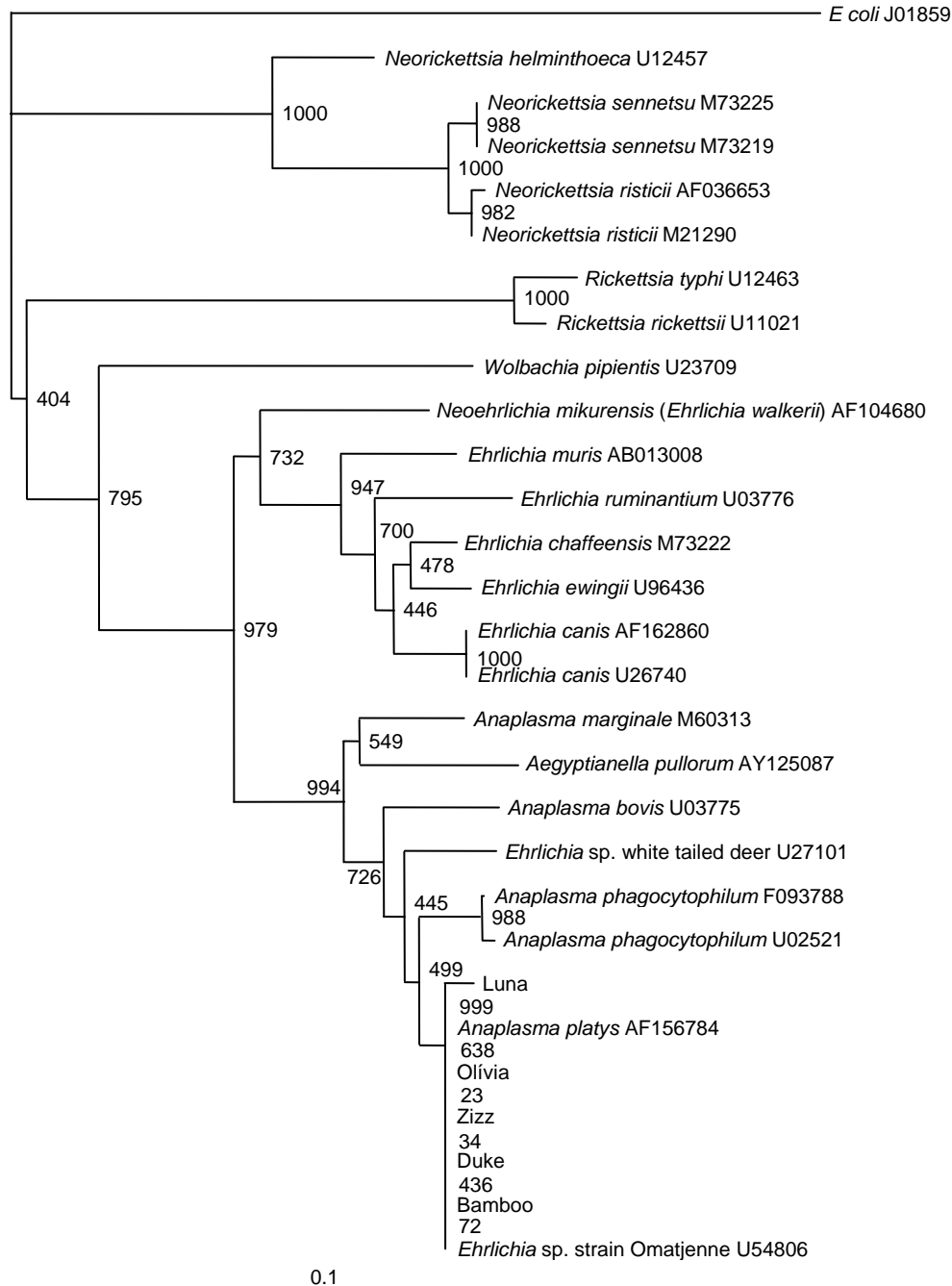
TABLE 1. Dogs presented with *Anaplasma* active infections detected by IFA and PCR.

Dog No.	Sex ^a	Age ^b	Breed	Clinical signs	Hematologic abnormalities ^c	IFA ^d	PCR ^e			Other tick-borne infections ^g
							16S rDNA	groESL	Msp2	
1- Babylon	F	8y	Cross-breed	Fever (39.4°C), lymphadenopathy, pale mucosa	A, Lc, T	<80; 1,280	-	-	-	Ec
2- Bamboo	M	3y	Cross-breed	Lymphadenopathy, pale mucosa, weight loss, diarrhea, vomit	A, T	320	+	+	-	-
3- Black	F	2 y	Pequinois	Fever (39.3°C), lymphadenopathy, pale mucosa	A, T	<80; 320	-	-	-	-
4- Duke	M	4y	Doberman	Fever (40.5°C), lymphadenopathy, pale mucosa	A, T	<80	+	+	-	-
5- Luna	F	1 y	Boxer	Fever (40.1 °C), lymphadenopathy	T	<80; 80	+	+	-	-
6- Nina	F	5y	Pincher	Fever (40.4), lymphadenopathy, pale mucosa	A, T	80; 1280	-	-	-	Rc
7- Olívia	F	3 m	Serra da Estrela Mountain Dog	Fever (39.6°C), lymphadenopathy, pale mucosa	A, T	<80	+	+	-	Rc
8- Sniper	M	1 y	Pittbull	Fever (41.4°C), lymphadenopathy	A, L, T	<80; 80	-	-	-	Ec
9- Zizzi	M	1y	Cross-breed	Fever (40.1°C), lymphadenopathy, anorexia	A, Lc, T	<80	+	+	-	-

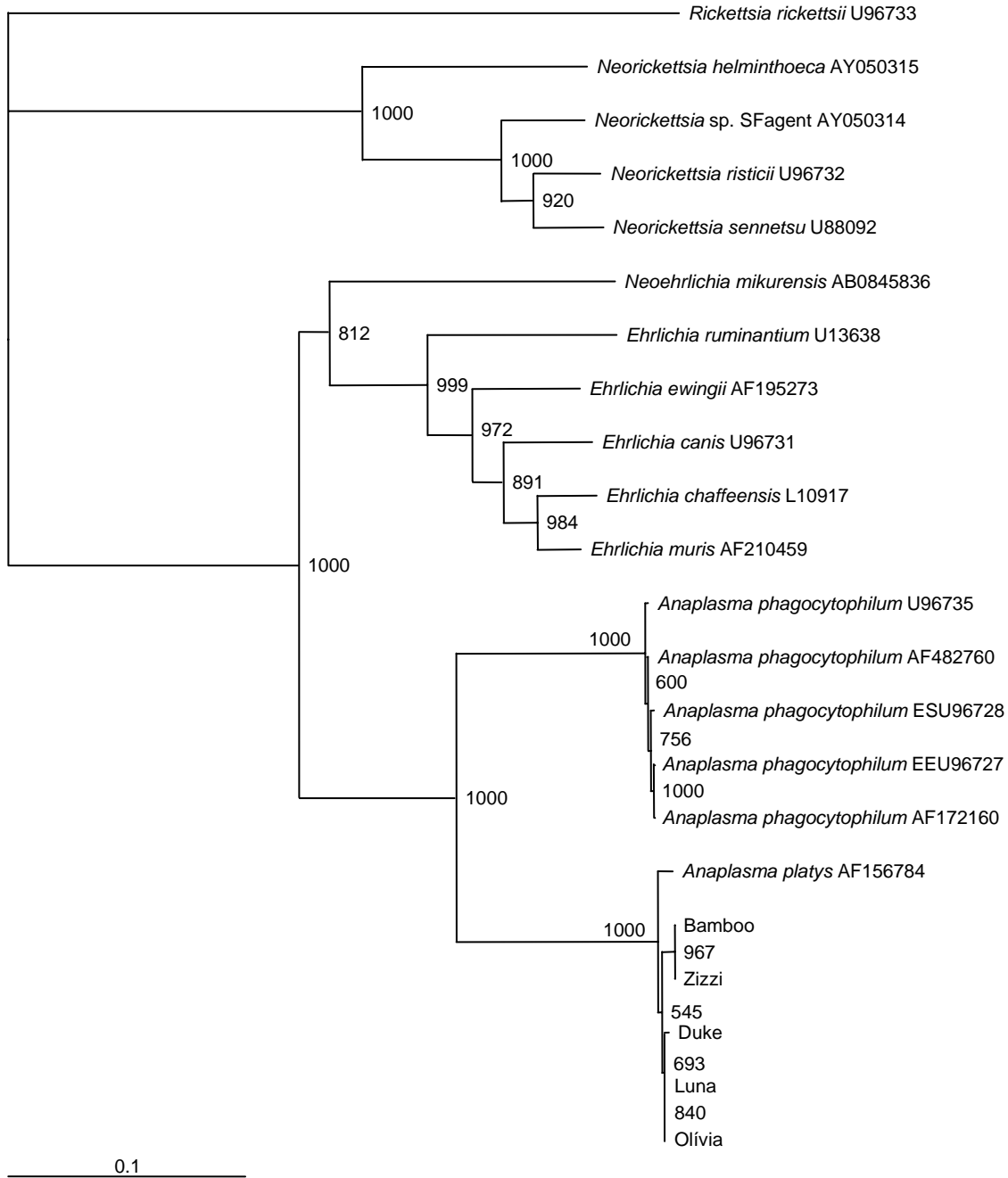
^aM male, F female; ^by year, m month; ^cA anemia $<5,5 \times 10^6 /\mu\text{l}$; Lc leukocytosis $> 17 \times 10^3 /\mu\text{l}$; L leukopenia $<6 \times 10^3 /\mu\text{l}$; T thrombocytopenia $<200 \times 10^3 /\mu\text{l}$; ^dIFA titer(s) of available plasma samples; ^eGenes tested by PCR; ^gResults of previous PCR testing has detected active infection with Ec *Ehrlichia canis* and Rc *Rickettsia conorii* (Alexandre, 2006).

FIGURE 1. Phylogenetic relationships between *A. platys* sequences detected in this study other Anaplasmataceae based on partial nucleotide sequences of the *rrs* (A) and *groESL* (B). The scale bar represents substitution rates of 10 per each 100 nucleotides.

A) *rrs*

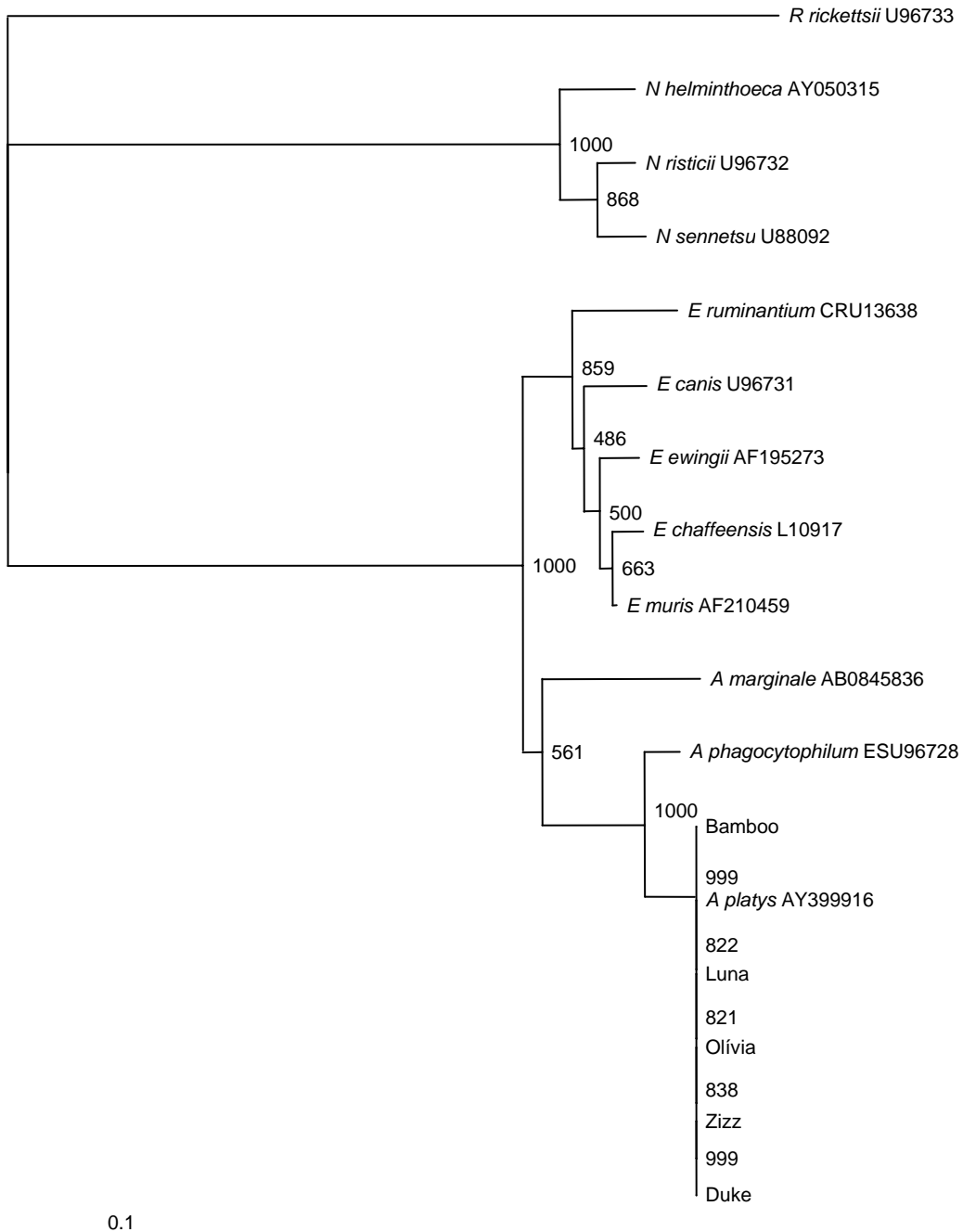


B) *groESL*



0.1

FIGURE 2. Dendrogram demonstrating the similarity among GroEL amino acid sequences derived from *A. platys*-infected Portuguese dogs compared to other Anaplasmataceae species. Note that despite the nucleotide heterogeneity found among the Portuguese dogs (Figure 1), the amino acid sequences and therefore GroEL protein structure are predicted to be identical.



CHAPTER V

HUMAN EXPOSURE TO *ANAPLASMA PHAGOCYTOPHILUM*

5.1. HUMAN EXPOSURE TO *ANAPLASMA PHAGOCYTOPHILUM* IN PORTUGAL

SANTOS AS, BACELLAR F, DUMLER JS

SHORT REPORT

ANNALS OF NEW YORK ACADEMY OF SCIENCES 2006; 1078:100-05

Human Exposure to *Anaplasma phagocytophilum* in Portugal

A.S. SANTOS,^a F. BACELLAR,^a AND J.S. DUMLER^b

^a*Centro de Estudos de Vetores e Doenças Infecciosas (CEVDI), Instituto Nacional de Saúde Dr. Ricardo Jorge, Águas de Moura, Portugal*

^b*Division of Medical Microbiology, Department of Pathology, The Johns Hopkins University School of Medicine, Baltimore, Maryland, USA*

ABSTRACT: A retrospective study to detect *Anaplasma phagocytophilum* antibodies by indirect immunofluorescence (IFA) and Western blot (WB) assay was conducted in 367 potentially exposed patients from Portugal. The study included 26 patients with confirmed Lyme borreliosis (LB), 77 with suspected LB, 264 seronegative patients studied for possible tick-transmitted LB and boutonneuse fever (LB/BF) infection, and 96 healthy blood donors. Overall, patients with LB and suspected LB ($n = 2$ [7.7%] and $n = 6$ [7.8%], respectively) were more often seropositive ($n = 8$ [7.8%]; $P < 0.001$), whereas only 1 (0.4%; $P = 0.046$) patient in the LB/BF seronegative group had confirmed disease. This study is the first evidence of human exposure to *A. phagocytophilum* or an antigenically similar bacterium in Portugal, and suggests that LB patients are significantly more likely to contact *A. phagocytophilum*.

KEYWORDS: serologic study; *Anaplasma phagocytophilum* exposure; Lyme borreliosis; Portugal

INTRODUCTION

Human granulocytic anaplasmosis (HGA) is an emerging tick-borne illness caused by *Anaplasma phagocytophilum*. In Portugal, the bacterium is present in both *Ixodes ricinus* and *I. ventralloi* ticks,¹ but no data concerning the occurrence of HGA are available. Because *I. ricinus* frequently bite humans, we conducted a retrospective study of *A. phagocytophilum* antibodies in potentially exposed patients.

Address for correspondence: Ana Sofia Santos, Centro de Estudos de Vetores e Doenças Infecciosas, Instituto Nacional de Saúde Dr. Ricardo Jorge, Avenida da Liberdade 5, 2965-575 Águas de Moura, Portugal. Voice: +351-265-912222; fax: +351-265-912568; +351-265-912155.
e-mail: ana.santos@insa.min-saude.pt

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MATERIAL AND METHODS

Sera from clinically ill individuals submitted to CEVDI's laboratory during 2002 for Lyme borreliosis (LB) and boutonneuse fever (BF) testing were used. The study included 26 patients with confirmed LB, 77 with suspected LB, 264 seronegative patients studied for possible tick-transmitted (LB/BF) infection, and 96 healthy blood donors. The first two cohorts included all confirmed and suspected LB cases with available sera.² The third cohort was a random sample comprising 25% of LB/BF seronegative patients detected monthly during the year. Institutional Review Board approval was obtained for these studies. Antibodies against *A. phagocytophilum* were detected by indirect immunofluorescence (IFA) and Western blot (WB) assays, as described previously.^{3,4} *A. phagocytophilum* Webster and *Ehrlichia chaffeensis* Arkansas strains were used as antigen. *E. chaffeensis* cross-reactivity was evaluated in seropositive samples. The criteria for seropositivity were IFA titer ≥ 80 and WB reactivity with bands between 42–49 kDa for *A. phagocytophilum* and between 23–30 kDa for *E. chaffeensis*.^{3,4} Confirmed *A. phagocytophilum* exposure was defined as a fourfold higher IFA titer to specific antigen than to *E. chaffeensis* or when IFA and WB were positive. Possible exposure was defined as a single IFA titer of ≥ 80 or less than fourfold titer difference between specific antigen and *E. chaffeensis*, and no specific WB bands. For statistical analysis, independence of proportions of reactive patient samples was compared between groups and the test population using the Chi-square test. *P* values of <0.05 were considered significant.

RESULTS

A total of 419 sera were obtained from 367 patients for serologic testing, not including 96 sera obtained from healthy blood donors. In 323 patients (88%) only one serum sample was available. Serologic results are summarized in TABLES 1 and 2 and in FIGURE 1. Confirmed and possible exposures to *A. phagocytophilum* were present in 1 (1%) and 3 (3%) of 96 blood donors, respectively. Patients with possible exposure were not more likely to have clinical findings ($P = 0.10$, χ^2 test); thus, only confirmed patients were considered infected. Overall, 2.2% (10/463) individuals had confirmed exposure. Patients with LB or suspected LB were significantly more likely to have *A. phagocytophilum* confirmed ($P \leq 0.002$). Of 367 studied, patients with LB ($n = 2$ [7.7%]) and suspected LB ($n = 6$ [7.8%]) together ($n = 8$, [7.8%]) were more often seropositive ($P < 0.001$), whereas only one (0.4%; $P = 0.046$) patient in the LB/BF seronegative group had confirmation. *E. chaffeensis* cross-reactions were detected only in three patients and only in the suspected LB group. No statistically significant differences in age, gender, and province were noted between the *A. phagocytophilum*-confirmed and -seronegative individuals; the

TABLE 1. Serologic testing results for *A. phagocytophilum* and *E. chaffeensis*

Study groups ^a	No. tested patients/ no. reactive	No. confirmed (%) / no. possible (%) exposure	
		<i>A. phagocytophilum</i>	<i>E. chaffeensis</i>
Patients with defined LB	26/5	2(7.7) / 3(11.5)	—
Patients with suspected LB	77/11	6 (7.8) / 2 (2.6)	— / 3(3.9)
Seronegative LB/BF patients	264/4	1(0.4) / 3(1.1)	—
Blood donors	96/4	1(1) / 3(3.1)	—

^a LB = Lyme borreliosis; BF = Boutonneuse fever.

median age of confirmed patients was 42 years, 66.6% were women and 55.5% came from Estremadura province. However, among patients in Estremadura province, *A. phagocytophilum*-confirmed cases more often resided in Oeiras than in other locations ($P < 0.001$).

DISCUSSION

A. phagocytophilum is transmitted by *Ixodes* ticks and shares these vectors with other human infectious agents, such as *Borrelia burgdorferi* (etiologic agent of LB). This ecological characteristic of *A. phagocytophilum* allowed us to focus the study on patients with clinical and laboratory evidence of confirmed or suspected LB in order to detect potential HGA. HGA results in an acute, generally self-limited, nonspecific febrile illness, characterized by headache and myalgias, often accompanied by systemic symptoms and signs and hematological abnormalities such as thrombocytopenia, leukopenia, elevated serum hepatic transaminases, and/or elevated serum C-reactive protein concentrations. This nonspecific presentation is common with other tick-borne illnesses, justifying the inclusion of an additional patient group with clinical suspicion of LB or BF but lacking laboratory confirmation for these diagnoses. In this report we have found that significantly higher proportions of patients with suspected/confirmed LB had confirmed exposure to *A. phagocytophilum* than did the overall population. Our results corroborate previous findings, and show that the prevalence of *A. phagocytophilum* infection among Portuguese LB patients (7.8%) is in the range of 2–21% as described in other European countries.⁵ However, the evaluation is partly impaired by the lack of analysis of paired sera that underestimates prevalence. Cultivation of Portuguese strains could also help to improve serologic tests. In conclusion, these data provide evidence that Portuguese *A. phagocytophilum* strains infect and evoke immune responses in tick-exposed humans, and that LB patients are significantly more likely to acquire *A. phagocytophilum* infection. The possibility of coinfection with both pathogens and comorbidity is worthy of clinical consideration.

TABLE 2. Epidemiological and clinical data from patients with confirmed exposure to *A. phagocytophilum*

Patient groups ^a	Gender ^{b/} age (year) ^c	Origin of residence ^d	Clinical presentation/ laboratory findings ^e (days)	Onset (days)	No. sera tested (time interval) ^f	<i>A. phagocytophilum</i> serology	
						IFA titer (Ig class)	WB result ^g
Defined LB	1 F/63	Elvas; Alto Alentejo	Febrile illness/—	—	2 (68 days)	80(IgG); 1280(IgG)	—
	2 F/57	Oeiras; Estremadura	—	—	1	640(IgG)	+
Suspected LB	3 M/U	Algarve	—	—	2 (13 days)	320(IgG)	+
	4 M/74	Oeiras; Estremadura	—	—	1	320(IgG)	+
	5 F/67	Lisboa; Estremadura	Vasculitis	—	1	320(IgM)	+
Seronegative LB/BF	6 F/9	Oeiras Estremadura	—	—	1	160(IgG)	+
	7 M/50	Oeiras; Estremadura	—	—	1	160(IgM)	+
	8 F/31	V F Xira; Ribatejo	—	—	3 (112 days)	80(IgG)	+
	9 F/19	F Foz; Beira Litoral	Febrile illness/ LT	8	1	80(IgM)	+

^aLB = Lyme borreliosis; BF = Boutonneuse fever; ^bM = male; F = female; ^cU = unknown; ^dPatient locality and province; ^eLT = Elevated liver transaminases; ^fAverage in days between consecutive sera samples; ^gWestern blot result for polyvalent antibodies testing.

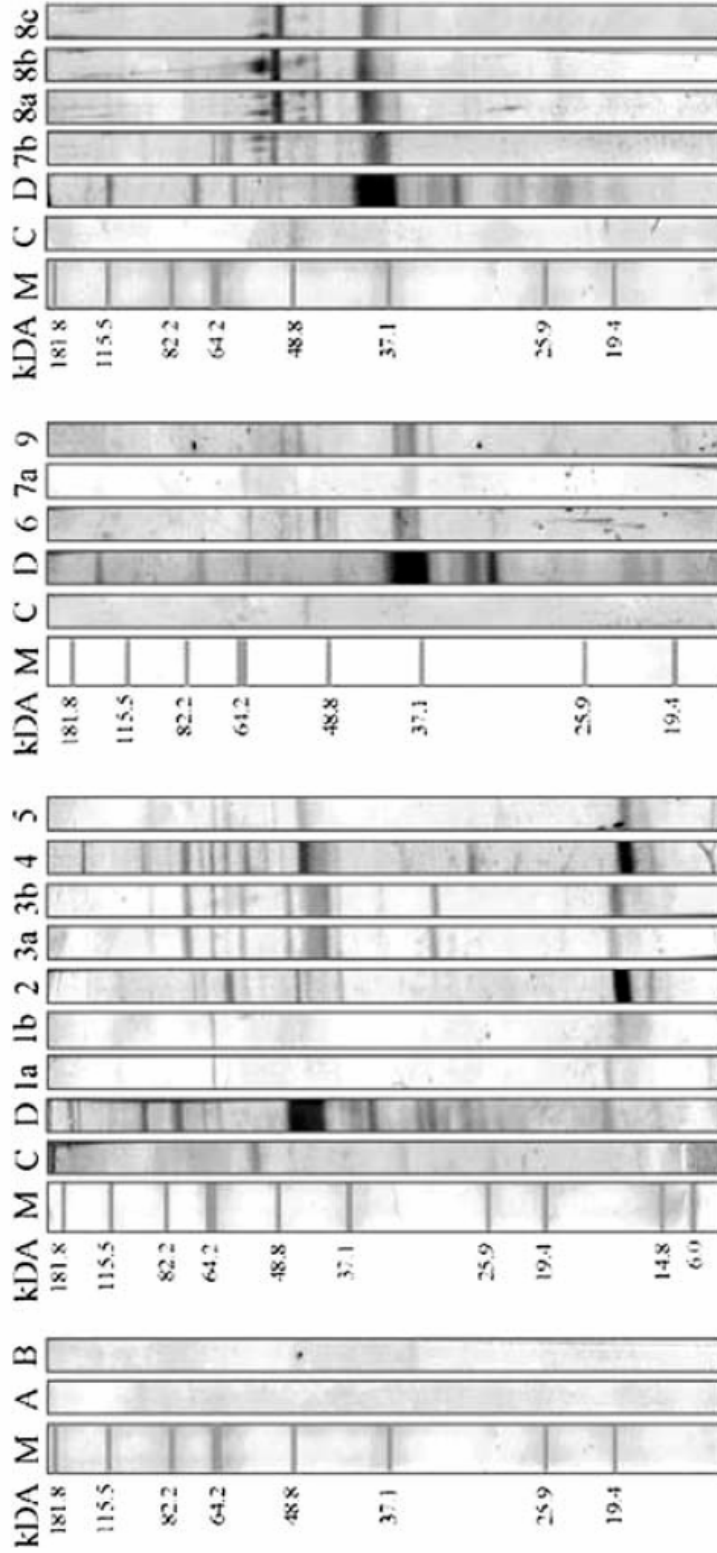


FIGURE 1. Western blot results for *A. phagocytophilum* IFA-positive patients.

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5.2. SIX YEARS OF ANAPLASMATACEAE SERODIAGNOSIS IN HUMANS.
DATA FROM A STATE LABORATORY, PORTUGAL

SANTOS AS, DE SOUSA R, LOPES DE CARVALHO I, NÚNCIO MS, DUMLER JS, BACELLAR F

RESEARCH ARTICLE

IN SUBMISSION

Six years of Anaplasmataceae serodiagnosis in humans. Data from a state laboratory, Portugal

Santos AS¹, De Sousa R¹, Lopes de Carvalho I¹, Nuncio MS¹, Dumler JS², Bacellar F¹

¹Centro de Estudos de Vectores e Doenças Infecciosas, Instituto Nacional de Saúde Dr. Ricardo Jorge, Lisboa, Portugal;

²Division of Medical Microbiology, Department of Pathology, The Johns Hopkins University School of Medicine, Baltimore, Maryland, USA.

Corresponding author: Ana Sofia Pereira dos Santos. Centro de Estudos de Vectores e Doenças Infecciosas, Instituto Nacional de Saúde Dr. Ricardo Jorge, Edifício LEMES, Avenida Padre Cruz, 1649-016 Lisboa, Portugal;

Tel: +351 217 508 125; Fax: +351 217 508 521

e-mail: ana.santos@insa.min-saude.pt

ABSTRACT

The present work summarizes the available data concerning Anaplasmataceae diagnosis, including *Anaplasma phagocytophilum* and *Ehrlichia chaffeensis*, performed at the the Center for Vector and Infectious Diseases Research, National Institute of Health Dr. Ricardo Jorge (CEVI/INSA) during 2000-2006. As part of routine diagnosis, CEVI/INSA prospectively investigated the presence of antibodies by indirect immunofluorescent assay (IFA) against *E. chaffeensis* from 2000-2006 and against *A. phagocytophilum* in 2006. Sera archived in 2000-2005 from patients with suspected Anaplasmataceae infection were also retrospectively studied by IFA for *A. phagocytophilum*. Positive sera were subsequently screened by PCR to detect Anaplasmataceae active infections. Investigation of active infection by PCR and *in vitro* isolation were also performed on whole-blood samples submitted in 2006. A total of 619 sera from 425 patients was tested. Overall, antibodies to *E. chaffeensis* and *A. phagocytophilum* were detected in 5.6% (24/425) of patients. Serologic reactions to *A. phagocytophilum* were detected in 70.8% (17/24), to *E. chaffeensis* in 12.5% (3/24), or to both antigens in 16.6% (4/24) of cases. The majority had stable or less than four-fold changes in antibody titer between consecutive samples. *A. phagocytophilum* seroconversion was observed in only one patient, fulfilling criteria for recent infection, although this patient also seroconverted to *Coxiella burnetii*. Neither *A. phagocytophilum* nor *E. chaffeensis* active infections were detected by PCR. Laboratory testing for other tick-borne agents or related bacteria also provided evidence for bartonellosis and acute Q fever in one and five *A. phagocytophilum*-seropositive patients, respectively, for rickettsiosis in two *E. chaffeensis*-seropositive patients, and for acute and chronic Q fever in two patients with both *A. phagocytophilum* and *E. chaffeensis* antibodies. Moreover one patient with stable *A. phagocytophilum* titer seroconverted to *C. burnetii*, which was later isolated from the patient's blood sample. These findings could represent false positive cross-reactions to shared antigens, antibodies induced by active dual infections, or past exposures to Anaplasmataceae species and other agents. Regardless, the results argue for continued development of improved diagnostics and integrated analysis of diagnostic tests for patients with suspected tick-borne disease.

RUNNING TITLE

Human Anaplasmataceae serodiagnosis, Portugal

KEYWORDS

Laboratory diagnosis; Human Anaplasmataceae infections; *Ehrlichia chaffeensis*; *Anaplasma phagocytophilum*;

INTRODUCTION

Human infections caused by bacteria belonging to the family Anaplasmataceae (Class α -proteobacteria, Order Rickettsiales), represent some of the best examples of emerging vector-borne diseases. Sennetsu fever (SF), documented in Japan in 1954 (Misao & Kobayashi, 1955), was the first human disease known to be caused by a member of the Anaplasmataceae family. This usually mild mononucleosis-like illness is caused by *Neorickettsia* (formerly *Ehrlichia*) *sennetsu*, likely acquired after ingestion of raw fish infested by infected trematodes. The infection occurs only in limited areas of the Far East, rarely outside Japan and Malaysia, and no deaths have been reported.

In 1986, human monocytic ehrlichiosis (HME) was reported in a patient from Central Arkansas. The infection was caused by a previously unknown tick-borne agent, closely related to the animal pathogen *E. canis* that was later named *Ehrlichia chaffeensis* (Maeda *et al.*, 1987; Anderson *et al.*, 1991; Dawson *et al.*, 1991). Additionally, other tick-borne Anaplasmataceae of veterinary importance were also described as causes of human infection. In the early 1990's, cases of human granulocytic anaplasmosis (HGA) (formerly human granulocytic ehrlichiosis [HGE]) were reported from Minnesota and Wisconsin (Bakken *et al.*, 1994; Chen *et al.*, 1994). The exact nature of the causative agent, originally named "HGE agent", remained uncertain for several years until its unification with the animal pathogens *E. phagocytophila* and *E. equi* into a single species, *Anaplasma phagocytophilum* (Dumler *et al.*, 2001, 2005).

In 1996, *E. canis* - the etiologic agent of canine monocytic ehrlichiosis was isolated from an apparently healthy man (Perez *et al.*, 1996), and was later associated with several symptomatic infections (Perez *et al.*, 2006) in Venezuela. More recently, in 1999 *E. ewingii*, the etiologic agent of canine granulocytic ehrlichiosis was also identified as a human disease agent in US, mostly in immunocompromised patients (Buller *et al.*, 1999). Of the above human diseases caused by pathogens assigned to Anaplasmataceae family, HME and HGA are now considered the most important due to the number of cases annually reported in US, the potential for fatal outcome and the broad worldwide geographic distribution of the etiologic agents, especially in Europe.

In Portugal, the potential involvement of Anaplasmataceae species in human disease was first suggested by David de Moraes and coworkers (1991), with the description of a case fulfilling serologic criteria for active *E. chaffeensis* infection. Additionally, a study performed on Madeira Island designed to clarify the importance of *Ixodes ricinus* as a vector of tick-borne agents showed for the first time *A. phagocytophilum* DNA in Portuguese *I. ricinus* ticks (Nuncio *et al.*, 2000). A project was then initiated to evaluate whether *A. phagocytophilum* could be an important pathogen in the country and confirmed its presence not only on Madeira Island but also in mainland *Ixodes* ticks (Santos *et al.*, 2004), and the presence of antibodies against this agent in patients with tick-borne diseases (Santos *et al.*, 2006). The potential for human exposure to Anaplasmataceae in Portugal justified the implementation of laboratory diagnostics for these tick-borne agents by the Center for Vector and Infectious Diseases Research from the National Institute of Health Dr. Ricardo Jorge (CEVDI/INSA). This work summarizes all available data concerning *E. chaffeensis* and *A. phagocytophilum* diagnostics performed in CEVDI/INSA during 2000-2006.

MATERIAL AND METHODS

Patient Samples. This study includes patients from which at least one biological sample, including whole-blood and/or serum, was received at CEVDI/INSA during 2000 to 2006 for laboratory diagnosis of *A. phagocytophilum* and/or *E. chaffeensis* infection. The samples were received either from state hospitals, public health centers, or directly from physicians practicing in diverse regions of the country.

Serology. An indirect immunofluorescent assay (IFA) was used for serologic diagnosis of

Anaplasmatataceae infections. The presence of antibodies against *E. chaffeensis* was studied prospectively in all available sera as part of CEVDI/INSA routine diagnosis conducted from 2000-2005. For *A. phagocytophilum*, laboratory diagnosis was available only in 2006; thus, sera archived during 2000-2005 from patients with suspected Anaplasmatataceae infection were studied retrospectively. Institutional Review Board approval was obtained for this retrospective study. In 2006, sera received for either *A. phagocytophilum* or *E. chaffeensis* testing were examined prospectively for antibodies against both agents. IFA was performed according to CEVDI/INSA procedures, as previously described (Santos *et al.*, in submission). Briefly, sera were diluted in PBS and incubated for 30 min at 37°C using commercial *A. phagocytophilum* and *E. chaffeensis* antigen slides (Focus Diagnostics, Cypress CA, USA). The retrospective study was performed using *A. phagocytophilum* Webster strain antigen slides prepared in-house (Santos *et al.*, in submission). A second incubation for 30 min at 37°C with fluorescein isothiocyanate (FITC)-labelled rabbit anti-human immunoglobulin M (IgM) and polyvalent IgA,G,M conjugates (Dako Cytomation, Denmark) were used to identify bound antibodies resulting in homogeneous fluorescence of Anaplasmatataceae morulae. The IFA was interpreted as positive whenever titers of IgM ≥ 80 or IgA,G,M ≥ 80 for *A. phagocytophilum* or when IgM ≥ 32 or IgA,G,M ≥ 64 for *E. chaffeensis* were found. All reactive samples were serially diluted to determine the end-point titer, which was expressed as the reciprocal of the serum dilution. Positive and negative sera were included on every antigen slide as IFA controls.

Molecular analysis. Polymerase chain reaction (PCR) was used to attempt detection of *A. phagocytophilum* and *E. chaffeensis* DNA in EDTA-blood samples received at CEVDI/INSA during 2006. Additionally, Anaplasmatataceae IFA-positive sera were tested by PCR. Since treatment information was missing on the majority of submission forms accompanying samples, molecular analysis was performed only on the first sample that more likely represented the acute or active phase of infection at time of presentation to the physician and prior to antibiotic therapy. Genomic DNA was extracted from 200 μ l of buffy-coat or serum using the Qiamp Blood Kit procedure (Qiagen GmbH, Germany). Known negative samples were included as controls with every set of 1 - 4 sample extractions. Nested or single tube PCR reactions targeting both the *A. phagocytophilum* and *E. chaffeensis* *groESL* operon, and *A. phagocytophilum* *rrs* (16S rRNA gene) and *msp2* (*p44*) genes were performed as previously described (Sumner *et al.*, 1997; Massung *et al.*, 1998;

Caspersen *et al.*, 2002) in a total volume of 50 μ l containing 1 μ M of each primer, 2.5 U of Taq DNA polymerase, 200 μ M of each deoxynucleotide triphosphate, 50 mM KCl 10 mM Tris-HCl pH 8.3, 1.5 mM Mg^{2+} (Eppendorf MasterTaq Kit, Germany), and 10 μ l DNA extract (or 1 μ l of first stage amplicon in nested PCR reactions). In each run, known negative (including the extraction controls and water) and positive samples were used as controls. Prevention of cross-contamination was managed by using pipette tips with filter barriers, and by performing PCR in 3 separate rooms (extraction, master mix preparation, and amplification/ electrophoresis).

Isolation attempts. During 2006, isolation of *A. phagocytophilum* and *E. chaffeensis* was attempted from patients for whom an EDTA or heparinized blood sample was available at the time of their initial presentation, using the culturing methods previously described (Dawson *et al.*, 1991; Goodman *et al.*, 1996). Briefly, for *A. phagocytophilum* isolation, approximately 0.5 ml of whole-blood or 0.2 ml of crude buffy coat recovered after blood sedimentation by gravity or low speed centrifugation, was directly inoculated into flasks with HL-60 cells maintained at a final concentration of 2×10^5 cells/ml in RPMI 1640 medium (Gibco, Invitrogen™, UK), supplemented with 1% FBS (Gibco, Invitrogen™, UK) and 2 mM L-glutamine (Gibco, Invitrogen™, UK). The cultures were incubated at 37°C in a 5% CO₂ atmosphere and checked twice weekly to adjust cell concentrations and to investigate infection. Microbial growth was ascertained by microscopy of cytocentrifuged culture aliquots stained by Diff-Quik (Medion Diagnostics GmbH, Germany). *E. chaffeensis* isolation was performed by direct inoculation of whole-blood or crude buffy coat onto monolayers of DH82 cells, maintained in minimum essential medium (MEM; Gibco, Invitrogen™, UK) supplemented with 10% FBS, 2 mM L-glutamine (Gibco, Invitrogen™, UK), 2 mM sodium pyruvate (Gibco, Invitrogen™, UK) and non-essential aminoacids (MEM NEAA; Gibco, Invitrogen™, UK) at 37°C and 5% CO₂. Twice weekly, the medium was changed and infection monitored as described above.

Differential Diagnosis. For Anaplasmataceae IFA-positive patients, when requested by the physician, data concerning CEVD/INSA tested for other tick-borne agents or related bacteria such as *Bartonella* spp., *Borrelia burgdorferi sensu lato*, *Rickettsia* spp., and *Coxiella burnetii* were also included in the presented work. Routine laboratory diagnosis of active infections by the latter agents depended on the type of sample submitted, but was usually based on serology (IFA, ELISA;

or WB), molecular analyses (PCR) and/or isolation attempts. Based on the agent suspected, the techniques used included: i) IFA and *gltA* gene PCR for Bartonella spp. (Norman *et al.*, 1995; Sander *et al.*, 2001); ii) IFA or ELISA followed by confirmatory WB of suspected or positive samples, 5S (*rrf*)-23S(*rrl*) intergenic spacer and *flgB* PCR, and isolation by direct inoculation in BSK-II medium for *B. burgdorferi* s.l. (Johnson *et al.*, 1992; Rijpkema *et al.*, 1995; Lopes de Carvalho & Nuncio, 2006); iii) IFA and transposon-like repetitive region PCR for *C. burnetii* (Williems *et al.*, 1994; Maurin & Raoult, 1999); and iv) IFA, *ompA* and *gltA* PCR, and isolation on Vero E6 shell-vials for *Rickettsia* spp. (Regnery *et al.*, 1991; Bacellar *et al.*, 2003; De Sousa *et al.*, 2006).

Criteria for laboratory confirmation. *CEVDI/INSA*'s case definition criteria for bartonellosis, Lyme borreliosis (LB), Q fever, rickettsiosis, HGA and HME are based on published guidelines, with slight modifications in some cut-off values according to the background reactivity as determined by the National Institute of Health for the Portuguese population (Maurin & Raoult, 1999; Walker *et al.*, 2000; Sander *et al.*, 2001; Brouqui *et al.*, 2004; Lopes de Carvalho & Nuncio, 2006; EUCALB). Thus, given an adequate epidemiologic and clinical context, a confirmed laboratory case is defined by: i) agent isolation in culture, or ii) positive PCR result with the demonstration of agent-specific DNA by subsequent amplicon sequencing, or iii) demonstration of a seroconversion or \geq four-fold increase in antibody titer between acute and convalescent samples. A single high titer also suggests disease, such as for bartonellosis and rickettsiosis (IFA IgM \geq 32 and IgG \geq 128), acute Q fever (IFA phase II IgM \geq 50 and IgG \geq 200), chronic Q fever (IFA phase I titer of IgG \geq 800) and Lyme disease [IFA IgM \geq 32 and/or IgG \geq 256, Elisa IgM and/or IgG \geq 5, according to Virion ELISA Kit (Sirion, Germany), followed by the demonstration of 2 of 3 IgM bands and/or 5 of 10 IgG bands in western blots].

RESULTS

From 2000 to 2006, a total of 619 sera samples from 425 patients were received by *CEVDI/INSA* for Anaplasmataceae infection diagnostic testing. In 125 patients (29.4%), more than one serum was available for testing. Moreover, all "first" blood samples received during 2006 that were collected in the proper anticoagulant were additionally used for PCR testing (n=6) and/or isolation

attempts in DH82 and HL-60 cells (n=16). In patients with Anaplasmataceae IFA-positive results, the first serum sample was also used for DNA preparation and PCR testing.

Overall, Anaplasmataceae IFA-positive reactions were detected in 5.6% (24/425) of patients, with seropositivity values ranging from 2.0% (in 2000) to 11.6% (in 2003) (Figure 1). Seropositive patients were found to react with either *A. phagocytophilum* in 70.8% (17/24) of the cases, *E. chaffeensis* in 12.5% (3/24), or with both antigens in 16.6% (4/24). However neither *A. phagocytophilum* nor *E. chaffeensis* active infections were detected by agent isolation or PCR in any sample tested during 2006. Moreover, the PCR analysis of IFA-positive sera was negative in all cases.

A detailed analysis of available data from patients that reacted only with *A. phagocytophilum* antigens revealed that almost all had polyvalent antibody titers ranging from 80 to 320 (Table 1). The only exception was patient no. 12/2005 who had a single serum sample with both IgM and IgA,G,M IFA titers of 80 and 320, respectively. Evolution of antibody titers was demonstrated among 7 of the 17 cases, showing stable IFA titers in 4 (57.1%), two-fold decreases in titers in 2 (28.6%) and seroconversion in 1 (14.3%; patient no. 11/2004).

Tests for other tick-borne agents or related bacteria conducted by CEVDI/INSA when requested by the physician provided laboratory evidence of bartonellosis in 1 case and acute Q fever in 5 cases. Nondiagnostic results were obtained in 11 cases. A suggestive IFA-titer of *Bartonella* sp. active infection was detected in a single serum from patient no. 2/2001 (IgM \geq 32 and IgG \geq 256, data not shown in Table 1) who also had a polyvalent *A. phagocytophilum* antibody titer of 320. Acute Q fever-compatible titers were present in 3 patients, showing either single polyvalent *A. phagocytophilum* antibody titers of 80 (patient no. 12/2004) and 160 (no. 20/2006), or a two-fold decrease in IFA-titer from 160 to 80 (no. 17/2005). Of interest is the observation that patient no. 11/2004 seroconverted to both *A. phagocytophilum* and *C. burnetii*, as evidenced by phase II IgM \geq 50 and IgG \geq 200 titers (data not shown in Table 1) in the second serum sample that are diagnostic of acute Q fever. Additionally, patient no. 15/2006, who presented with a stable IgA,G,M IFA-titer of 160 but was PCR-negative for *A. phagocytophilum* DNA in both buffy coat and serum, also had a seroconversion to *C. burnetii*, and a buffy coat PCR that was positive for this latter agent. Moreover, the inoculation of buffy coat into HL-60 cells resulted in the isolation of *C. burnetii*. The agent isolation was initially detected by microscopic observation of cytocentrifuged culture aliquots (Figure 2), and subsequently confirmed by using species-specific PCR (Williems *et al.*, 1994). The partial sequences of transposon-like repetitive region of *C. burnetii* obtained from

this isolate are available in GenBank under the accession number EU009657. Table 1 presents all the available data from *A. phagocytophilum* IFA-positive patients detected during 2000-2006.

Among the 3 patients who had *E. chaffeensis* antibodies alone, stable IgA,G,M titers were found in two cases (patient nos. 18/2001 and 19/2002) and stable IgA,G,M and IgM titers in another case (no. 20/2005) (Table 2). In the first two patients, a seroconversion and compatible titers against *Rickettsia* spp. were found when sera were tested by IFA using *R. conorii* Malish strain antigen, supporting the laboratory diagnosis of rickettsiosis. For patient no. 20/2005 who presented with stable IgM and IgA,G,M *E. chaffeensis* titers in consecutive samples, no diagnostic laboratory tests were obtained. Moreover, the small amount of first sample serum was insufficient for DNA extraction and PCR analysis.

For four patients with both *A. phagocytophilum* and *E. chaffeensis* antibodies, stable polyvalent antibody titers (\leq two-fold change) were observed (Table 3). Other laboratory tests demonstrated *C. burnetii* antibodies with titers consistent with acute (patient no. 21/2004) and chronic infections (patient no. 23/2005). In 2 other cases, differential testing was inconclusive, although patient no. 24/2006 had a stable *C. burnetii* titer, serodiagnostic criteria for active infection were not fulfilled (phase II IgM \geq 50 IgG $<$ 200 and phase I IgM \geq 50 IgG 400, data not shown in Table 3). Patient no. 19/2005 had the highest polyvalent titers in this study for *A. phagocytophilum* and *E. chaffeensis*, 640 and 256, respectively. Moreover he also had very high titers against *C. burnetii* (phase II IgM 200 and IgG 51,200, phase I IgM 100 and IgG 25,600; data not shown in Table 3), which in the clinical context of prolonged disease and endocarditis was highly supportive of a diagnosis of chronic Q fever.

DISCUSSION

Since the report of *E. chaffeensis* in a Portuguese man (David de Morais *et al.*, 1991), CEVDI/INSA has included IFA testing for this Anaplasmataceae as a routine laboratory diagnostic available for the community. In the last 6 years (2000-2006), a mean of 61 requests were received annually for *E. chaffeensis* testing, representing 3.1 to 7.4% of the total number of requests received annually for serodiagnosis at CEVDI/INSA. In addition, the recent detection of *A. phagocytophilum* in Portuguese *Ixodes ricinus* and *I. ventralloi* ticks (Nuncio *et al.*, 2000; Santos *et al.*, 2004) and the possibility of human exposure (Santos *et al.*, 2006) have stimulated further

research in this field and led to the implementation in 2006 of routine laboratory diagnostic testing for this Anaplasmataceae family member. The potential for cross-reaction between *E. chaffeensis* and *A. phagocytophilum*, as previously documented in both HME and HGA case series (Bakken *et al.*, 1996; Wong *et al.*, 1997; Comer *et al.*, 1999; Walls *et al.*, 1999; Lotric-Furlan *et al.*, 2006), imposes that all sera received based on a clinical suspicion of infection with either Anaplasmataceae be tested for both. Moreover, archived sera received during 2000-2005 for *E. chaffeensis* serodiagnosis were also analysed retrospectively for antibodies against *A. phagocytophilum*. This cross-testing study demonstrated a higher proportion of IFA seropositivity to *A. phagocytophilum* (17 patients) than to *E. chaffeensis* (3 patients). Reactivity to both agents was additionally found in 4 patients. These results are in accordance with those obtained in several seroprevalence studies performed on European populations (farmers, hunters, tick-exposure residents and patients with febrile illness with ascribed aetiology) and which suggest a greater exposure to *A. phagocytophilum* or an antigenically related agent, than to *E. chaffeensis* (Dumler *et al.*, 1997; Thomas *et al.*, 1998; Groen *et al.*, 2002). In spite of *E. chaffeensis* serological reactions among patients with febrile illnesses after tick-bite, no definitive evidence of human infection has yet been obtained by either DNA amplification or agent isolation (Lotric-Furlan *et al.*, 2006).

Despite the serological reactions to both *A. phagocytophilum* and *E. chaffeensis* found here, no active infections caused by either agent was definitively proven by laboratory testing. In fact, all isolation attempts using available buffy coat samples and PCR testing of IFA-positive sera for the above mentioned agents were unsuccessful. Nevertheless it is important to state that direct diagnosis suffered from constraints that could have influenced the final results. For example, isolations in both HL-60 and DH82 cells were only routinely attempted in 2006. Moreover, for the great majority of seroreactive patients, an adequate whole-blood sample for direct testing was not provided. Even using known sensitive PCR approaches, the ability to amplify small amounts of target DNA (Sumner *et al.*, 1997; Massung *et al.*, 1998; Caspersen *et al.*, 2002) from archived sera of known positive patients is only 14% sensitive, a significant limitation to this approach (Comer *et al.*, 1999). In addition, very little information about antecedent treatment that could reduce Anaplasmataceae DNA was available, further confounding detection methods. Thus, despite negative results in both culture and sensitive molecular detection methods, the possibility of false-negative results can not be excluded.

Despite the lack of direct confirmation of Anaplasmataceae active human infections, one patient seroconverted to *A. phagocytophilum* antigen in consecutive samples, fulfilling serological,

criteria for a confirmed case. However, when tested for other tick-borne or related agents by physician request and presumptive diagnosis, one patient also seroconverted to *C. burnetii* developing an antibody titer in the second serum that was alone highly presumptively diagnostic for acute Q fever. Additionally, other patients with serological reactivity to *A. phagocytophilum* alone or in association with *E. chaffeensis* also had laboratory diagnostic results compatible for Q fever in 6 cases and for bartonellosis in 1 case. Of interest was the direct confirmation of Q fever in 1 patient by isolation of *C. burnetii* in HL-60 cells and by PCR detection of *C. burnetii* DNA in buffy coat and culture samples. The HL-60 cells are currently known as an *in vitro* cellular target for *A. phagocytophilum* cultivation, due to its tropism for polymorphonuclear leucocytes. These cells are derived from a patient with promyelocytic leukaemia, but they can also be induced to terminal differentiation into either monocyte/macrophage-like cells or neutrophil-like cells by stimuli such as all-trans Retinoic acid (granulocyte differentiation) or Vitamin D3 (monocyte/macrophage differentiation), and even long-term culture. The fact that our cultures were maintained ≥ 1 month after inoculation might have led to HL-60 monocyte/macrophage differentiation, as this agent is known to preferentially target cells from the mononuclear lineage.

The possibility of cross-reactivity between non-related agents has been already addressed. Brouqui and coworkers (2001), in an evaluation trial of serodiagnosis by IFA testing using distinct *A. phagocytophilum* from different sources as well as varying antigen preparations demonstrated cross-reactions in patients with confirmed Q fever and bartonellosis. In the present series, Q fever was the main disease identified in cross-reactions with *A. phagocytophilum*, although the results of an internal CEVDI/INSA study performed using serum from confirmed *C. burnetii* cases demonstrated that not all patients present with Anaplasmataceae cross-reactive samples (data not shown). Whether these findings represent a distinct cross-reactive potential for different *C. burnetii* strains that is directed toward common antigens such as heat shock proteins, distinct host immune responses to infections, or antibody induced by active dual or past exposures to both *A. phagocytophilum* and *C. burnetii*, remains to be ascertained.

In Portugal, Q fever was recognized in 1948 (Fonseca *et al.*, 1949 in Santos *et al.*, 2007), and has been listed as a reportable disease since 1999 (<http://www.dgsaude.pt>). On average, 0.14 cases per 10^5 inhabitants are reported annually (1999-2003), however official reports may not accurately reflect the true Q fever incidence and little information is available regarding *C. burnetii* natural history in Portugal (Santos *et al.*, 2007). Domestic mammals, especially cattle, sheep, goats, dogs and cats are regarded as the most important reservoirs for human infection, and the

pathogen is usually acquired by aerosol contamination (Maurin and Raoult, 1999). Although tick-exposure is not considered relevant in the epidemiology of Q fever human cases, ticks are thought to play an important role in the maintenance of agent's enzootic cycle among wild animals (Maurin & Raoult, 1999). Several tick species have been found infected with *C. burnetii* (Maurin & Raoult, 1999) and the isolation of this agent from *I. ricinus* has been reported in Europe (Rehacek *et al.*, 1994; Jacomo *et al.*, 2002). Moreover, *A. phagocytophilum* coinfections with *Bartonella henselae* and *Babesia* spp. have also been sporadically reported in *Ixodes* ticks (Adelson *et al.*, 2004; Holden *et al.*, 2006). Thus, like other *Ixodes*-borne agents that share vector ticks, such as *B. burgdorferi* s.l., *A. phagocytophilum* and *C. burnetii* or other agent's enzootic cycles might potentially overlap. A previous study of Portuguese patients with confirmed and suspected LB showed a significant association of with *A. phagocytophilum* seropositivity when comparing to controls (Santos *et al.*, 2006). The additional identification of *A. phagocytophilum* seroreactivity among patients with confirmed Q fever and the fact that *I. ricinus* is one of the most frequently reported tick species parasitizing humans in Portugal, underscores the need for further investigation regarding the potential exposure of humans to several *Ixodes*-borne agents in Portugal.

Another interesting finding of this work was the detection of antibody titers only to *E. chaffeensis* antigen in 2 patients who presented with compatible laboratory diagnostics for rickettsiosis. Thus far, the apparent lack of any definitive *E. chaffeensis* identification by DNA detection or agent isolation in most European countries, as in Portugal, suggests exposure to other *Ehrlichia* spp. as a possible explanation for the serological reactions. *Rhipicephalus sanguineus*, one of the most prevalent tick species in Portugal, is a recognized vector of the two *Rickettsia conorii* strains causing Mediterranean spotted fever (MSF) (Bacellar, 1999; Santos-Silva *et al.*, 2006). This disease is presently the most important rickettsial infection in Portugal due not only to its high reported incidence and associated fatality rates, but also because of the broad-geographic distribution of cases throughout Portugal (Amaro *et al.*, 2003; De Sousa *et al.*, 2003). Additionally, *R. sanguineus* is a recognized vector of the canine Anaplasmataceae pathogen, *Ehrlichia canis*. Canine disease due to *E. canis* infection has long been suggested by several serological studies and was definitively proven by a PCR-based study of a clinically-ill Portuguese dog population (Alexandre *et al.*, in submission). Thus, the likely contact of *R. sanguineus* with humans and their potential for harbouring an *Ehrlichia* sp. might belie serological reactions detected using antigens of the closely related *E. chaffeensis* given the absence of irrefutable proof for its presence. In fact, *E.*

canis can evoke immune responses in Venezuelan patients with both asymptomatic and symptomatic infections (Perez *et al.*, 1996, 2006). Thus serological cross-reactions after *E. canis* exposure in humans could be considered as a possible explanation for antibodies reactivity with *E. chaffeensis*, although the human pathogenic potential of this canine agent deserves considerable further investigation.

In conclusion, although no definitively confirmed Anaplasmataceae infection was detected in the present study it is suggested that in Portuguese patients with a clinical suspicion of tick-borne disease or related illness, exposure to *A. phagocytophilum*, or a close related agent, is more likely to occur than to *E. chaffeensis*, or other *Ehrlichia* spp. Moreover, serological reactions to *A. phagocytophilum* antigen in patients with confirmed Q fever and to *E. chaffeensis* in patients with rickettsiosis were recognized. Whether these findings reflect serological cross-reactions, coinfections, or present/past exposure deserves further investigation. A continuing integrated analysis of Anaplasmataceae and other tick-borne or related agent laboratory diagnostics, when justified by clinical suspicion, is indispensable to better understand the present results. Moreover, the potential for native Anaplasmataceae infections in residents at risk for tick-borne disease, especially due to *A. phagocytophilum*, or imported cases associated with international travelers to European- or US-endemic areas, suggests the need for continuing active surveillance.

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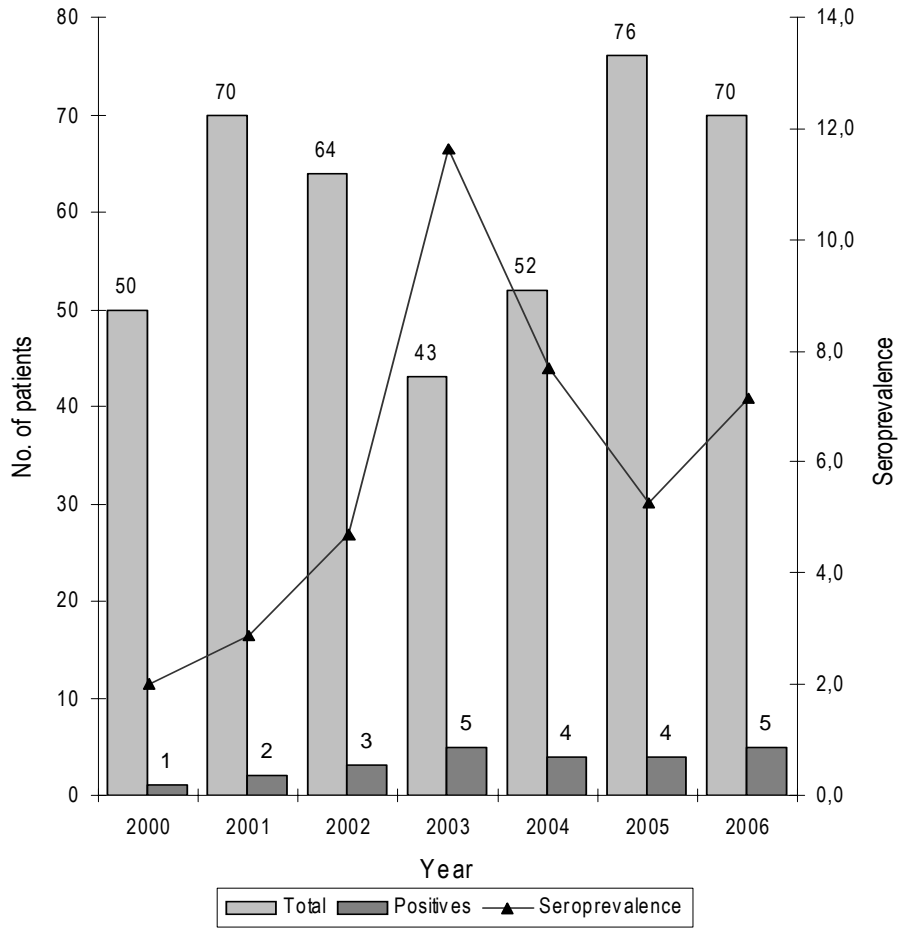


FIGURE 1. Number of patients that had at least one sera sample submitted to *CEVDI/INSA* with a request for *A. phagocytophilum* and/or *E. chaffeensis* diagnosis during 2000-2006.

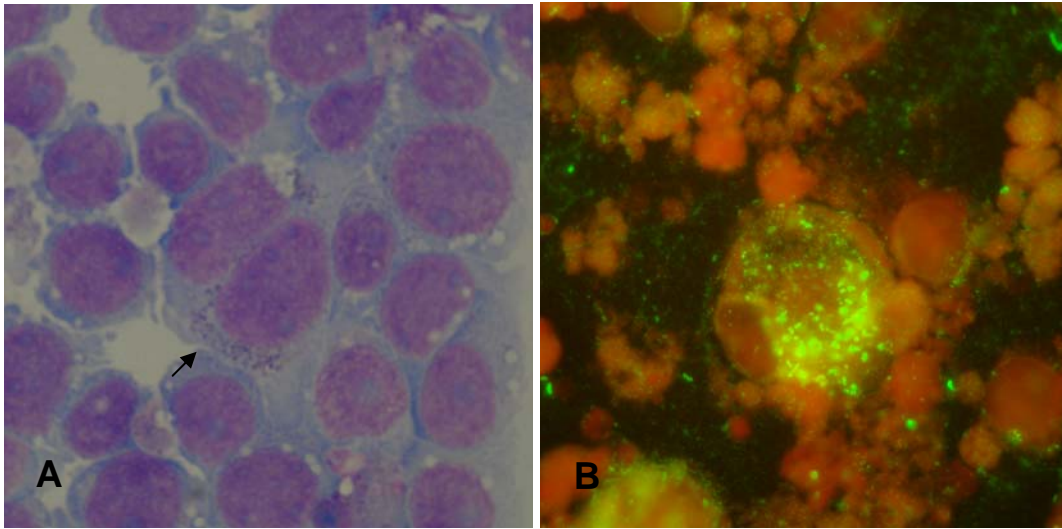


FIGURE 2. Light microscopic appearance of *C. burnetti* human isolate in HL-60 cells. Culture cytocentrifuge preparations stained by Diff-Quik (A) and by IFA, using a positive control sera (B). Arrow indicate intracytoplasmic inclusions filled with numerous bacteria, 1000X magnification.

TABLE 1. Patients with positive results for *A. phagocytophilum* in serologic tests (2000-2006).

Patient No./ Year	Gender/Age(y)/ Residence ^a	Clinical information ^b	Sample date	<i>A. phagocytophilum</i>			Other pathogen tests ^c	Interpretation of laboratory diagnosis
				IFA (IgM/IgA,M,G)	PCR (Blood/Sera)	Isolation (HL60)		
1/2000	M/52/Lisboa	Febrile illness	06/Jul	-/80	NA/-	NA	Ec (S -)	Inconclusive
2/2001	F/NA/Lisboa	Febrile illness	19/Jun	-/320	NA/-	NA	Ba (S +); Ec, Rk (S -)	Bartonellosis (compatible titers)
3/2002	F/NA/Santarém	Febrile illness	04/Apr	-/160	NA/-	NA	Ec, Rk (S -)	Inconclusive
4/2002	M/43/Setúbal	NA	12/Aug	-/80	NA/NA	NA	Ec, Rk (S -)	Inconclusive
5/2003	M/35/Lisboa	NA	21/Jun	-/80	NA/-	NA	Ec, Rk (S -)	Inconclusive
6/2003	M/64/Santarém	Febrile illness	02/Jun	-/80	NA/-	NA	Ec, Rk (S -)	Inconclusive
			09/Oct	-/80			Ec, Rk (S -)	
7/2003	M/44/Lisboa	Polyarthralgia	13/Mar	-/80	NA/-	NA	Ec, Rk (S -)	Inconclusive
8/2003	M/49/Évora	Febrile illness	10/Apr	-/80	NA/-	NA	Ec, Rk (S -)	Inconclusive
			17/Apr	-/80			Ec, Rk (S -)	
			23/Sep	-/80			Cb; Ec, Rk (S -)	
9/2003	M/40/Évora	Arthritis	26/Dec	-/160	NA/-	NA	Ec, Rk (S -)	Inconclusive
			19/Feb	-/80			Bb, Ec, Rk (S -)	
10/ 2004	M/NA/Évora	NA	05/Nov	-/80	NA/-	NA	Cb (S +); Ec, Rk (S -)	Acute Q fever (compatible titers)

TABLE 1 (cont.). Patients with positive results for *A. phagocytophilum* in serologic tests (2000-2006).

Patient No./ Year	Gender/Age(y)/ Residence ^a	Clinical information ^b	Sample date	<i>A. phagocytophilum</i>			Other pathogen tests ^c	Interpretation of laboratory diagnosis
				IFA (IgM/IgA,M,G)	PCR (Blood/Sera)	Isolation (HL60)		
11/2004	M/NA/Setúbal	Febrile illness	16/May	-/-	NA/-	NA	Cb, Ec (S -); Rk (S/P/I -) Cb (S +); Ec, Rk (S -)	Acute Q fever (seroconversion);
			18/Jul	-/80				
12/2005	M/60/Évora	Polyarthralgia	09/Jun	80/320	NA/-	NA	Cb, Ec (S -); Rk (S/P/I -)	Inconclusive
13/2005	F/51/Lisboa	Febrile illness	06/Feb	-/160	NA/-	NA	Cb (S +); Ec, Rk (S -) Cb (S +); Ec, Rk (S -)	Acute Q fever (compatible titers)
			25/Feb	-/80				
14/2006	F/68/Évora	Febrile illness	13/Mar	NA	NA/NA	NA	Ec, Rk (S -) Cb (S +); Ec, Rk (S -)	Acute Q fever (compatible titers)
			03/Apr	-/160				
15/2006	F/39/Faro	Febrile illness	27/Jun	-/160	-/-	-	Cb (S -; P +); Bb (S -); Ec, Rk (S/P/I -) Cb (S +); Bb, Ec, Rk (S -)	Acute Q fever (seroconversion; <i>C. burnetii</i> isolation on HL60; DNA detection in both culture, and buffy coat)
			03/Jul	-/160				
16/2006	F/53/Coimbra	Febrile illness	14/Nov	-/80	NA-	NA	Ba; Cb, Ec, Rk (S -) Ba; Cb, Ec, Rk (S -)	Inconclusive
			30/Nov	-/80				
17/2006	F/NA/NA	Sepsis	29/Nov	-/80	-/-	-	Bb, Cb, Ec, Rk (S/P -)	Inconclusive

(-) Negative result; (+) Positive result; (NA) Not available sample; ^aDistrict of residence; ^bClinical information available in submission forms; ^cAvailable information regarding other tick-borne agents or related bacteria tested in CEVD/INSA according to physician suspicion - (Bb) *Borrelia burgdorferi* s.l., (Cb) *Coxiella burnetii*, (Ba) *Bartonella* spp., (Ec) *Ehrlichia chaffeensis*, (Rk) *Rickettsia* spp. The laboratory diagnosis was based in (S) serology, (P) PCR testing and (I) isolation attempts.

TABLE 2. Patients with positive results for *E. chaffeensis* in serologic tests (2000-2006).

Patient No./ Year	Gender/Age(y)/ Residence ^a	Clinical information ^b	Sample date	<i>E. chaffeensis</i>			Other pathogen tests ^c	Interpretation of laboratory diagnosis
				IFA (IgM/ IgA,M,G)	PCR (Blood/Sera)	Isolation (DH82)		
18/2001	F/NA/Évora	NA	17/Aug	-/64	NA/-	NA	Ap, Rk (S -)	Rickettsiosis (seroconversion)
			18/Oct	-/64			Ap (S -); Rk (S +)	
19/2002	F/NA/Évora	Febrile illness	20/Sep	-/64	NA/-	NA	Ap (S -); Rk (S +)	Rickettsiosis (compatible titers)
			18/Oct	-/64			Ap (S -); Rk (S +)	
20/2005	F/29/Évora	Febrile illness	30/Jun	128/128	NA/NA	NA	Ap, Cb (S -); Rk (S/P/I -)	Inconclusive
			21/ Jul	128/128			Ap, Cb, Rk (S -)	

(-) Negative result; (+) Positive result; (NA) Not available sample; ^aDistrict of residence; ^bClinical information available in submission forms; ^cAvailable information regarding other tick-borne agents or related bacteria tested in CEVDI/INSA according to physician suspicion – (Ap) *Anaplasma phagocytophilum*, (Bb) *Borrelia burgdorferi s.l.*, (Cb) *Coxiella burnetii*, (Ba) *Bartonella* spp., (Rk) *Rickettsia* spp. The laboratory diagnosis was based in (S) serology, (P) PCR testing and (I) isolation attempts.

TABLE 3. Patients with positive results for both *A. phagocytophilum* and *E. chaffeensis* in serologic tests (2000-2006).

Patient No./ Year	Gender/Age(y)/ Residence ^a	Clinical information ^b	Sample date	Anaplasmataceae PCR (Blood/Sera)	<i>A. phagocytophilum</i>		<i>E. chaffeensis</i>		Other pathogen tests ^c	Interpretation of laboratory diagnosis
					IFA (IgM/ IgA,M,G)	Isolation (HL60)	IFA (IgM/ IgA,M,G)	Isolation (DH82)		
21/2004	F/60/Évora	Febrile illness with rash	25/Mar	NA/NA	NA	NA	NA	NA	Rk (S -)	Acute Q fever (compatible titers)
			30/Mar		-/80		-/64		Cb (S +); Rk (S -)	
			06/May		-/80		-/128		Cb (S +); Rk (S -)	
22/2004	M/33/Lisboa	NA	02/Jun	NA/NA	NA	NA	-/128	NA	Cb (S -); Rk (+)	Inconclusive
			13/Jun		-/160		-/64			
23/2005	M/52/Évora	Endocarditis	23/Aug	NA/-	-/640	NA	-/256	NA	Cb (S +); Rk (S -)	Chronic Q fever (compatible titers)
			08/Sep		-/320		-/128		Cb (S +); Rk (S -)	
			29/Sep		-/320		-/128		Cb (S +); Rk (S -)	
			13/Dec		-/320		-/128		Cb (S +)	
24/2006	M/58/Évora	NA	19/Dec	-/-	-/640	-	-/128	-	Cb (S +); Rk (S/I -)	Inconclusive

(-) Negative result; (+) Positive result; (NA) Not available sample; ^aDistrict of residence; ^bClinical information available in submission forms; ^cAvailable information regarding other tick-borne agents or related bacteria tested in *CEVDI/INSA* according to physician suspicion - (Cb) *Coxiella burnetii*, (Rk) *Rickettsia* spp. The laboratory diagnosis was based in (S) serology, (P) PCR testing and (I) isolation attempts.

CHAPTER VI

FINAL REMARKS AND FUTURE PERSPECTIVES

FINAL REMARKS AND FUTURE PERSPECTIVES

This thesis continues earlier studies on *Ehrlichia* species infections started at *Centro de Estudos de Vectores e Doenças Infecciosas, Instituto Nacional de Saúde Dr. Ricardo Jorge (CEVDI/INSA)* during the 1990s. It focuses on methodological training, especially regarding *A. phagocytophilum*. Much of the work was under the guidance of Professor John Stephen Dumler, initially at the *Unité des Rickettsies - Faculté de Médecine, Marseille - France*, and later continued in the *Division of Medical Microbiology, Department of Pathology, The Johns Hopkins University School of Medicine, Baltimore, Maryland - USA*. As presented in Chapter II, the technical training included the integration of research teams resulting in broad studies of Anaplasmataceae, such as **“Distribution of “*Ehrlichia walkeri*” in *Ixodes ricinus* (Acari:Ixodidae) from the Northern Part of Italy”**, conducted while training at the *Unité des Rickettsies*. The opportunity to work and learn in Research Units devoted to Anaplasmataceae was essential for the proposed objectives of this thesis, allowing technology transfer and development of this area research investigation at *CEVDI/INSA*. Establishing the foundations for a concerted study on *A. phagocytophilum* enabled cooperation in a Spanish study partially developed by our laboratory **“Detection of a non-pathogenic variant of *Anaplasma phagocytophilum* in *Ixodes ricinus* from La Rioja, Spain”**, and permitted the fundamental study of *A. phagocytophilum* in Portugal, presented in Chapters III to V either as published articles, or as original studies submitted for publication in scientific journals.

The study of vector ticks potentially involved in *A. phagocytophilum* enzootic cycles, addressed in Chapter III, was based on collaborative field-work developed in coordination with other research teams of *CEVDI/INSA* in order to promote a fuller understanding of ticks and tick-borne agents of potential Public Health relevance in Portugal. Several regions of the country were selected for the field-trials, either because *Ixodes* species were known to be present, or because specific interest in a given tick-borne disease was expressed for integration with ongoing projects. Nevertheless, it is important to state that several areas of interest were not covered by this study due to time restrictions or high cost usually associated with this kind of research.

The majority of ticks included in the present study were obtained by flagging vegetation in selected collection sites. Additional specimens were also collected from parasitized domestic and

wild animals, as well as from humans. The analysis of questing ticks generally allows a better assessment of the tick-borne agent's prevalence in a given environment, by reducing the potential bias introduced by infected host blood resulting in positive results when vector competence for pathogen replication and transmission is uncertain. Moreover, the study of free-living ticks has additional informative value with regard to the potential of a given species to sustain the agent transstadially, which is one of the fundamental requirements considered for competence as a vector. Regardless, important information can also be obtained with the analysis of ticks in their parasitic phase, especially regarding the potential role of wild and domestic animals as feeding-support for hematophagous arthropods of interest and their involvement in an infectious agent's natural cycles when serving as either susceptible vertebrate host or reservoir.

One conclusion of this study was that *A. phagocytophilum* persists on Madeira Island, Madeira Archipelago. The presence of this agent was first reported in questing *I. ricinus* collected on the Island by Nuncio and coworkers (2000) and observed again in field work performed during this study. The estimated prevalence of *A. phagocytophilum* on Madeira Island ticks was 4 - 7.5%, which is in the range of 0 – 57.1% described in questing *I. ricinus* from other European countries, as detailed in Chapter 1 - State of the Art. Studies using a greater number of samples, and targeting different seasons, locations and habitats were identified as important requirements for confirming levels of infection and to better investigate the natural cycles of the agent on the Island. Two projects have already been submitted to obtain government financial support to continue research on Madeira Island. Another interesting finding was the detection of a natural focus of *A. phagocytophilum* that involves other *Ixodes* species - *I. ventalloi* in Baixa de Palmela (Setúbal District, mainland). Infected ticks were obtained from both vegetation and a stray cat (*Felis catus domesticus*). This was the first documentation of *A. phagocytophilum* infection in *I. ventalloi* ticks. Moreover, it added domestic cats to the national list of vertebrate hosts parasitized by this tick species and potentially involved in *A. phagocytophilum* natural cycles. The highlighted findings are presented in the article **“Detection of *Anaplasma phagocytophilum* DNA in *Ixodes* ticks (Acari:Ixodidae) from Madeira Island and Setúbal District, Mainland Portugal”**. This association is now reinforced by the detection of additional *I. ventalloi* parasitizing cats in Lisboa and also in Santarém District, where another tick was found infected with *A. phagocytophilum*, as summarized in **“PCR-based survey of *Anaplasma phagocytophilum* in Portuguese ticks (Acari: Ixodidae)”**.

The continued study of Portuguese ticks suggests that *A. phagocytophilum* is not widely distributed but is concentrated in certain environments that either sustain it or possibly allow its continuous introduction. As noted by several authors, wild birds could play a role in the introduction and/or dispersion of *A. phagocytophilum* infected ticks to widespread regions (Alekseev *et al.*, 2001a; Bjoersdorff *et al.*, 2001; Daniels *et al.*, 2002; De la Fuente *et al.*, 2005a). Investigation of this aspect was started during this study, but only a limited number of ticks have been analysed so far. Ticks were collected from wounded birds, recovered in two rehabilitation centers in Lisboa and Setúbal District (mainland), and all specimens were found to be negative for *A. phagocytophilum* in spite of the detection of other tick-borne bacteria, as stated in "Ticks Parasitizing Wild Birds in Portugal: Detection of *Rickettsia aeschlimannii*, *R. helvetica* and *R. massiliae*". Nevertheless, a collaborative agreement between CEVDI/INSA and Instituto de Conservação da Natureza e da Biodiversidade (ICNB) will provide new opportunities for continuing evaluations of the potential for resident, occasional migrant, or migratory birds to maintain ticks and tick-borne agents in Portugal.

During the four years of this study, ticks were obtained from several sampling areas within seven mainland districts, Bragança, Braga, Leiria, Lisboa, Portalegre, Santarém and Setúbal, and also from Madeira Island. The majority of ticks were obtained in collections directed toward areas where the existence of *Ixodes* species was previous documented, as in the Lisboa, Leiria and Setúbal Districts, and on Madeira Island. Additional specimens were obtained as part of ongoing projects with other specific interests, such as from sampling areas in Bragança District. This region was included in a CEVDI/INSA project because it had the highest incidence of MSF reported during 1989-2003, yet little was known about the *Rickettsia* species that circulated in this region of the country or about their prevalence in ticks. In Portugal, MSF is the most important tick-borne disease with an incidence rate of 8.9 per 10⁵ inhabitants over 1999-2003 (De Sousa *et al.*, 2003). The disease is caused by bacteria belonging to the complex *Rickettsia conorii* which are transmitted by the brown-dog tick, *R. sanguineus* (Bacellar, 1996; Bacellar *et al.*, 1999a, 1999b; De Sousa *et al.*, in press). This tick is widely distributed on the mainland, and according to Baptista's prediction maps, *Rhipicephalus* spp. are especially prevalent in the South, in the Centre and also in Northern inner regions of the country coinciding with the majority of districts reporting the highest prevalences of MSF (De Sousa *et al.*, 2003; Baptista, 2006). By contrast, *I. ricinus* has a more restricted distribution occurring in the littoral region increasing from South to the North (Baptista, 2006). In fact, the samples collected in Bragança District were in accordance with Baptista's data,

showing a low prevalence of *Ixodes* species; although several rickettsiae were found in the studied arthropods, no *A. phagocytophilum* infection was detected. These preliminary results are presented in “Ticks and tick-borne rickettsiae surveillance in Montesinho Natural Park, Portugal” and the results from an additional sample of ticks that was further tested for *A. phagocytophilum* are included in the article that summarized all the tick study work: “PCR-based survey of *Anaplasma phagocytophilum* in Portuguese ticks (Acari: Ixodidae)”.

Additionally, the study of *Portalegre* District reinforced the observation of a limited number of *Ixodes* spp. among inland regions of the country when compared to littoral areas. The field work in *Portalegre* were performed in a similar manner as those in *Lisboa* and *Setúbal* districts, i.e. focused in the spring season and carried out over the same number of days, but in those littoral districts *Ixodes* species were found to be generally more abundant. Regardless, due to the exploratory rather than exhaustive nature of this work, it cannot exclude the occurrence of natural foci of *A. phagocytophilum* cycles among inland regions. Although the Continental and Mediterranean climates that generally characterize the North and Southern inland regions are regarded as limiting factors for maintenance of *Ixodes* spp. populations, when compared to the littoral dominated by an oceanic influence, local favourable environmental conditions have been identified. In fact, several authors documented the presence of *I. ricinus*, the main European vector of *A. phagocytophilum*, in all inland districts of Portugal (Dias, 1994; Caeiro, 1999). Interestingly, also in littoral areas *Ixodes* spp. do not seem to present a regular distribution, as in the example of the District of *Leiria* where only a limited number of specimens were obtained. Again, this patchy distribution may relate to the strict ecological requirements that characterize *Ixodes* spp., so it is possible that some microenvironments that sustain these ticks are not identified when performing sample collections even in areas where these ticks are expected to occur. *Madeira Island* and *Tapada Nacional de Mafra (TNM)*, a confined Natural Park belonging to *Lisboa* District, remain as the few exceptions of this, presenting an abundant tick fauna dominated by *I. ricinus*.

The importance of adequate ecological conditions for the maintenance of *A. phagocytophilum* enzootic cycles, starting with the existence of competent vectors of the genus *Ixodes*, has been demonstrated in all Northern hemisphere countries where this agent is present. Only sporadic reports document *A. phagocytophilum* in other genera of ticks and mites (Des Vignes *et al.*, 1999; Fernandez-Soto *et al.*, 2001; Goethert & Telford, 2003; Holden *et al.*, 2003; Kim *et al.*, 2003; Sarih *et al.*, 2005; Cao *et al.*, 2006; Skoracki *et al.*, 2006), but thus far no study

has proven their role in the agent's transmission, as reviewed in Chapter I. This ecological requirement is also shown here by the exclusive association of *A. phagocytophilum* with *Ixodes* spp., in spite of screening of several other ticks species, some even collected in the same area as infected *Ixodes* ticks, such as Baixa de Palmela in Setúbal District. This study included *Dermacentor marginatus*, *D. reticulatus*, *Hyalomma lusitanicum*, *Haemaphysalis inermis*, *H. punctata*, *Rhipicephalus bursa*, *R. pusillus*, and the *R. sanguineus* group, which represents 75% of the non-*Ixodes* species present in Portugal, as described in “**Carraças associadas a patologias infecciosas em Portugal**” (Appendix 1).

Regardless, competent *Ixodes* ticks are found in many regions beyond the areas of pathogen endemicity, and seasonal fluctuations in *A. phagocytophilum*-endemic foci have also been reported. Discrepancies between the presence of vector ticks and pathogen spatial and temporal distribution are not well understood but could be related to arthropod feeding behaviour and reservoir-host dynamics (Swanson *et al.*, 2006). A patchy distribution of *A. phagocytophilum* was also documented in this study. The best example of this phenomenon is shown in *TNM* in opposition to Madeira Island. As previously mentioned, both areas sustain abundant populations of *I. ricinus*, but no active infections by *A. phagocytophilum* were found in *TNM* in the arthropod sampling in spite of the detection of other Rickettsiales associated with *I. ricinus*, as presented in “**Detection of *Rickettsia helvetica* and other Spotted Fever Group Rickettsiae in *Ixodes ricinus* from Tapada Nacional de Mafra, Portugal**”. Of interest is the observation that both *TNM* and Madeira Island sustain a great variety of another *I. ricinus*-borne agent, *B. burgdorferi* s.l. including: *B. afzelii*, *B. burgdorferi* s.s., *B. garinii*, *B. lusitaniae* and *B. valaisiana* in Madeira Island (Matuschka *et al.*, 1994, 1998; Nuncio, 2001; Lopes de Carvalho *et al.*, in submission); *B. afzelii*, *B. garinii*, *B. lusitaniae*, and *B. valaisiana* in *TNM* (Baptista *et al.*, 2004, 2006). The apparent lack of *A. phagocytophilum* transovarial transmission in ticks directs attention to competent vertebrates, especially feeding hosts for larvae and nymphs, as critical in the natural maintenance of *A. phagocytophilum* active cycles. Thus, the patchy distribution of *A. phagocytophilum* seems to be multifactorial and probably depends on the existence of both competent vector ticks and reservoir hosts. However, *TNM* possesses a mammal population with small and large-size animals, including rodents, insectivores, carnivores, lagomorphs, and artiodactyls (wild boars, fallow deer and elks), that are capable of acting as both feeding support for ticks and as potential reservoirs for *A. phagocytophilum*. Thus, this aspect alone apparently does not seem to be a limiting factor for

agent maintenance. If further research confirms that the absence of *A. phagocytophilum* in *TNM* is not the result of seasonal fluctuation or methodologic approaches, other aspects should be considered as determinants of the agent's presence and maintenance.

Another interesting finding was the detection of *A. phagocytophilum* variant genotypes in Portuguese ticks. Analysis of *A. phagocytophilum* *rrs*, *groESL* and *msp2* (*p44*) partial gene sequences obtained from positive ticks demonstrated nucleotide polymorphisms, especially in *groESL* and *msp2*. *A. phagocytophilum* sequences found in Madeira Island *I. ricinus* suggest a close relationship with North American strains isolated from humans, and also with those detected in Central and Northern Europe. Yet, these were divergent from genotypes found in mainland *I. ventralloi*, which represent new variant genotypes of unknown pathogenicity, as detailed in "PCR-based survey of *Anaplasma phagocytophilum* in Portuguese ticks (Acari: Ixodidae)".

The existence of *A. phagocytophilum* genotypes with distinct geographic origins, reservoir hosts and possibly pathogenicity is a significant matter of interest in the scientific community. Ongoing research suggests that genotypes identified in human disease are identical or closely related to those infecting other non-ruminant animals, such as horses, dogs and possibly cats. It is proposed that these genotypes are maintained in an enzootic cycle that is dependent on ticks and small mammals, such as rodents. Thus, to complement the ecological study of *A. phagocytophilum* and address the existence of variant genotypes potentially involved in human granulocytic anaplasmosis in Portugal, several animal populations that could act as reservoirs (rodents) or susceptible hosts (horses and dogs) were screened for active infections, as presented in Chapter IV. To maximize resources and limit the time-consuming and costly collection of samples, biological specimens were obtained from ongoing *CEVD/INSA* projects or from other independent studies performed by Institutional partners.

The study of potential reservoirs addressed five of the twelve rodent species that are known to inhabit Portugal (Madureira & Ramalhinho, 1981; McDonald & Barret, 1999), including *Apodemus sylvaticus*, *Mus musculus*, *M. spretus*, *Rattus norvegicus* and *R. rattus*. The majority of these species are regarded as hosts for both *I. ricinus* and *I. ventralloi* (Dias, 1994; MM Santos-Silva, personal communication) and were captured in Arrábida, Mafra and Gerês in mainland, Santana and Seixal in Madeira Island, areas where *Ixodes* ticks are known to be present. The additional inland area of Mértola was also included in this study. Antibodies against *A. phagocytophilum* or a closely related agent were detected in *M. spretus* sera from all mainland

sampling areas where this mouse was captured (Arrábida, Mafra and Mértola). The greatest number of seropositive animals was found during spring but, despite the capture season no other proportion with statistically significant was observed, probably due to the limited number of rodents analysed. Spring is recognized as the season when *M. spretus* are most active and is also regarded as the time of the year when *A. phagocytophilum* infections or reinfections occur in rodents (Stafford *et al.*, 1999; Castro *et al.*, 2001). However, active infections by *A. phagocytophilum* were not detected in seropositive animals, as presented in **“Detection of antibodies against *Anaplasma phagocytophilum* in wild-rodents, Portugal”**.

Whether the *M. spretus* seropositivity reflects residual antibodies from past *A. phagocytophilum* infections or active infections with bacteremia lower than detection thresholds deserves a more detailed investigation. The occurrence in ticks of *A. phagocytophilum* ruminant-like genotypes that are regarded to have limited infective potential for rodents was suggested by Massung and coworkers (2003b), and could explain the inability to detect active infection in *M. spretus*. In fact, the dominant ruminant strain (Ap-variant 1) was identified in *I. ricinus* collected from cattle in Spain, as demonstrated in the collaborative study **“Detection of a non-pathogenic variant of *Anaplasma phagocytophilum* in *Ixodes ricinus* from La Rioja, Spain”**. Although ruminant populations were not addressed in this thesis and all genotypes detected in ticks had sequence polymorphisms distinct from the Ap-variant 1 and other ruminant variants, the existence of genotypes with limited infective potential for rodents and other non-ruminants can not be excluded. In this regard, it is of interest the spatial proximity between the area defined as Arrábida in this rodent study, and Baixa de Palmela, where *I. ventalloi* were found infected with a new *A. phagocytophilum* genotype for which pathogenicity potential is unknown. Moreover, in Mafra no *A. phagocytophilum*-infected *Ixodes* spp. could be identified despite the presence of seropositive mice. Thus, the possibility of cross-reactions with antigenically similar agents should also be considered as another explanation for the *M. spretus* serologic results. As further discussed in this chapter, *A. platys*, that is closely related to *A. phagocytophilum*, was recently identified in a Portuguese dog population that had *A. phagocytophilum* serologic reactions. Although the enzootic cycle of this agent remains largely unknown, active infections in rodents are documented in other countries (Chae *et al.*, 2003; Kim *et al.*, 2006).

An important unexplained aspect is the lack of *A. phagocytophilum* detection in Madeira Island rodents despite the documented persistence of this agent in *I. ricinus* ticks in that location. The possibility of inadequate rodent sampling exists due to i) the limited number analysed

compared to the total number of captures, ii) the limited collection studies restricted to only two locations on the Island, or iii) the potential that other unexamined small or medium size animals serve as feeding support for *Ixodes* spp. In fact, both *I. ricinus* and *I. ventraloi* have been detected parasitizing several other feral animals beside rodents, including birds, and members of the Order Carnivora, Erinaceomorpha, Lagomorpha and Soricomorpha (Dias, 1994; MM Santos-Silva, personal communication). Such uncertainties argue for further investigation of *A. phagocytophilum* cycles on Madeira Island.

With regard to possible infections in domestic animals, equine samples were obtained during routine evaluations for serosurveillance of 10 mainland districts, and, seropositive animals were identified in 6, including Braga, Faro, Lisboa, Portalegre, Santarém and Setúbal. Even though no significant association was found between seroprevalence rates and horse origin, age groups or gender, an active *A. phagocytophilum* infection was detected by molecular analysis in one seropositive mare from Faro District, Algarve region, Southern mainland. Nucleotide sequences obtained from this animal exhibited a high degree of similarity to strains involved in human disease, as presented in **“Serological survey and molecular detection of *Anaplasma phagocytophilum* infection in Portuguese horses”**. Additionally, a population of dogs from Algarve region was also tested for active *A. phagocytophilum* infections. These animals were presented to veterinarian with clinical signs compatible of tick-borne disease; the great majority were seroreactive for *A. phagocytophilum*. In five animals the serological criteria for *A. phagocytophilum* active infection were fulfilled by either seroconversion or four-fold increase in antibody titers. Regardless, molecular analysis failed to detect any active *A. phagocytophilum* infections but *A. platys* DNA was found in two seropositive (one presenting seroconversion for *A. phagocytophilum* antigen) and three seronegative animals, as presented in **“Anaplasmataceae as etiologic agents of canine tick-borne disease in Portugal”**.

Horses and dogs are two of the non-ruminant animals that have been documented with granulocytic anaplasmosis in both North American and European areas where *A. phagocytophilum* is known to exist (Engvall *et al.*, 1996; Greig *et al.*, 1996; Madigan *et al.*, 1996; Pusterla *et al.*, 1998a; Bullok *et al.*, 2000; Tozon *et al.*, 2003; Von Loewenich *et al.*, 2003b; Alberti *et al.*, 2005; Lester *et al.*, 2005; Shaw *et al.*, 2005). Identification of infections in these animals is also regarded as a surrogate predictor of human disease. This study provided the first definitive evidence of *A. phagocytophilum* infections in Portuguese horses and suggests the potential occurrence of HGA in

Portugal as well. Despite the lack of active infections in dogs, the close contact of these animals with humans argues for continued evaluations. In a study of patients with dermatological lesions resulting from infection by *Ixodes*-borne agent *B. burgdorferi* s.l., 1/3 of the individuals owned companion animals, especially dogs but also cats, birds and rodents (Franca, 2004). Moreover, these data add *A. platys* to the list of Anaplasmataceae that circulate in Portugal and emphasize the importance of veterinarians considering not only equine granulocytic anaplasmosis but also canine infectious cyclic thrombocytopenia in the differential diagnosis of tick-borne diseases in Portugal.

Molecular analyses demonstrate that *A. phagocytophilum* with genotypes closely related to those known to cause human disease were found only in *I. ricinus* from Madeira Island and in a horse from the Algarve region. These two geographic regions are well known as tourist destinations and also as nidification or resting sites for several migratory bird species, suggesting the possibility of tick-borne agent introduction, a concept that deserves much more study.

The potential occurrence of human Anaplasmataceae infections in Portugal was first proposed by David de Moraes and coworkers (1991). These authors described a febrile patient with negative serological results for typhoid fever, brucellosis, MSF and LB, stable titers for *C. burnetii*, but a >four-fold decrease in *E. chaffeensis* antibodies in three consecutive samples. This finding was reported in the same year that *E. chaffeensis* was first isolated in the US and prior to the published description of the first cases of human granulocytic anaplasmosis; thus, evaluation for *A. phagocytophilum* infection was not performed. The diagnosis was made possible as a consequence of pioneering research initiated at CEVDI/INSA by Armindo Filipe, the coordinator of a study of emerging tick-borne agents and their potential impact on human diseases. The determination and enthusiasm of these investigators were undoubtedly the stimuli for development of Anaplasmataceae and other emerging tick-borne disease research in Portugal. In fact, two years before the report of this case that fulfilled serological criteria for *E. chaffeensis* infection, the same investigators documented the first clinical case of LB in Portugal (David de Moraes, 1989).

Since the report of the first Portuguese *E. chaffeensis* case, CEVDI/INSA has included *E. chaffeensis* IFA as a routine laboratory test available for the community, and over the last year, this was also extended to include testing for *A. phagocytophilum*. Moreover, within the scope of this thesis, the technological exchange with The Johns Hopkins University School of Medicine.

permitted the implementation of direct tests, including molecular and culture techniques that were performed on an experimentally basis in 2006 and are now being used routinely. In order to alert the practicing medical community about the emergence of Anaplasmataceae, two review articles were published regarding this subject. The first focused on the epidemiological, clinical manifestations, diagnosis and treatment of HME (David de Moraes, 1992a). More recently, in response to the increasing detection of *A. phagocytophilum* infections in Europe, an update “Ehrlichiose granulocítica humana. Conceitos actuais” (Appendix 2) was published. To better address whether *A. phagocytophilum* is involved in human infection in Portugal, Chapter V of this thesis is devoted to analysis of biological samples received annually at CEDVII/INSA from patients with suspected tick-borne disease.

The occurrence of *A. phagocytophilum* and HGA positively correlates with the geographic distribution of other *Ixodes*-borne agents and associated diseases, such as *B. burgdorferi s.l.*, *Babesia microti* and *B. divergens*, and TBE virus. This correlation is demonstrated by coinfections in ticks (Swanson *et al.*, 2006), the geographic convergence of diseases (CDC, 2001-2006; Dumler, 2005), and increasing recognition of human coinfections (Nadelman *et al.*, 1997; Horowitz *et al.*, 1998a; Krause *et al.*, 2003; Moss & Dumler, 2003; Hermanowska-Szpakowicz *et al.*, 2004; Lotric-Furlan *et al.*, 2005, 2006; Grzeszczuk *et al.*, 2006b). Thus, the first study addresses *A. phagocytophilum* infections in Portuguese patients and is based on a retrospective serological evaluation of samples received in 2002 from individuals with confirmed or suspected LB. Given the non-specific presentation of HGA that is in common with other-tick borne illnesses, an additional cohort representing patients with clinical suspicion of LB/MSF, but lacking laboratory confirmation for these diagnoses was also included. Indeed, this study demonstrated a significantly higher proportion of *A. phagocytophilum* seropositive patients among those with suspected/confirmed LB when compared to the overall population and the control cohort, defined by healthy blood-donors. Although no statistically significant differences in age, gender, or province of origin were noted between *A. phagocytophilum* –seropositive and –seronegative individuals, the majority of samples came from Estremadura region, and among these positive results were more often found in patients who resided in Oeiras than in other locations. Regardless, only a 63 year-old female from Elvas, Alto Alentejo region, who presented with fever and had a >four-fold increase in *A. phagocytophilum* IFA titer in two consecutive samples collected 68 days apart, fulfilled the HGA laboratory diagnostic criteria for active infection (Walker *et al.*, 2000; Brouqui *et al.*, 2004). These

results are presented in the article **“Human exposure to *Anaplasma phagocytophilum* in Portugal”**.

This study corroborated previous reports that document a higher *A. phagocytophilum* seroprevalence in at-risk populations, in this case, documented LB patients (reviewed in detail in Chapter I, State of the art). Regardless, for the majority of seropositive patients, *A. phagocytophilum* diagnostic criteria could not be fulfilled because of the lack of paired serum samples. Moreover, application of direct laboratory tests that could definitively confirm HGA, such as isolation and molecular analysis, were not applicable due to the retrospective character of the study and the inavailability of appropriate samples when *A. phagocytophilum* testing was eventually available. The association of seropositivity with Oeiras residence in patients from the Estremadura region is worthy of further consideration. Interestingly, the first human isolate of *B. burgdorferi* s.l. in Portugal, identified as *B. lusitaniae*, was obtained from a patient residing in Oeiras (Collares-Pereira *et al.*, 2004; Franca, 2004). Oeiras is located near the urban perimeter of Lisboa city and is one of the administrative divisions of Lisboa District, a littoral area where *Ixodes* spp. are known to occur. This district is also described in several studies as having the highest number of laboratory-confirmed cases of LB in Portugal (Franca, 2004; Baptista, 2006; Lopes de Carvalho & Nuncio, 2006), and Oeiras is mentioned in Franca's work (2004) as the residence place of at least three LB patients. The authors discussed potential biases for these results, focusing on the possibility that some patients could acquire infection in districts or countries other than their area of residence while working or in leisure activities (Franca, 2004), or biased by the more ready access to samples from patients of South Central and Southern regions due to the locations of health institute partners and research units where these studies were conducted (Baptista, 2006; Lopes de Carvalho & Nuncio, 2006). Nevertheless, the possibility of Lisboa District to be an endemic area for *Ixodes*-borne disease, requires further evaluation.

An additional study analysed available data concerning Anaplasmataceae diagnoses performed in CEVDI/NSA during 2000-2006, as presented in **“Six years of Anaplasmataceae serodiagnosis in humans. Data from a state laboratory, Portugal”**. IFA tests for *E. chaffeensis* were performed prospectively as part of routine laboratory diagnosis. Potential cross-reactions between *E. chaffeensis* and *A. phagocytophilum*, as previous documented in both HME and HGA case series (Bakken *et al.*, 1996c; Wong *et al.*, 1997; Comer *et al.*, 1999a; Walls *et al.*, 1999; Lotric-Furlan *et al.*, 2006), prompted testing of samples received based on clinical suspicion of infection

for both agents. Thus, archived sera received during 2000-2005 for *E. chaffeensis* serodiagnosis were analysed retrospectively for the presence of antibodies against *A. phagocytophilum*. In 2006, serological testing was performed prospectively and in parallel for both agents. Such testing demonstrated a higher proportion of *A. phagocytophilum* than *E. chaffeensis* seropositive samples, although reactivity to both agents was also found. These results are in accordance with seroprevalence studies on European population, which suggest greater exposure to *A. phagocytophilum* or an antigenically related agent (Dumler et al, 1997; Groen et al, 2002). For the majority of seropositive patients that had paired sera, stable antibody titers or less than four-fold titer changes were observed. Only one male patient from Setúbal District seroconverted for *A. phagocytophilum*, fulfilling serological criteria for a confirmed case. However neither *A. phagocytophilum* nor *E. chaffeensis* active infections could be detected in the samples analysed by direct techniques.

This study also analysed the results among *A. phagocytophilum* and/or *E. chaffeensis* seropositive patients of tests requested by physicians for other tick-borne agents or related bacteria that were conducted at CEVDI/INSA. These supplemental laboratory tests provided serological evidence of bartonellosis in one and acute Q fever cases in five *A. phagocytophilum*-seropositive individuals, rickettsiosis in two *E. chaffeensis*-seropositive patients, and individual cases of acute and chronic Q fever in two patients with both *A. phagocytophilum* and *E. chaffeensis* antibodies. Moreover, culture attempts using samples from a patient with stable *A. phagocytophilum* titers and a *C. burnetii* seroconversion resulted in the isolation of *C. burnetii* in HL-60 cells. Of interest was the observation of another patient with *C. burnetii* seroconversion that also fulfilled serologic criteria for the diagnosis of active *A. phagocytophilum* infection. Whether reactivity to multiple vector-borne agents represents cross-reactivity to shared antigens, such as heat shock proteins or antibodies induced by active coinfection or past exposures to one or more Anaplasmataceae, *C. burnetii*, *Rickettsia* spp., or *Bartonella* spp., remains to be ascertained.

Fifteen years have past since the findings of David de Moraes and coworkers (1991), but the question still remains about the interpretation of serologic reactivity to Anaplasmataceae observed among Portuguese patients. For at least *A. phagocytophilum*, potential exists for human infection given identification of genotypes that are similar or closely related to those associated to HGA. However, the possible presence of *E. chaffeensis* or other *Ehrlichia* spp. of medical interest can not be excluded, since this aspect was not investigated. Continued integrated analysis of the results of laboratory diagnostic tests for Anaplasmataceae and other tick-borne infections, with a

special emphasis on applications of direct approaches is indispensable to better understand whether active infections with these agents occur in Portugal. Moreover, the potential for imported cases associated with international travellers to European- or US-endemic areas, underscores the need for continuing active surveillance and vigilance.

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APPENDIXES

**APPENDIX 1. CARRAÇAS ASSOCIADAS A PATOLOGIAS INFECCIOSAS EM
PORTUGAL**

SILVA MM, SANTOS AS, FORMOSINHO P, BACELLAR F

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CARRAÇAS ASSOCIADAS A PATOLOGIAS INFECCIOSAS EM PORTUGAL

M.^a MARGARIDA SILVA, A SOFIA SANTOS, PERPÉTTUA FORMOSINHO, FÁTIMA BACELLAR
Centro de Estudos de Vectores e Doenças Infecciosas, Instituto Nacional de Saúde Dr. Ricardo Jorge. Lisboa.

RESUMO

Os ixodoideos, também designados por carraças, são artrópodes hematófagos estritos ectoparasitas de vertebrados terrestres. Estes artrópodes estão presentes em quase todas as regiões zoogeográficas. Embora sejam considerados zoonóticos, são várias as espécies associadas à transmissão ao Homem de importantes agentes etiológicos, responsáveis pelo aparecimento de diversas doenças infecciosas. Julgamos por isso oportuno, contribuir desta forma para uma revisão dos aspectos relevantes, relacionados com a caracterização destes artrópodes, como vectores de agentes infecciosos em Portugal, abordando aspectos biológicos, ecológicos e epidemiológicos com interesse em Saúde Pública.

Palavras-Chave – Ixodídeos; Agentes transmitidos por ixodídeos; Saúde Pública; Portugal

SUMMARY**TICKS ASSOCIATED TO INFECTIOUS PATHOLOGIES IN PORTUGAL**

Ticks are hematophagous arthropods that parasitize terrestrial vertebrates. They are world wide, living in almost all terrestrial regions. Although mainly associated to animals, there are several tick species that bite humans and transmit tick-borne agents causing important infectious disease. In this paper the authors revise the most outstanding aspects of those arthropods as vectors of infectious pathogens in Portugal, focusing biologic, ecologic and epidemiologic features with Public Health interest.

Key-Words – Ticks; Tick-borne pathogens; Public Health; Portugal

INTRODUÇÃO

Os ixodódeos, vulgarmente designados por carraças, são artrópodes ectoparasitas hematófagos estritos. Existem em quase todas as regiões zoogeográficas, parasitando uma ampla variedade de hospedeiros como mamíferos, aves, répteis e anfíbios. São conhecidas aproximadamente 850 espécies distribuídas por três famílias: Nuttalliellidae, Argasidae e Ixodidae. *Nuttalliella namaqua*, é o único representante da família Nuttalliellidae. É uma espécie rara, apenas conhecida na África do Sul, que possui características intermédias entre os elementos das outras famílias e cujo papel na transmissão de agentes infecciosos é desconhecido^{1,2}. Na família Argasidae são conhecidas cerca de 170 espécies que, pela ausência de escudo dorsal, são designadas argasídeos ou “carraças de corpo mole”. Da família Ixodidae fazem parte cerca de 650 espécies de ixodódeos, vulgarmente designados por “carraças de corpo duro” pela presença de escudo dorsal. Nestas duas últimas famílias, cerca de 10% das espécies conhecidas estão associadas à transmissão ao Homem e a outros vertebrados, de agentes patogénicos responsáveis por várias doenças infecciosas como rickettsioses, borreliososes, ehrlichioses, tularémia, arboviroses, babesioses, entre outras patologias¹. Contudo, é a família Ixodidae a que se reveste de maior importância médica pelo número de espécies implicadas na transmissão de agentes patogénicos, facto que nos levou a considerar uma revisão sobre este tema.

Ixodódeos

O ciclo biológico dos ixodódeos compreende quatro fases evolutivas: uma fase inactiva - ovo e três fases activas - larva, ninfa e adulto (macho ou fêmea) (Figura 1). Durante as fases activas, os ixodódeos alternam entre períodos de intensa actividade (procura de hospedeiro e alimentação) e períodos não activos (metamorfose e diapausa), necessitando sempre de uma refeição de sangue para passarem ao estado evolutivo seguinte. Ao notável sucesso destes artrópodes, como vectores potenciais de agentes patogénicos, são associadas características biológicas singulares^{2,3} (Quadro I), que os colocam, imediatamente a seguir aos mosquitos, como os artrópodes vectores de maior importância em Saúde Pública^{1,2}.

Vectores mecânicos / Vectores biológicos

Na transmissão efectiva do agente infeccioso os ixodódeos podem actuar quer como vectores mecânicos, quer como vectores biológicos⁴. No primeiro caso, a sobrevivência do agente depende da sua capacidade para suportar as condições do tracto digestivo do artrópode, até ser transmitido ao hospedeiro vertebrado. O agente patogénico não se multipli-



Fig 1 - Fases evolutivas do ciclo de vida dos ixodódeos.
Legenda: 1-ovo; 2-larva; 3-ninfa; 4-macho; 5-fêmea.

Quadro I - Características biológicas mais importantes dos ixodódeos (adaptado de Sonenshine, 1991)

IXODÓDEOS	Hematofagia obrigatória (larvas, ninfas e adultos)
	Apresentam ciclos de vida mono, di e trifásicos, consoante necessitam de se alimentar em um, dois ou três hospedeiros vertebrados ^a
	A alimentação é um processo geralmente lento o que propicia um alargado período de interacção com o hospedeiro
	Todas as fases de desenvolvimento ingerem grandes volumes de sangue
	Digestão gradual e intracelular, que ocorre sem a presença de enzimas no lúmen intestinal
	Existência de transmissão transtadial ^b ou transmissão horizontal
	Existência de transmissão transovárica ^c ou transmissão vertical
	Existência de um sistema sensorial desenvolvido ^d
	Diapausa ^e
	Grande longevidade e elevadas taxas de prolificidade
Distribuição por quase todos os habitats terrestres e reduzido número de predadores naturais	

^a No caso do ciclo monofásico todas as fases de desenvolvimento do artrópode alimentam-se no mesmo hospedeiro, ao contrário do ciclo difásico, em que apenas as fases imaturas partilham o mesmo hospedeiro. Contudo, mais de 90% das espécies apresentam ciclos trifásicos (em que cada fase de desenvolvimento se alimenta num hospedeiro diferente), o que aumenta a probabilidade de serem infectadas e a capacidade de transmitir a infecção.

^b As metamorfoses não envolvem a degeneração e regeneração total de cada órgão, pelo que, os microorganismos sobrevivem à muda de fase evolutiva, processo denominado por transmissão transtadial ou transmissão horizontal.

^c Em algumas associações ixodódeo/agente infeccioso ocorre a invasão do sistema reprodutor, permitindo assim a transmissão da infecção à prole, processo denominado por transmissão transovárica. Neste caso os ixodódeos são considerados também, para além de vectores, reservatórios naturais do agente.

^d Um sistema sensorial bem desenvolvido permite aos ixodódeos detectar a presença de potenciais hospedeiros (quer pelas suas emissões de dióxido de carbono, ácido láctico, amoníaco e outros odores, como pelas vibrações que causam). Deste modo, podem ocupar posições estratégicas, em trilhos de passagem, que aumentam as probabilidades de sucesso no encontro com novos hospedeiros.

^e Adaptação que lhes permite a sobrevivência em ambientes desfavoráveis.

ca no vector e o artrópode apenas o transmite mecanicamente, de um hospedeiro vertebrado para outro. No caso em que o ixodódeo é vector biológico, o agente infeccioso invade o

CARRAÇAS ASSOCIADAS A PATOLOGIAS INFECCIOSAS EM PORTUGAL

corpo do artrópode, proliferando nos seus tecidos antes de ser transmitido a um outro hospedeiro vertebrado. Esta situação é a mais frequente, verificando-se para a maioria dos agentes associados a estes artrópodes^{4,5}.

Capacidade vectorial/Competência dos vectores

Para a avaliação da eficácia de um ixodídeo como vector existem dois parâmetros principais: a capacidade vectorial e a competência do vector. A capacidade vectorial é a habilidade que uma determinada espécie tem, no tempo e no espaço, para transmitir o agente patogénico. Factores como a dimensão da população dos artrópodes, a longevidade, o número de posturas e o próprio comportamento alimentar afectam a capacidade vectorial de uma determinada população. A competência de um vector é a capacidade intrínseca que um ixodídeo tem para manter a infecção e consequentemente transmitir biologicamente o agente infeccioso, durante a alimentação. A Organização Mundial de Saúde, em 1985, definiu “vector competente” como aquele que possui um limiar de infecção baixo, que apresenta um reduzido período de incubação extrínseca⁹) e uma elevada eficácia de transmissão⁶. Assim, para que um ixodídeo possa ser considerado um vector competente de determinado agente infeccioso é necessário que apresente evidências, não só da sua manutenção, mas também da capacidade de o transmitir a um hospedeiro susceptível.

Infecção/transmissão do agente infeccioso

A infecção de um ixodídeo com um agente infeccioso pode ocorrer através de vários processos, nomeadamente por: I. transmissão transtadial e/ou transovárica; II. alimentação num hospedeiro vertebrado infectado; III. *cofeeding*^{b)}.

De um modo geral, a transmissão do agente infeccioso a um hospedeiro vertebrado deve-se à picada de um ixodídeo infectado, com a consequente inoculação de secreções salivares contendo o agente. Porém, e dependendo da natureza do agente infeccioso, a transmissão também pode ocorrer, nas seguintes situações: I. Quando o ixodídeo se alimenta, estando as suas peças bucais contaminadas com sangue infectado, proveniente de um hospedeiro ao qual se fixou anteriormente, mas no qual não completou a refeição; II. Quando o ixodídeo infectado liberta fezes contaminadas, sobre a descontinuidade cutânea, resultante do acto alimentar ou quando ocorre o seu esmagamento sobre esse local; III. Quando o ixodídeo infectado é deglutido^{4,5}.

Embora os ixodídeos sejam zoofílicos, têm sido observadas, com alguma frequência, diferentes espécies a parasitar o Homem, e que têm sido implicadas na transmissão de diversos agentes patogénicos (Quadro II). Esta situação não é atribuída a uma tendência antropofílica, mas sim à oportunidade de contacto com o Homem, o qual se torna um hospedeiro accidental.

Agentes patogénicos	Doença	Distribuição geográfica	Principais vectores
Vírus			
Encefalite transmitida por carraça (TBE)	Meningoencefalite	Europa, Ásia	<i>Ixodes ricinus</i> , <i>I. persulcatus</i>
Febre hemorrágica Crimeia-Congo (CCHF)	Febre hemorrágica	Europa, Ásia, África	<i>Hyalomma marginatum marginatum</i> , <i>H. m. rufipes</i> , <i>Haemaphysalis</i> spp.
Febre da carraça do Colorado (CTF)	Doença febril sistémica	América do Norte	<i>Dermacentor andersoni</i>
Bactérias			
<i>Rickettsia</i>			
<i>Rickettsia rickettsii</i>	Febre exantemática das Montanhas Rochosas	América do Norte Central e do Sul	<i>Dermacentor</i> spp., <i>Amblyomma</i> spp., <i>Rhipicephalus</i> spp.
<i>R. conorii</i>	Febre botanosa ou escaro-nodular	Sub-região Mediterrânica Ásia e África	<i>Rhipicephalus</i> spp., <i>Haemaphysalis</i> spp., <i>Amblyomma</i> spp., <i>Hyalomma</i> spp.
<i>R. japonica</i>	Febre exantemática oriental	Japão	<i>Haemaphysalis</i> spp.
<i>R. africae</i>	Febre da carraça africana	África	<i>Amblyomma hebraeum</i>
<i>R. slovaca</i>	Tibola (Linfadenopatia causada pela picada da carraça)	Europa	<i>Dermacentor marginatus</i>
<i>R. helvetica</i>	Perimiocardite crónica	Europa	<i>Ixodes ricinus</i>
<i>Ehrlichia</i>			
<i>Ehrlichia chaffeensis</i>	Ehrlichiose monocítica humana	EUA	<i>Amblyomma americanum</i>
<i>Anaplasma phagocytophilum</i>	Ehrlichiose granulocítica humana (HGE)	EUA Europa	<i>Ixodes scapularis</i> <i>I. ricinus</i>
<i>Borrelia</i>			
<i>Borrelia burgdorferi</i> s.l.	Borreliose de Lyme	EUA Europa África Austrália	<i>Ixodes scapularis</i> , <i>I. pacificus</i> <i>I. ricinus</i> , <i>I. persulcatus</i> <i>I. persulcatus</i> <i>I. holocyclus</i>
Outras bactérias			
<i>Francisella tularensis</i>	Tuarémia	Europa, Ásia, África, América do Norte	<i>Haemaphysalis leporipalustris</i> , <i>Dermacentor marginatus</i> , <i>D. variabilis</i> , <i>D. andersoni</i> , <i>D. americanum</i> <i>Rhipicephalus</i> spp.
<i>Coxiella burnetii</i>	Febre Q	Europa, Ásia, África, América do Norte	
Protozoários			
<i>Babesia</i>			
<i>Babesia microti</i>	Babesiose humana	EUA	<i>I. scapularis</i>
<i>B. divergens</i>	Babesiose humana	Europa	<i>I. ricinus</i>

Os agentes patogénicos podem ser encontrados em focos naturais, que envolvem diversas espécies roedores e outros mamíferos silváticos. A infecção humana resulta do contacto do Homem com esses ambientes, através de actividades relacionadas com a profissão (agricultura, pastorícia, etc.) ou de lazer (campismo, caça, passeios pedestres, etc.). Contudo, alguns agentes podem ainda estabelecer focos secundários rurais ou urbanos (como é o caso das rickettsias), em que diversos mamíferos domésticos e roedores, que vivem na dependência humana, desempenham um papel importante. Neste caso, pode ocorrer infecção sem contacto do Homem com os focos naturais⁵.

No Homem, a infecção resulta na maioria dos casos da picada do ixodídeo infectado. Considera-se no entanto, que é necessário existir um determinado período de fixação do artrópode para haver uma transmissão efectiva do agente infeccioso ao homem. Por exemplo, no caso de agentes rickettsiales pode ser de 6-20h⁷. Na maioria dos casos, qualquer uma das formas evolutivas dos ixodídeos é capaz de transmitir o agente infeccioso, sendo particularmente importantes as fases imaturas que, pelas suas reduzidas dimensões, são dificilmente detectadas. É, sobretudo, ao estado de ninfa que se deve grande parte das infecções no Homem. Para além da picada, também está descrita na literatura a infecção por contaminação de descontinuidades cutâneas ou de mucosas, quer com fluidos corporais dos artrópodes infectados, por exemplo quando se procede à desparasitação de animais, quer com as fezes dos ixodídeos (esta última situação ocorre concretamente com artrópodes infectados por *Coxiella sp.* ou *Francisella sp.*)³. Convém ainda referir que, para alguns agentes, a infecção humana não resulta exclusivamente do contacto com os ixodídeos. A infecção com o vírus TBE (Tick-borne encephalitis), pode ser adquirida pela ingestão de produtos derivados de animais infectados, nomeadamente leite⁸. Adicionalmente, *Coxiella sp.* e

Francisella sp. são espécies muito resistentes às condições ambientais, podendo contaminar os solos e reservas de água. Deste modo, a infecção humana pode resultar do contacto com estes ambientes e/ou com fluidos biológicos contaminados, provenientes da manipulação de animais infectados³.

Principais espécies ixodológicas com interesse médico

Portugal apresenta condições climáticas, ecológicas e ambientais favoráveis ao desenvolvimento de várias espécies ixodológicas. Actualmente, estão identificadas 21 espécies classificadas na família Ixodidae, das quais várias são reconhecidos vectores de agentes etiológicos causadores de doença no Homem (Quadro III). Pela importância que alguns destes *taxa* representam, em termos de Saúde Pública, realçaremos algumas das espécies de ixodídeos que apresentam um papel, real ou potencial, na transmissão de agentes infecciosos ao Homem (Quadro IV, Figura 2).

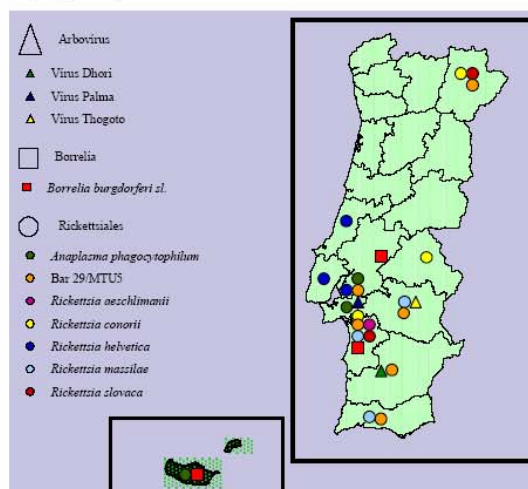


Fig. 2 – Localização dos microrganismos isolados /detectados em ixodídeos

Quadro III - Sistemática das espécies de Ixodidae existentes em Portugal e seus hospedeiros preferenciais.

Família Ixodidae				
Género				
<i>Rhipicephalus</i>	<i>Ixodes</i>	<i>Dermacentor</i>	<i>Hyalomma</i>	<i>Haemaphysalis</i>
Espécie / Hospedeiro preferencial				
<i>R. sanguineus</i> / Canídeos domésticos	<i>I. ricinus</i> / Mamíferos silváticos	<i>D. marginatus</i> / Bovinos		
<i>R. turanicus</i> / Ovinos	<i>I. hexagonus</i> / Mamíferos silváticos	<i>D. reticulatus</i> ¹ / Canídeos domésticos e silváticos	<i>H. lusitanicum</i> / Bovinos	<i>H. punctata</i> / Mamíferos domésticos e silváticos
<i>R. pusillus</i> / Pequenos mamíferos silváticos	<i>I. vespertilionis</i> / Quirópteros		<i>H. marginatum</i> / Bovinos	<i>H. inermis</i> / Mamíferos silváticos
<i>R. bursa</i> / Caprinos	<i>I. ventrali</i> / Pequenos mamíferos silváticos			<i>H. hispanica</i> / Pequenos mamíferos silváticos
<i>R. annulatus</i> ² / Bovinos	<i>I. bivariv</i> / Pequenos mamíferos silváticos			
	<i>I. canisuga</i> / Mamíferos silváticos			
	<i>I. simplex</i> / Quirópteros			
	<i>I. acuminatus</i> / Pequenos mamíferos silváticos			
	<i>I. frontalis</i> / Aves silváticas			

¹ Espécie também denominada por *Boophilus annulatus*; ² Espécie anteriormente denominada por *Dermacentor pictus*

CARRAÇAS ASSOCIADAS A PATOLOGIAS INFECCIOSAS EM PORTUGAL

Quadro IV – Microrganismos detectados/ isolados de ixodídeos em Portugal.

Espécie ixodológica (Vector/Reservatório)	Agente Etiológico	Patologia associada	Patogenia em Portugal	Assinalado em Portugal
<i>Dermacentor marginatus</i>	<i>Rickettsia slovaca</i>	Tibola	Desconhecida	Bacellar <i>et al</i> , 1995
	<i>Borrelia burgdorferi</i> sl	Borreliose de Lyme	Conhecida	Baptista <i>et al</i> , 2004
<i>Haemaphysalis punctata</i>	Vírus Palma	–	Desconhecida	Filipe <i>et al</i> , 1994
	<i>Rickettsia aeschlimanii</i>	–	Desconhecida	Bacellar <i>et al</i> , 1999
<i>Hyalomma marginatum</i>	Vírus Dhori	–	Desconhecida	Filipe & Casals, 1979
	<i>Borrelia burgdorferi</i> sl	Borreliose de Lyme	Conhecida	Baptista <i>et al</i> , 2004
<i>Ixodes ricinus</i>	<i>Anaplasma phagocytophilum</i>	Ehrlichiose granulocítica humana	Desconhecida	Santos <i>et al</i> , 2004a
	<i>Borrelia burgdorferi</i> sl	Borreliose de Lyme	Conhecida	Núncio <i>et al</i> , 1993
	<i>Rickettsia helvetica</i>	Perimiocardite crónica	Desconhecida	Bacellar <i>et al</i> , 1999
<i>Ixodes ventralis</i>	<i>Anaplasma phagocytophilum</i>	Ehrlichiose granulocítica humana	Desconhecida	Santos <i>et al</i> , 2004a
	<i>Rickettsia helvetica</i>	Perimiocardite crónica	Desconhecida	Bacellar <i>et al</i> , 1999
<i>Rhipicephalus sanguineus</i>	<i>Rickettsia conorii</i>	Febre botonosa ou escaro-nodular	Conhecida	Bacellar <i>et al</i> , 1995
	<i>R. massiliae</i>	–	Desconhecida	Bacellar <i>et al</i> , 1995
	Vírus Thogoto	–	Desconhecida	Filipe & Calisher, 1984
<i>Rhipicephalus turanicus</i>	<i>Rickettsia massiliae</i>	–	Desconhecida	Bacellar <i>et al</i> , 1995
	Bar 29/MTU5	–	Desconhecida	Bacellar <i>et al</i> , 1995

Género *Rhipicephalus*

Neste género encontra-se classificada uma das espécies de maior importância no nosso País, *Rhipicephalus sanguineus*. Esta é uma espécie que existe em quase todas as regiões do mundo, com a excepção das zonas circumpolares. Este ixodídeo encontra-se distribuído de Norte a Sul do País estando, do ponto de vista ecológico, adaptado a uma grande variedade de climas e hospedeiros vertebrados. Parasita numerosos animais silváticos e todas as espécies de animais domésticos, estando particularmente associada ao cão doméstico - *Canis familiaris*^{9,10}. Do ponto de vista biológico, *R. sanguineus* tem uma evolução do tipo trifásico^e) e ditrópico^d), sendo as formas adultas exofílicas^e) e as imaturas endofílicas, evoluindo habitualmente nos locais onde os hospedeiros se refugiam.

Porém, no caso em que as populações de ixodídeos vivem em estrita dependência do seu hospedeiro preferencial (o cão doméstico), o ciclo alimentar manifesta-se essencialmente de forma monotrópica e endofílica, alojando-se tanto as formas imaturas com os adultos nos canis ou dentro das próprias habitações do Homem. As maiores densidades populacionais foram encontradas nos meses mais quentes (Julho e Agosto), pelo que, esta espécie, está melhor adaptada a temperaturas altas, não sendo exigente quanto a humidade relativa, sobrevivendo com facilidade em climas secos. As formas adultas são encontradas em quase todos os meses do ano, com um incremento na altura de Primavera/Verão, resultante de uma maior actividade e abundância do vector. A maior actividade das formas imaturas está sobretudo concentrada nos meses de verão. Quando as condições ambientais (temperatura,

humidade relativa, fotoperíodo) são favoráveis esta espécie pode completar anualmente 2 ou 3 ciclos de vida, com posturas na ordem dos 5000 ovos.

A *R. sanguineus* cabe-lhe a transmissão de estirpes do complexo-*Rickettsia conorii*, agentes da febre botonosa ou escaro-nodular^{11,12} que, no nosso País, é a principal doença associada a ixodídeos. Classificada como uma doença de declaração obrigatória, apresenta uma taxa de incidência de $9.8/10^5$ habitantes sendo uma das mais elevadas face aos países da bacia do Mediterrâneo¹³. A febre botonosa apresenta um período de incubação de aproximadamente uma semana, muitas vezes assintomático, após o qual surge um quadro clínico de início súbito caracterizado por cefaleias, mialgias, artralgias e prostração acentuadas. Podem ainda ocorrer sintomas gastrointestinais, tais como vómitos e diarreia. Após uma semana, aparecem manchas na pele - o exantema maculo-papular, que atinge as palmas das mãos e as plantas dos pés, podendo poupar a face. No local da picada da carraça forma-se uma escara, lesão com crosta negra de 0,5–2 cm de diâmetro, com halo eritematoso. Contudo, pode ter um aspecto pustuloso ou ser apenas uma pápula eritematosa de pequeno diâmetro¹⁴.

De *R. sanguineus* foram ainda isoladas outras rickettsias, consideradas não patogénicas como *R. massiliae* (também isolada de *R. turanicus*) e um agente ainda sem nomenclatura oficial, Bar 29/MTU5^{11,16}. Este ixodídeo está também associado a *Coxiella burnetti* (agente etiológico da febre Q). Embora este último agente infeccioso circule em território nacional e já tenha sido por nós detectado em *Rhipicephalus spp.* (assim como em *Haemaphysalis spp.*) por técnicas de biologia molecular,

ainda não foi possível o seu isolamento. A febre Q é uma doença polimorfa, quando aguda pode apresentar-se como uma pneumonia ou um síndrome gripal ou pode tornar-se crónica e manifestar-se por endocardite, infecção valvular, osteomielite e hepatite crónica. Geralmente, *C. burnetti* é transmitida ao Homem por aerossóis de produtos animais infectados e não pela picada do artrópode, não estando excluída a hipótese das suas fezes manterem o agente viável e ser uma fonte de infecção.

A partir de *R. sanguineus* foi também possível o isolamento de agentes virais nomeadamente o vírus Thogoto¹⁵, cuja responsabilidade na patologia de doenças infecciosas ainda não está esclarecida (Quadro IV).

Género *Ixodes*

No género *Ixodes*, é a espécie *Ixodes ricinus* que se reveste de maior importância médica. Este ixodídeo apresenta uma grande área de expansão, ocupando toda a Europa, bem como a África Mediterrânica e a Ásia Menor. Em Portugal, embora com uma distribuição desigual, pode ser encontrado de Norte a Sul, predominantemente nas regiões e/ou locais que apresentem uma cobertura vegetal considerável e onde se verifiquem elevados níveis de humidade relativa (acima de 90%). É uma espécie muito dependente do estado higrométrico do ar e da temperatura, cujo equilíbrio lhe é essencial. A insuficiência de cobertura vegetal e as temperaturas elevadas comprometem a vitalidade das formas evolutivas, levando-as a procurar refúgios apropriados à sua sobrevivência e a utilizar, frequentemente, mecanismos de defesa como a diapausa. Esta espécie apresenta uma excepcional capacidade de adaptação a diversos hospedeiros, parasitando tanto mamife-

ros domésticos como silváticos, aves e alguns lacertídeos, sendo também frequentemente detectada a parasitar o Homem^{9,10}. Do ponto de vista biológico é uma espécie de evolução trifásica, exofílica e politrópica. A sua actividade estende-se por todo o ano, porém com alguma sazonalidade. As formas adultas estão activas durante os períodos menos quentes do ano (Setembro/Março) interrompendo a actividade durante o período de Verão. Ao contrário, as formas imaturas têm maior actividade nos meses de Primavera/Verão (Abril/Junho), justificando a sazonalidade observada nas doenças associadas a este artrópode. Na Natureza *I. ricinus* apresenta um ciclo de vida anual, podendo estender-se até três anos, com posturas não superiores a 3000 ovos.

I. ricinus é o principal vector de *Borrelia burgdorferi* sl, agente etiológico da borreliose de Lyme. Esta patologia é considerada multissistémica e multifásica, com sintomatologia variável, podendo ser enquadrada segundo o predomínio das manifestações em: síndromas febris, sintomatologia predominantemente dermatológica, osteo-articular e neurológica, atingindo preferencialmente a pele, as articulações, o sistema nervoso e o coração. Numa fase precoce da doença, o diagnóstico clínico baseia-se na presença do *eritema migrans* (lesão dermatológica característica) que, quando presente, é suficiente para estabelecer o diagnóstico clínico. Até ao momento, a borreliose de Lyme é a única doença comprovadamente associada a *I. ricinus* no nosso país, porém, esta espécie poderá ter um papel relevante na transmissão de outros agentes infecciosos. Deste ixodídeo têm sido isoladas estirpes de *Rickettsia helvetica*^{11,16} agente que em outras regiões da Europa foi associado a periomocardite crónica e à morte

Quadro IV – *Microrganismos detectados/ isolados de ixodídeos em Portugal*

Espécie ixodológica (Vector/Reservatório)	Agente Etiológico	Patologia associada	Patogenia em Portugal	Assinalado em Portugal
<i>Dermacentor marginatus</i>	<i>Rickettsia slovaca</i>	Tibola	Desconhecida	Bacellar et al, 1995
	<i>Borrelia burgdorferi</i> sl	Borreliose de Lyme	Conhecida	Baptista et al, 2004
<i>Haemaphysalis punctata</i>	Vírus Palma	—	Desconhecida	Filipe et al, 1994
<i>Hyalomma marginatum</i>	<i>Rickettsia aeschlimanii</i>	—	Desconhecida	Bacellar et al, 1999
	Vírus Dhori	—	Desconhecida	Filipe & Casals, 1979
	<i>Borrelia burgdorferi</i> sl	Borreliose de Lyme	Conhecida	Baptista et al, 2004
<i>Ixodes ricinus</i>	<i>Anaplasma phagocytophilum</i>	Ehrlichiose granulocítica humana	Desconhecida	Santos et al, 2004a
	<i>Borrelia burgdorferi</i> sl.	Borreliose de Lyme	Conhecida	Núncio et al, 1993
	<i>Rickettsia helvetica</i>	Periomocardite crónica	Desconhecida	Bacellar et al, 1999
<i>Ixodes ventralis</i>	<i>Anaplasma phagocytophilum</i>	Ehrlichiose granulocítica humana	Desconhecida	Santos et al, 2004a
	<i>Rickettsia helvetica</i>	Periomocardite crónica	Desconhecida	Bacellar et al, 1999
<i>Rhipicephalus sanguineus</i>	<i>Rickettsia conorii</i>	Febre botonosa ou escaro-nodular	Conhecida	Bacellar et al, 1995
	<i>R. massiliae</i>	—	Desconhecida	Bacellar et al, 1995
	Vírus Thogoto	—	Desconhecida	Filipe & Calisher, 1984
<i>Rhipicephalus turanicus</i>	<i>Rickettsia massiliae</i>	—	Desconhecida	Bacellar et al, 1995
	Bar 29/MTU5	—	Desconhecida	Bacellar et al, 1995

de jovens adultos¹⁷.

Estudos recentes, revelaram ainda a presença nesta espécie de *Anaplasma phagocytophilum*^f (agente também detectado em *I. ventraloi*)¹⁹. Este agente é responsável por uma zoonose designada anaplasmose granulocítica humana (actual designação para ehrlichiose granulocítica humana), que ocorre principalmente nos Estados Unidos mas que também já foi assinalada em algumas regiões da Europa²⁰. Esta doença costuma cursar com quadros febris moderados, geralmente de prognóstico benigno, acompanhados de uma sintomatologia inespecífica como febre, arrepios, mal-estar geral, cefaleias e mialgias, entre outros, e alterações hematológicas como trombocitopenia, leucopénia e aumento dos valores das transaminases²¹. Convém ainda salientar o facto de *I. ricinus* estar associado à virose provocada pela actividade do vírus TBE que é sem dúvida a arbovirose mais importante que afecta o Homem na Europa²². A maioria das infecções por este vírus são assintomáticas, contudo podem evoluir para uma infecção do sistema nervoso central. Neste caso, a doença apresenta um curso bifásico, em que a primeira fase é caracterizada por febre, cefaleias, náuseas, vómitos e uma segunda fase com sinais e sintomas de meningite e meningoencefalite. Este ixodídeo está também implicado na transmissão de protozoários do género *Babesia*, que noutros países europeus tem sido implicado em casos de babesiose humana. Muito embora este agente ainda não tenha sido detectado no nosso país a sua presença em Espanha²³ deixa em aberto a possibilidade da sua ocorrência no território nacional.

Género *Dermacentor*

Neste género, *Dermacentor marginatus* é a espécie que mais se destaca, quer pela frequência com que é detectada, quer pelo variado número de hospedeiros que parasita, abrangendo, praticamente, todos os mamíferos domésticos, uma variada gama de animais silváticos e o Homem^{9,10}. Esta espécie encontra-se presente na Europa, Ásia Central e no Norte de África, estando em Portugal distribuída por todo o País.

Ocorre em regiões de clima temperado e seco, no entanto suporta com facilidade temperaturas mais elevadas, não sendo também muito exigente em humidade.

Do ponto de vista biológico, *D. marginatus* é uma espécie de ciclo trifásico e ditrópico, com as formas adultas exofílicas e as fases imaturas endofílicas. As formas adultas apresentam uma maior actividade na altura do Outono/Inverno e os estados imaturos de larva e ninfa na Primavera/Verão. No entanto, poder-se-ão encontrar todas as fases de desenvolvimento em qualquer época do

ano. Na Natureza esta espécie realiza um ciclo de vida por ano, com posturas que podem chegar até aos 7000 ovos.

Embora com menor relevância que as espécies anteriormente referidas *Dermacentor marginatus* também tem sido associada à parasitação do Homem. A partir desta espécie, foi isolada *Rickettsia slovaca*, agente que no nosso país apresentou uma elevada prevalência^{16,24}. *R. slovaca*, tida como uma rickettsia não patogénica, é hoje associada a uma nova patologia denominada TIBOLA (tick-borne lymphadenopathy ou linfadenopatia causada pela picada de carraça)²⁵. As manifestações clínicas são descritas como uma reacção no local da picada, geralmente localizada na cabeça, em pápula ou vesícula que evolui para uma lesão exsudativa, necrótica, formando-se uma crosta e alopecia, acompanhada de adenopatias cervicais e submaxilares. Um dos sintomas, febre baixa, pode persistir por meses e a alopecia por anos²⁵. Importa no entanto referir que até ao momento não foram descritos casos de TIBOLA em Portugal.

Género *Hyalomma*

Em Portugal é sem dúvida a espécie *Hyalomma marginatum* a que assume um papel preponderante dentro deste género. Esta espécie apresenta uma larga distribuição geográfica, sendo muito comum na Ásia, em algumas regiões de África e nos países da orla do mediterrâneo. Este ixodídeo ocorre de Norte a Sul do País e do ponto de vista biológico é considerado uma espécie de ciclo quer trifásico quer bifásico, endofílica ou exofílica, monotrópica ou ditrópica, consoante o tipo de hospedeiros que parasita. As fases adultas são encontradas, frequentemente, a parasitar animais domésticos, nomeadamente, bovinos^{9,10}. As formas imaturas, larvas e ninfas, têm sido encontradas a parasitar aves²⁶, podendo também ocorrer em pequenos animais silváticos como ouriços-caixeiros e coelhos^{9,10}. Em Portugal, o Homem também surge como hospedeiro desta espécie, sendo este trabalho o primeiro registo desta ocorrência. Em termos climáticos esta espécie está adaptada a climas quentes e secos, não sendo por isso muito exigente do ponto de vista higrométrico. O período de maior actividade das formas adultas é durante a Primavera–Verão, enquanto as formas imaturas de larvas e ninfas são encontradas, com maior facilidade, no final do Verão e durante o período do Outono–Inverno. Na Natureza, *H. marginatum* pode realizar mais de um ciclo de vida anual, com posturas na ordem dos 11.000 ovos.

H. marginatum está associado ao isolamento da *Rickettsia aeschlimanii*²⁷ cuja intervenção na patologia das doenças infecciosas ainda não está totalmente averiguada em Portugal. Em França, estão descritos al-

guns casos clínicos associados a esta rickettsia, acompanhados de febre, escara, exantema cutâneo e linfangite. Todos os casos ocorreram na Primavera e estão relacionados com a migração de aves que introduziram o vector infectado²⁸. Nesta espécie regista-se também o isolamento do vírus Dhori, cuja responsabilidade em patologias humanas não está ainda esclarecida²⁹. Em outros Países, nomeadamente na ex-União Soviética, Mauritânia, Senegal, Egipto e Grécia, *H. marginatum* está associado à transmissão de outros vírus, nomeadamente o vírus da febre hemorrágica Crimeia-Congo.

Género *Haemaphysalis*

Haemaphysalis punctata é a espécie que se destaca dentro deste género. Embora não haja registos, no país, da sua presença no Homem, foi já encontrada numa variada gama de animais domésticos, ocorrendo também em animais silváticos e em aves^{9,10}. A área de distribuição desta espécie, engloba toda a Europa e os países africanos da orla Mediterrânica, nomeadamente Egipto, Líbia, Tunísia, Argélia e Marrocos. Em Portugal encontra-se distribuída de Norte a Sul. Do ponto de vista biológico, *H. punctata* é uma espécie de ciclo trifásico, exofílica e politrópica. As formas adultas tem maior actividade no período de Outono-Inverno, ao contrário dos estados imaturos de larva e ninfa cujo período de maior actividade é a Primavera-Verão. Prefere zonas de clima temperado a frio, não sendo muito exigente nas condições de humidade relativa. Na Natureza esta espécie apresenta um ciclo de vida anual, com posturas na ordem dos 3000 ovos.

A partir de *H. punctata* foi possível isolar um agente serologicamente caracterizado como um novo vírus, pertencente ao grupo antigénico Bhanja, denominado por vírus Palma³⁰. Até ao momento, não está esclarecido qual o papel que este vírus pode desempenhar em Saúde Pública. Sabe-se, porém, que outras espécies de ixodídeos, nomeadamente, *D. marginatus* e *R. sanguineus* podem também permitir laboratorialmente a sobrevivência deste vírus³¹.

CONSIDERAÇÕES FINAIS

A integração dos estudos de sistemática e ecobiologia dos ixodídeos, a par da identificação de microrganismos patogénicos de que são vectores e reservatórios naturais, é a grande aposta que vem sendo desenvolvida há quase duas décadas pela equipa do Centro de Estudos de Vectores e Doenças infecciosas, Instituto Nacional de Saúde Dr. Ricardo Jorge. Estes esforços concertados são indispen-

sáveis para o desenvolvimento de programas de planeamento e controlo dos ixodídeos e das doenças por estes vectorizadas, possibilitando o delineamento de zonas de potencial risco para o Homem.

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FOOTNOTES

- a) Período que medeia a transmissão do agente infeccioso após a sua ingestão por meio da refeição sanguínea.
- b) Processo através do qual ixodídeos infectados e não infectados, se alimentam num determinado hospedeiro e em que a distância que os separa é inferior a um centímetro, o que os obriga a partilhar a mesma área alimentar.
- c) Cada fase evolutiva parasita um hospedeiro diferente.
- d) Um ciclo biológico ditrópico significa que as formas imaturas se alimentam-se num determinado tipo de hospedeiro, geralmente micromamíferos ou pequenos mamíferos silváticos, enquanto as formas adultas procuram hospedeiros de maior porte. No caso de ser monotrópico todas as fases evolutivas se alimentam-se no mesmo tipo de hospedeiro. Num ciclo politrópico todas as fases evolutivas têm uma grande capacidade de adaptação e podem-se alimentar-se em diversos hospedeiros.
- e) Refere-se à dispersão da espécie relativamente ao local onde eclodiram. Assim formas adultas exofílicas significa que os adultos se podem afastar do local em que eclodiram ao contrário das formas endofílicas.
- f) *Anaplasma phagocytophilum* é a actual designação para Ehrlichia phagocytophila, E. equi e agente da ehrlichiose granulocítica humana¹⁸.
- l) Espécie também denominada por Boophilus annulatus

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CARRAÇAS ASSOCIADAS A PATOLOGIAS INFECCIOSAS EM PORTUGAL

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APPENDIX 2. EHRLICHIOSE GRANULOCÍTICA HUMANA: CONCEITOS ACTUAIS

SANTOS AS, BACELLAR F, DAVID DE MORAIS J

REVISION ARTICLE

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Ehrlichiose Granulocítica Humana

Conceitos actuais

A. Santos¹, F. Bacellar¹, J. David de Moraes²

¹ Centro de Estudos de Vectores e Doenças Infecciosas, Instituto Nacional de Saúde Dr. Ricardo Jorge, Águas de Moura.

² Departamento de Ecologia, Universidade de Évora, Évora.

EHRlichiose HUMANA

A ehrlichiose é uma doença infecciosa tradicionalmente associada aos animais, que afecta diversos mamíferos domésticos e silváticos. É conhecida há mais meio século, desde a descrição da ehrlichiose canina em 1935¹ e da ehrlichiose bovina e ovina em 1936². Nas últimas décadas, esta doença tem merecido um interesse crescente em medicina humana, o que veio conduzir a intensas investigações nesta área até então considerada exclusivamente do âmbito veterinário.

Em termos etiológicos, a ehrlichiose é causada por bactérias Gram negativas intracelulares obrigatórias, que se desenvolvem no interior dos vacúolos fagossómicos de células eucariotas³. O ciclo de transmissão destes microrganismos inclui a infecção tanto de artrópodes vectores (essencialmente carraças) como de hospedeiros vertebrados. Nestes últimos, são infectadas predominantemente as células de origem hematopoiética, com excepção dos eritrócitos. Em termo taxonómicos, estes microrganismos foram reunidos num único grupo: o género *Ehrlichia* (pertencente à tribo Ehrlichia-eae, família Rickettsiaceae, ordem Rickettsiales). Estudos filogenéticos, com base em técnicas de biologia molecular, têm vindo a demonstrar a sua heterogeneidade e a proximidade de alguns dos seus membros com outros microrganismos. Assim, foi proposta a reclassificação de algumas ehrlichias no género *Neorickettsia* e no género *Anaplasma*, mantendo-se no género *Ehrlichia* apenas algumas das espécies originalmente descritas⁴ (vide Quadro I). Compreender-se-á, pois, que quando

estamos, na verdade, do ponto de vista etiológico, a utilizar um termo que inclui afinal ehrlichioses propriamente ditas mas também anaplasmoses humanas, designativo este que, em rigor, deveríamos utilizar, e que por certo terá tendência a impor-se no futuro.

Embora, o primeiro caso de ehrlichiose humana (febre de Sennetsu) tenha sido documentado no Japão, em 1954,⁵ a doença foi considerada de reduzida importância médica. Na verdade, esta ehrlichiose causada por *Neorickettsia (Ehrlichia) sennetsu* é pouco frequente e de gravidade moderada, não havendo registos de mortalidade associados, ocorrendo apenas em áreas limitadas do Extremo Oriente, raramente fora do Japão. Só nas últimas décadas do século XX, com a descoberta de outras ehrlichias associadas a patologias humanas de gravidade variável no Ocidente, é que foi radicalmente alterada a forma como a comunidade científica encarava a problemática da ehrlichiose humana.

Em 1986, foi diagnosticada pela primeira vez a ehrlichiose monocítica (ou monocitotrópica) humana (EMH), nos E.U.A.⁶ Esta doença foi associada a uma nova espécie, designada por *Ehrlichia chaffeensis*.^{7,8} Mais tarde, em 1994, foram descritos os primeiros casos de ehrlichiose granulocítica (ou granulocitotrópica) humana (EGH).⁹ Como a identidade exacta do agente envolvido nesta doença era desconhecida, foi adoptada a designação de "agente da EGH". Em 1996, foram descritos na Venezuela casos de infecção humana por um agente semelhante a *Ehrlichia canis* (agente etiológico da ehrlichiose monocítica canina).¹⁰ Mais recentemente, em 1999, também *Ehrlichia ewingii* (conhecido agente da ehrlichiose

granulocítica canina) foi implicada em casos de ehrlichiose humana nos E.U.A.¹¹ Actualmente, a EMH e a EGH são consideradas as ehrlichioses humanas mais importantes em Saúde Pública, não só pela sua alargada distribuição geográfica, mas também pela casuística que lhes está associada. Estas ehrlichioses ocorrem essencialmente nos Estados Unidos, havendo também registos da sua presença noutros pontos do globo. Na Europa, existem referências de infecção humana por um agente imunologicamente semelhante a *E. chaffeensis* em Portugal,¹² Espanha¹³ e Bélgica.¹⁴ Porém, estudos recentes apontam para que seja a EGH a ter um papel de relevo nos países europeus.

Com a presente revisão da EGH pretendemos alertar os clínicos para os principais aspectos epidemiológicos e clínicos, bem como para o diagnóstico e tratamento desta ehrlichiose, à semelhança do que já havia sido feito, por um de nós, para a EMH.¹⁵

EHRlichiose GRANULOCÍTICA HUMANA

ETIOLOGIA

Como já foi referido, a ehrlichiose granulocítica humana é causada por um agente que permaneceu, até há bem pouco tempo, sem nomenclatura oficial, tendo sido designado por agente da EGH. Nos anos seguintes ao seu isolamento, foram reunidos dados genéticos,^{16,17} antigénicos^{18,19} e biológicos que sugeriam a existência de uma estreita relação com *Ehrlichia phagocytophila* (agente da febre da carraça dos ruminantes) e *Ehrlichia equi* (agente da ehrlichiose granulocítica equina), defenden-

do-se que representariam diferentes estirpes de uma única espécie. Actualmente essa hipótese está confirmada, e além disso há evidências da proximidade genética entre estes microrganismos e os anaplasmas, o que levou a que fosse proposta a sua reclassificação no Género *Anaplasma*, como uma única espécie, com a designação de *Anaplasma phagocytophilum*²⁴ (vide Fig. 1).

EPIDEMIOLOGIA

Desde que foi descrita pela primeira vez no Minnesota e Wisconsin, em 1994, a EGH têm vindo a ser sucessivamente identificada em diversos estados americanos, apresentando actualmente uma vasta distribuição geográfica nos Estados Unidos. Ao contrário da EMH, que está confinada à região Sul e Sudoeste, esta ehrlichiose ocorre predominantemente na região Nordeste e Noroeste do País, apresentando nas áreas endémicas uma frequência semelhante à verificada para a borreliose de Lyme.²⁵ O principal ixodídeo vector é *Ixodes scapularis*, também implicado na transmissão de *Borrelia burgdorferi* (agente etiológico da borreliose de Lyme) e de *Babesia microti* (associada a casos de babesiose humana). O ciclo epidemiológico do agente envolve pequenos roedores e ruminantes silváticos, principalmente veados, que servem de hospedeiros vertebrados aos artrópodes vectores.^{23,24,25,26,27} Esta doença afecta um largo espectro de mamíferos, incluindo equídeos, ruminantes, canídeos e o Homem.^{28,29,30,31} A infecção humana está associada ao contacto com o ixodídeo vector. No entanto, a descrição de um caso de infecção perinatal³² e a associação da doença à manipulação de carne fresca de cervídeos³³ realça a

existência de vias alternativas de infecção.

O crescente interesse por este tema e o desenvolvimento de linhas de investigação a nível mundial revelaram evidências significativas de que EGH não está confinada apenas aos Estados Unidos, ocorrendo também noutros países, principalmente da Europa. O contacto com *A. phagocytophilum* (estirpe agente da EGH) foi detectado em estudos serológicos realizados no Reino Unido,³⁴ Suíça,³⁵ Noruega,³⁶ Suécia³⁷ e Espanha.³⁸ Estudos moleculares também identificaram a presença de ADN específico do agente em carraças *Ixodes ricinus* capturadas na Itália,³⁹ Suécia,⁴⁰ França,⁴¹ Eslovénia,⁴² Alemanha,⁴³ Holanda,⁴⁴ Suíça,⁴⁵ Portugal⁴⁶ e Espanha⁴⁷. Há também uma referência à detecção de ADN específico em ácaros *Neotrombicula autumnalis* em Espanha.⁴⁸ Estes dados sugerem que *A. phagocytophilum* apresenta uma larga distribuição geográfica na Europa, partilhando o mesmo biótopo que o agente da borreliose de Lyme e sendo transmitido pelo mesmo ixodídeo vector (*I. ricinus*). Embora a sua associação a patologias humanas seja, até à data, reduzida,^{34,40} julga-se provável que esta realidade possa estar subavaliada devido possivelmente à falta de sensibilização dos clínicos e à escassez de laboratórios com o diagnóstico específico.

CLÍNICA

O tempo médio de incubação da ehrlichiose humana cifra-se em cerca de oito dias.³⁹ Comparativamente com a ehrlichiose monocítica, a ehrlichiose granulocítica costuma cursar com quadros clínicos mais moderados (vide Quadro II). A sintoma-

tologia mais frequente da EGH inclui febre, arrepios, mal-estar geral, cefaleias e mialgias, podendo estas ser muito intensas. Cerca de metade dos doentes podem também apresentar anorexia, náuseas, vômitos, dores abdominais, diarreia, tosse e artralgias.³⁹ Em menos de 10% dos casos pode coexistir rash cutâneo.^{34,35} Embora raramente, o quadro clínico pode evoluir para rabdomiólise, miocardite, falência respiratória aguda, shock séptico, polineuropatia desmielinizante, meningite asséptica e meningoencefalite.^{34,35,36,38,45,47,48} Os casos mais graves e que requerem períodos mais prolongados de internamento hospitalar respeitam muitas vezes a indivíduos idosos, diabéticos, pacientes com doenças vasculares do colagénio, imunodeprimidos e casos de diagnóstico tardio de ehrlichiose.³⁹ Estão também referidas complicações importantes do quadro clínico em indivíduos a quem foi administrada terapêutica antibiótica prévia com co-trimoxazol, como aliás acontece nas rickettsioses em geral.³⁹ A mortalidade na EGH cifra-se entre 0,5 e 1%, enquanto na EMH costuma ser mais elevada: 2,7%.³⁹

DIAGNÓSTICO

A hipótese de ehrlichiose deverá ser posta face a quadros febris de origem incerta com:

- história de picada de ixodídeo e/ou exposição a ixodídeos em área endémica nas duas semanas prévias;
- existência de trombocitopenia e leucopenia;
- aumento dos valores das transaminases séricas.

Nestes casos os testes laboratoriais são imprescindíveis, visto ser virtualmente

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ORIGINAL ARTICLE

impossível o diagnóstico definitivo da EGH apenas com base em aspectos epidemiológicos e clínicos.⁶⁴ Os testes laboratoriais disponíveis são de dois tipos: directos, que visam a detecção do agente (exame microscópico, análise molecular e isolamento) ou indirectos, que detectam anticorpos produzidos na sequência da infecção (análises sero-imunológicas).⁶⁴

Como *A. phagocytophila* infecta células de origem mielocítica, apresentando um marcado tropismo por neutrófilos, sangue total com anti-coagulante (preferencialmente sem heparina) e aspirado medular (se clinicamente apropriado) são as amostras mais adequadas para a realização dos testes directos. Este material biológico deve ser obtido durante a fase aguda da doença, antes da instituição da terapêutica antibiótica. As amostras devem ser refrigeradas a 4°C, mantidas no recipiente de colheita para garantir condições de esterilidade (situação indispensável caso se pretenda fazer o isolamento do agente) e enviadas no frio para o laboratório (idealmente nas 24h subsequentes à colheita). As amostras de soro ou plasma dos doentes destinam-se apenas aos testes imunológicos. É importante salientar que 60% dos doentes com suspeita de ehrlichiose apresentam resultados serológicos negativos na fase aguda da doença, verificando-se que mais de 80% destes casos desenvolvem posteriormente níveis de anticorpos detectáveis.⁶⁵ O estudo da cinética dos anticorpos da EGH tem mostrado que o aparecimento de imunoglobulinas específicas ocorre durante a segunda semana de doença, verificando-se uma elevação dos títulos até às quatro a seis semanas, permanecendo elevados durante vários meses.^{64,65} É pois recomendável para os testes indirectos o envio de duas amostras de soro/plasma do doente: a primeira, o mais precocemente possível, seguida de uma segunda amostra colhida 4 a 8 semanas depois.⁶⁴

O exame microscópico é realizado por observação dos esfregaços de sangue periférico corados por Giemsa ou *Diff Quick* para pesquisa de agregados bacterianos intra-leucocitários (mórulas). No entanto, devido à leucopenia que frequentemente é observada durante a fase aguda da EGH e ao baixo nível de infecção celular é recomendável a realização de uma concentração leucocitária e a

Quadro 1 - Classificação actual e principais aspectos epidemiológicos dos agentes tradicionalmente associados a ehrlichioses

Agente etiológico	Doença	Vectores/Hospedeiros	Tropismo celular
Género Ehrlichia			
<i>E. canis</i>	Ehrlichiose monocítica canina	Íxodídeos/Canídeos	Leucócitos mononucleares
<i>E. chaffeensis</i>	Ehrlichiose monocítica humana	Íxodídeos/Cervídeos, canídeos e homem	Leucócitos mononucleares
<i>E. ewingii</i>	Ehrlichiose granulocítica canina	Íxodídeos/Canídeos e homem	Leucócitos polimorfonucleares
<i>E. muris</i>	Provoca esplenomegalia	Íxodídeos/Roedores	Leucócitos mononucleares
Género Anaplasma			
<i>A. phagocytophila</i> (<i>Ehrlichia phagocytophila</i>)	Febre da carraça dos ruminantes	Íxodídeos/Ruminantes	Leucócitos polimorfonucleares
<i>A. phagocytophila</i> (<i>Ehrlichia equi</i>)	Ehrlichiose granulocítica equina	Íxodídeos/Equídeos	Leucócitos polimorfonucleares
<i>A. phagocytophila</i> (agente da EGH)	Ehrlichiose granulocítica humana	Íxodídeos/Ruminantes, equídeos, canídeos e homem	Leucócitos polimorfonucleares
<i>A. bovis</i> (<i>Ehrlichia bovis</i>)	Ehrlichiose bovina	Íxodídeos/Ruminantes	Leucócitos mononucleares
<i>A. platys</i> (<i>Ehrlichia platys</i>)	Trombocitopenia cíclica infecciosa dos canídeos	Íxodídeos/Canídeos	Plaquetas
Género Neorickettsia			
<i>N. sennetsu</i> (<i>Ehrlichia sennetsu</i>)	Febre de Sennetsu	Tremátodos/Homem	Leucócitos mononucleares
<i>N. risticii</i> (<i>Ehrlichia risticii</i>)	Síndrome diarreico agudo dos equídeos	Tremátodos/Equídeos	Leucócitos mononucleares

observação de 800-1000 granulócitos por esfregaço.⁶⁴ Todavia, importará referir que, nos EUA, a detecção de mórulas na primeira semana, só ocorreu em cerca de 62% dos casos de EGH63 e que na Europa ela tem sido bastante mais rara.⁶⁴ Acrescenta-se ainda a possibilidade de ocorrerem falso positivos. A presença de granulações intra-leucocitárias (como granulações tóxicas ou corpos de Döhle) e a sobreposição de plaquetas ou partículas contaminantes poderão ser confundidas com mórulas de ehrlichia.⁶⁴ Assim, o exame microscópico não deverá por si só ser suficiente para confirmar o diagnóstico de EGH.

A análise molecular é uma alternativa. A reacção de polimerase em cadeia (PCR) é a técnica molecular de eleição para o diagnóstico da EGH. A sensibilidade desta técnica varia entre 67-87% e a especi-

ficidade é próxima dos 100%.⁶⁵ Existem diversos pares de oligonucleotídeos que podem ser usados na detecção das estirpes de *A. phagocytophila* por PCR. Na sua grande maioria amplificam segmentos do gene que codifica a sub-unidade 16S do ARN ribossomal ou a região do operão *groESL*.^{11,18}

O isolamento do agente é ainda outra técnica directa para confirmar o diagnóstico de EGH. A cultura de ehrlichias é correntemente realizada em células HL-60,⁶⁶ mas esta técnica só está disponível em laboratórios especializados. Demais, o crescimento das ehrlichias poderá levar vários dias ou até mais de duas semanas, tornando moroso o resultado da confirmação laboratorial.

Em termos práticos, é pois nas análises sero-imunológicas que muitas vezes assenta o diagnóstico definitivo de ehrl-

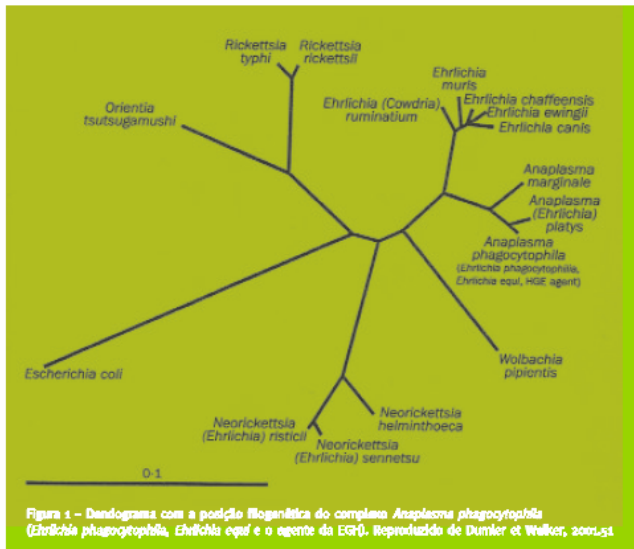


Figura 1 - Dendrograma com a posição filogenética do complexo *Anaplasma phagocytophilum* (*Ehrlichia phagocytophilum*, *Ehrlichia equi* e o agente da EGH). Reproduzido de Dumler et Walker, 2001.⁵¹

chiose. A pesquisa de imunoglobulinas das classes M e G por imunofluorescência indirecta (IFA) é a técnica aconselhada.⁶⁰ Devem ser usados como antígeno isolados de *A. phagocytophilum* (estirpes *E. phagocytophilum*, *E. equi* ou agente da EGH) e o limiar de positividade (diluição a partir da qual um soro deve ser considerado positivo) deve ser determinado por cada laboratório.⁶⁰ A sensibilidade da IFA nos casos de EGH confirmados por exame cultural é superior a 95%.⁶⁰ Outros testes serológicos como ELISA e imunoblot, com microrganismos purificados ou com proteínas recombinantes, estão a ser desenvolvidos e tudo indica que a curto prazo possam vir a ser aplicados correntemente no diagnóstico da EGH.^{60,61,62,70}

A confirmação laboratorial de um caso de EGH, com diagnóstico clínico compatível, é definida por: (i) seroconversão; (ii) alteração do título de anticorpos de pelo menos quatro vezes, relativamente ao título do soro inicial; (iii) detecção de mórulas no exame microscópico, associado a PCR positivo; (iv) isolamento do agente em cultura celular. Considera-se ainda como caso provável a detecção de mórulas intra-leucocitárias ou a presença de uma única amostra de soro com título superior ao limiar de positividade.^{60,62,71}

O Centro de Estudos de Vetores e Doenças Infecciosas (CEVDI) dispõe actualmente do teste de IFA para a detecção de infecções pelo agente EGH. Nesta análise é utilizado antígeno comercial (# IF 1402, Focus Technologies), bem como antígeno fornecido Prof. Stephen Dumler, da Divisão de Microbiologia Médica do Departamento de Patologia, Johns Hopkins Medical Institutions, EUA.

TRATAMENTO

Para além da terapêutica sintomática eventualmente necessária, o tratamento de escolha da ehrlichiose assenta na prescrição da doxiciclina. A dose habitualmente recomendada é de 100 mg, 2 vezes/dia, durante uma semana, ou mais três a cinco dias após a defervescência da febre. Todavia, em áreas endémicas de borreliose de Lyme, o tratamento deverá ser mantido, em princípio, durante duas a três semanas, dada a possibilidade de existência de infecção simultânea pelas duas zoonoses.^{61,72} Uma vez que o diagnóstico laboratorial poderá demorar algum tempo, frente a um caso de suspeita de ehrlichiose a terapêutica antibiótica apropriada deverá ser logo instituída.⁷³

In vitro, as ehrlichias mostraram-se também sensíveis à rifamicina e à rifampicina, sendo este último antibiótico

habitualmente preferido em grávidas infectadas.⁷⁴

As ehrlichias não evidenciaram sensibilidade às cefalosporinas, aminoglicosídeos, macrólidos e cloranfenicol,^{26,62} pelo que são questionáveis alguns pretensos bons resultados obtidos com tais antibióticos. Recorde-se que nos casos mais frustes de ehrlichiose a sintomatologia pode regredir espontaneamente sem qualquer terapêutica, além de poderem existir casos assintomáticos, como o atestam os inquéritos sero-epidemiológicos.

Como já antes dito, face a um diagnóstico presuntivo de ehrlichiose a terapêutica com co-trimoxazol deverá ser completamente banida.

COMENTÁRIO FINAL

No caso concreto de Portugal, a descoberta do agente da EGH em território nacional e a sua associação ao ixodídeo vector implicado na transmissão da *B. burgdorferi*⁴⁶ poderá ter amplas implicações em Saúde Pública.

A borreliose de Lyme só agora começou a merecer mais atenção por parte das entidades oficiais, sendo desde 1999 uma doença de declaração obrigatória.⁷⁵ Contudo, do universo de episódios febris supostamente relacionados com a borreliose de Lyme, apenas numa parte dos casos este diagnóstico é confirmado laboratorialmente.^{76,76} Assim, e à luz desta nova descoberta, é possível que algumas dessas situações "não conclusivas" sejam de facto resultantes da infecção humana por este novo agente. Deverá também ser considerada a possibilidade de infecções conjuntas do agente EGH e de *B. burgdorferi*, à semelhança do que se verifica noutros países onde estes dois agentes coexistem.^{77,78,79,80}

CORRESPONDÊNCIA

Ana Sofia Santos, Centro de Estudos de Vetores e Doenças Infecciosas, Instituto Nacional de Saúde Dr. Ricardo Jorge, 2965 Águas de Moura, Portugal. Telef. 265 912 222; Fax. 265 912 155; e-mail: ana.santos@insa.min-saude.pt

SUMÁRIO

A ehrlichiose humana representa um dos melhores exemplos de doenças infecciosas emergentes, com a ehrlichiose granulocítica humana (EGH) a merecer o papel de maior destaque na Europa. Esta doença é causada por um conhe-

ARTIGO ORIGINAL

ORIGINAL ARTICLE

cido agente de interesse veterinário *Anaplasma (Ehrlichia) phagocytophila*. Estudos recentes demonstraram que este agente ocorre em vários países europeus, designadamente Portugal, partilhando a mesma área geográfica do agente da borreliose de Lyme, e sendo transmitido pelo mesmo ixodídeo vector (*Ixodes ricinus*). Embora o número de casos de infecção humana por este agente seja até à data reduzido, os autores discutem o facto desta zoonose poder estar subavaliada devido possivelmente à falta de sensibilização dos clínicos e à escassez de laboratórios equipados para o diagnóstico específico. Este artigo aborda os principais aspectos epidemiológicos, clínicos, de diagnóstico e tratamento da EGH. Os autores pretendem também divulgar que o CEVDI tem à disposição técnicas serológicas para o diagnóstico laboratorial de EGH.

ABSTRACT

Human ehrlichiosis represent one of the best examples of newly emergent infectious diseases with human granulocytic ehrlichiosis (HGE) standing out as the most relevant in Europe. This disease is caused by a well-known veterinary pathogen *Anaplasma (Ehrlichia) phagocytophila*. Recent studies suggest that this agent may occur broadly across several European countries, including Portugal, within the same geographic range as the Lyme borreliosis agent and sharing the same vector tick (*Ixodes ricinus*). Although the number of human infection is few, the authors discuss the possibility that this zoonotic disease could be underestimated due to a lack of physician awareness and unavailability of current laboratory diagnosis. This article focuses on the epidemiology, clinical manifestations, diagnosis and treatment of HGE. The authors also point out that CEVDI has already available serologic tests for the diagnosis of HGE.

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Quadro II Principais aspectos epidemiológicos, clínico e laboratoriais distintivos das duas principais ehrlichioses humanas

	EGH	EMH
Agente etiológico	<i>Anaplasma phagocytophila</i>	<i>Ehrlichia chaffeensis</i>
Vector	<i>Ixodes</i> spp.	<i>Amblyomma americanum</i> <i>Dermacentor variabilis</i>
Principais hospedeiros	Homem, cervídeos, roedores, cavalos, cães	Homem, cervídeos, cães
Principal sintomatologia	Febre, mal-estar geral, cefaleias, mialgias	Idem, rash cutâneo, falência respiratória aguda, falência renal aguda, meningoencefalite
Mortalidade	0,5 a 1%	2,7%
Trofozoário celular	Neutrófilos	Monócitos/macrófagos
Presença de esférias	10 a 73%	0 a 1%
Cultura de células	HL60	DH82
Imunoblot	25, 40, 42, 44, 46, 65, 110 kD	22, 25, 27, 29, 44, 55, 66, 120 kD

Quadro adaptado de Bakken et Dumler, 2000 e Dumler et Walker, 2001.51,63

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