

1 **First detection and molecular identification of the zoonotic *Anaplasma capra* in**
2 **deer in France**

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4 Short title : *Anaplasma capra* in deer in France

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12

13 **Abstract**

14 Cervids are known to be reservoir of zoonotic tick-transmitted bacteria. The aim of this study was
15 to perform a survey in a wild fauna reserve to characterize *Anaplasma* species carried by captive red
16 deer and swamp deer. Blood from 59 red deer and 7 swamp deer was collected and analyzed over a
17 period of two years. A semi-nested PCR that targets the 23S rRNA was performed to detect and
18 characterise *Anaplasma* spp. and determine zoonotic species presence. *Anaplasma phagocytophilum*
19 was identified in 14/59 deer (23.7%) but not in swamp deer. Few sequences could not be assigned
20 to any particular species based on the 23S rRNA sequences. Nested PCR targeting *16S* rRNA, *gltA*
21 and *groEL* genes and sequencing analysis detected a recently reported zoonotic species, *Anaplasma*
22 *capra* in red deer as well as in swamp deer. This is the first reporting of the tick-borne zoonotic
23 bacterium *A. capra* in France, a species otherwise described only in China and Japan, in goats,
24 sheep, deer and japanese serows. Even if this bacterium may have been introduced in the Park with
25 infected imported animals, its local epidemiological cycle through tick transmission seems possible
26 as locally born deer were found infected. Diagnostic methods, especially molecular ones, should
27 take into account the potential infection of animals and humans with this species.

28

29 **Keywords :** *Anaplasma capra*, zoonotic tick-borne bacteria, red deer, swamp deer, 23S rRNA, 16S
30 rRNA, *groEL*, *gltA*

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34 **Introduction**

35 Bacteria of the genus *Anaplasma* are obligate intracellular parasites that replicate within the
36 vacuoles of diverse eukaryotic cells (monocytes, granulocytes, erythrocytes, endothelial cells).
37 These bacteria are mainly transmitted by ixodid ticks and multiply both in the invertebrate and
38 vertebrate hosts [1]. The genus *Anaplasma* includes 6 recognized species (*A. phagocytophilum*, *A.*
39 *bovis*, *A. centrale*, *A. marginale*, *A. ovis* and *A. platys*) responsible for anaplasmosis worldwide on a
40 large range of wild and domesticated vertebrates [1]. One species, *A. phagocytophilum*, described in
41 1994 in the USA as the agent of human granulocytic anaplasmosis (HGA), is now increasingly
42 detected worldwide [1]. In 2015, a second zoonotic and new species, proposed as *A. capra*, was
43 described in humans in China [2]. On a population of 477 patients with tick-bite history, six percent
44 (28 patients) were found infected with *A. capra* with non-specific febrile manifestations. Five of
45 them were hospitalized due to severe symptoms. General clinical features in human patients have
46 included febrile manifestations (fever, headache, malaise) as well as eschar, lymphadenopathy and
47 gastrointestinal symptoms [2].

48 Both *A. phagocytophilum* and *A. capra* infect diverse domestic (sheep and goats) and wild
49 ruminants (deer) species, which are considered as reservoirs. In a survey of tick-borne diseases in
50 captive and protected deer in France, we investigated the presence of *Anaplasma* species infecting
51 captive red deer (*Cervus elaphus*) and swamp deer (*Rucervus duvaucelii*). In the “Réserve de la
52 Haute Touche”, endangered species such as the swamp deer (CITES appendix I) are preserved. This
53 reserve is surrounded by a large forested and humid area, a biotope favorable to Ixodid ticks,
54 vectors of *A. phagocytophilum*.

55 **Methods**

56 *Animal sampling*

57 In 2015, a molecular survey of *Anaplasma* spp. infecting deer was started in the “Réserve de
58 la Haute Touche” Zoological Park, Indre, France (National Museum of Natural History). Blood

59 samples from 59 red deer and 7 swamp deer were collected between 2015 and 2017. They were
60 used for molecular detection and characterization of *Anaplasma* spp.. Blood was sampled at the
61 jugular vein at the occasion of animal care (treatments, vaccinations) or transfers (authorization 36-
62 145-002).

63 *Molecular detection and characterization of Anaplasma spp.*

64 Genomic DNA was extracted from blood according to previously described protocols [3]. We
65 detected *Anaplasmatatacae* by semi-nested PCR based on the 23S rRNA gene [4] and determined the
66 species by sequencing PCR positive amplicons. A new detected *Anaplasma* species was further
67 characterized using nested PCR and sequencing of the 16S rRNA, *gltA* and *groEL* genes (table 1).
68 Bidirectionnal sequencing was performed to ensure sequences, that were further analyzed by the
69 BLASTN (<http://www.ncbi.nlm.nih.gov/BLAST/>) and CLUSTAWL
70 (<https://www.ebi.ac.uk/Tools/msa/clustalo/>) programs.

71 **Results**

72 *Detection of Anaplasma spp. in deer blood*

73 Of the 66 heparine blood samples from red deer and swamp deer, 23S rRNA amplicons of the right
74 size were obtained for 28 samples. A BLASTn search of 23S rRNA sequences identified *A.*
75 *phagocytophilum* in 14 red deer (4/21 in 2015, 7/23 in 2016 and 3/15 in 2017) (prevalence of
76 23.7%) but not in swamp deer. Sequences (lengths between 430-476 bp) were more than 99.5%
77 identical (maximum two mismatches) to *A. phagocytophilum* strain HZ (GenBank accession
78 number NR_076399). Sequences from eleven amplicons (367 to 476 bp) were identical, with 99.8%
79 identities with *Ralstonia pickettii* (GenBank accession number CP001644). Three identical
80 sequences from two red deer and one swamp deer (3/66 - infection rate 4.5%) gave the highest
81 identities with “*Candidatus Anaplasma mediterraneum*” sequence (KY498330), described as a
82 potentially new *Anaplasma* species infecting sheep in Corsica [5] (table 2). Other genetic markers
83 often used to identify *Anaplasma* species were then tested to further characterize this *Anaplasma*
84 species never described in deer.

85 ***Further molecular characterization of the new Anaplasma spp. from deer in France***

86 Two *16S* rRNA identical sequences were obtained from red and swamp deer blood samples. They
87 had similarities of more than 99.6% with numerous *16S* rRNA *Anaplasma capra* sequences
88 deposited in GenBank. These sequences were obtained from sheep, goat, human blood and ticks
89 from China, as well as from cattle, sika deer, Japanese serows and ticks from Japan. Sequence
90 similarities with other known *Anaplasma 16S* rRNA sequences were lower than 99% (table 2).

91 As *Anaplasma capra groEL* and *gltA* sequences were also deposited in GenBank, we
92 amplified and sequenced these genes from our deer blood samples to better characterize this new
93 *Anaplasma*. The three *groEL* *Anaplasma* sequences from deer were identical and identity rates
94 ranged from 91.4 to 97.7% with the *A. capra groEL* sequences from China and Japan available in
95 GenBank (table 2). The similarities with *groEL* sequences from other related *Anaplasma* species (*A.*
96 *centrale*, *A. marginale*, *A. platys*, *A. phagocytophilum* and *A. ovis*) fell under 84%. The three *gltA*
97 *Anaplasma* sequences from deer differed by one nucleotide. The identity rates of the longest
98 sequence (729 bp) ranged from 87.9 to 98% with *A. capra gltA* sequences from Japan and China.
99 They were lower than 75% (61.4 to 74.6%) with *gltA* sequences from other *Anaplasma* species
100 (table 2). All these data confirmed the identity of the *Anaplasma* from French deer as belonging to
101 the *A. capra* species.

102 Partial sequences of the *16S* rRNA, *23S* rRNA, *groEL* and *gltA* from *A. capra* identified
103 from the swamp deer and one red deer were deposited in GenBank (accession numbers MH084717-
104 MH084724 with details in table 2).

105 ***Persistence of A. capra***

106 The persistence of deer infection by *A. capra* was analyzed by sampling blood from one of the two
107 infected red deer four months after the initial detection of this unexpected bacterial species. We
108 detected *A. capra*, with *23S* rRNA, *16S* rRNA, *groEL* and *gltA* sequences 100% identical to the first
109 identified *A. capra*, with the same distinct nucleotide in the *gltA* sequence as characterized 4 months
110 earlier.

111

112 **Discussion**

113 For about 40% of the positive conventional Anaplasmataceae spp. specific semi-nested
114 PCRs, sequences indicated amplification of *Ralstonia pickettii* 23S rRNA, highlighting a lack of
115 specificity of the semi-nested PCR used. As some of our negative controls were also positive, we
116 decided to sequence them and sequences corresponding also to *Ralstonia pickettii* were found. As
117 this bacteria is a frequent contaminant of all kind of solutions, including ultrapure water [6], our
118 results most probably correspond to *R. pickettii* contamination of the solutions we used for
119 extraction or PCR.

120 In this survey, we detected two *Anaplasma* species infecting deer. *A. phagocytophilum* was
121 detected with a rather moderate prevalence (23.7%) in red deer only. Prevalence of *A.*
122 *phagocytophilum* infection in wild red deer in Europe is highly variable, from 1.5% in Austria,
123 10.9% in Portugal, 40-75% in Italy, 80.8% in Spain, to 97.9 to 100% in central Europe (respectively
124 in Slovakia and Hungary) [7-13]. Captive deer are probably less prone to tick bites compared to
125 wild ones, due to grazing areas management. This result indicates anyway the contact of red deer
126 with ticks and the transmission of *A. phagocytophilum* in the Reserve. Swamp deer were found
127 uninfected with *A. phagocytophilum*, a result which could be attributed to the low number of
128 animals analyzed in the case of a low infection rate (7). There are no data about tick-transmitted
129 pathogens for this endangered species, so the susceptibility of swamp deer to *A. phagocytophilum* is
130 unknown. A recently described *Anaplasma* species, *A. capra* was detected and identified in both deer
131 species, with a much lower infection rate (4.5%). *A. capra* has already been detected in various
132 ruminant hosts (sheep, goats, cattle, sika deer, Japanese serows) but its localization was up to now
133 geographically restricted to China and Japan [14-17]. Human infection by this newly-described
134 species has been reported in northeast China, leading to patients hospitalisation [2]. The detection
135 and characterization of *A. capra* based on several molecular markers in our study represents the first
136 evidence of this potentially new zoonotic species in Europe (France) in two new hosts, red deer and

137 swamp deer. Species assignment to *A. capra* was based on *16S* rRNA homologies higher than 99%
138 [18].

139 The *23S* rRNA sequence from *A. capra* described in our study blasted with an unknown *Anaplasma*
140 species proposed as “*Candidatus Anaplasma mediterraneum*” from sheep in Corsica (France)[5].

141 Whether “*Candidatus Anaplasma mediterraneum*” corresponds in fact to *A. capra* could not be
142 determined, as the only other marker used in this study is *rpoB*, whereas we as most authors used a
143 combination of *16S* rRNA, *groEL*, *gltA* and *msp4* sequences to identify and characterize *Anaplasma*
144 *capra* [2, 15-17, 19-21].

145

146 We have detected *A. capra* in three different deer since 2015. The first infected and detected
147 red deer was a male originating from France (Theix) while the two others (red deer and swamp
148 deer) detected in 2017 and 2018 were both born inside the Park. Acquisition of a locally transmitted
149 *A. capra* is therefore probable for these two deer, even if *A. capra* may have been originally
150 introduced into the Park from an external source. The epidemiological cycle of *A. capra* seems
151 therefore to be completed locally. The low prevalence of infected deer in the Park might be due to
152 the introduction being recent. Ticks are the main vectors for *Anaplasma* species even if other
153 transmission routes have been described for some species (blood-sucking flies and transplacental
154 transmissions) [1]. Although *A. capra* has been detected in several tick species, *Ixodes persulcatus*
155 [2], *Rhipicephalus microplus* [19], *Haemaphysalis longicornis* [15,20] and *Haemaphysalis*
156 *qinghaiensis* [21], vectorial competence has not been proven yet. As most of these tick species are
157 not present in France, another tick species may be responsible for *A. capra* transmission in France.
158 The “Réserve de la Haute Touche” is located in a forested preserved area suitable for ticks and ticks
159 are commonly found feeding on the animals as well as questing on the vegetation (not shown).
160 Vector identification and vectorial competence remain to be elucidated.

161 In this study, we demonstrated the presence in France of the new species *A. capra* on two
162 new hosts. New studies are required, to examine its zoonotic ability, as non-zoonotic genetic

163 variants may exist as described in the case of *A. phagocytophilum* [1,3]. Diagnostic methods,
164 especially molecular ones, should take into account the potential infection of animals and humans
165 with this species, as molecular tools are often designed to specifically detect *A. phagocytophilum*.
166 To improve our knowledge on the epidemiological cycle of this bacterium in France, the vector tick
167 species should be identified, in order to evaluate the risks of transmission to humans. Deer could
168 therefore be considered as a potential reservoir for *A. capra*.

169

170 **Data Availability Statement**

171 Gene sequences are available in GenBank under accession numbers MH084717-MH084724.

172 **Competing interest**

173 All authors report no conflicts of interest relevant to this article. There was no external funding for
174 the study.

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181 **Author Contributions**

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185 **References**

- 186 1. Battilani M, De Arcangeli S, Balboni A, Dondi F. Genetic diversity and molecular epidemiology
187 of *Anaplasma*. Infect Genet Evol. 2017;49:195-211. doi: 10.1016/j.meegid.2017.01.021.
- 188 2. Li H, Zheng YC, Ma L, Jia N, Jiang BG, Jiang RR, et al. Human infection with a novel tick-borne
189 *Anaplasma* species in China: a surveillance study. Lancet Infect Dis. 2015;15:663-70. doi:
190 10.1016/S1473-3099(15)70051-4.
- 191 3. Jouglin M, Chagneau S, Faille F, Verheyden H, Bastian S, Malandrin L. Detecting and
192 characterizing mixed infections with genetic variants of *Anaplasma phagocytophilum* in roe deer
193 (*Capreolus capreolus*) by developing an *ankA* cluster-specific nested PCR. Parasit Vectors.
194 2017;10:377. doi: 10.1186/s13071-017-2316-0.
- 195 4. Dahmani M, Davoust B, Benterki MS, Fenollar F, Raoult D, Mediannikov O. Development of a
196 new PCR-based assay to detect Anaplasmataceae and the first report of *Anaplasma*
197 *phagocytophilum* and *Anaplasma platys* in cattle from Algeria. Comp Immunol Microbiol Infect
198 Dis. 2015;39:39-45. doi: 10.1016/j.cimid.2015.02.002.
- 199 5. Dahmani M, Davoust B, Tahir D, Raoult D, Fenollar F, Mediannikov O. Molecular investigation
200 and phylogeny of *Anaplasmataceae* species infecting domestic animals and ticks in Corsica, France.
201 Parasit Vectors. 2017;10:302. doi: 10.1186/s13071-017-2233-2.
- 202 6. Ryan MP, Pembroke JT, Adley CC. *Ralstonia pickettii*: a persistent gram-negative nosocomial
203 infectious organism. J Hosp Infect. 2006;62(3):278-84.
- 204 7. Cézanne R, Mrowietz N, Eigner B, Duscher GG, Glawischnig W, Fuehrer HP. Molecular analysis
205 of *Anaplasma phagocytophilum* and *Babesia divergens* in red deer (*Cervus elaphus*) in Western
206 Austria. Mol Cell Probes. 2017;31:55-58. doi: 10.1016/j.mcp.2016.07.003.

- 207 8. Pereira A, Parreira R, Nunes M, Casadinho A, Vieira ML, Campino L, Maia C. Molecular
208 detection of tick-borne bacteria and protozoa in cervids and wild boars from Portugal. *Parasit*
209 *Vectors*. 2016;9:251. doi: 10.1186/s13071-016-1535-0.
- 210 9. Ebani VV, Rocchigiani G, Bertelloni F, Nardoni S, Leoni A, Nicoloso S, Mancianti F. Molecular
211 survey on the presence of zoonotic arthropod-borne pathogens in wild red deer (*Cervus elaphus*).
212 *Comp Immunol Microbiol Infect Dis*. 2016;7:77-80. doi: 10.1016/j.cimid.2016.06.003.
- 213 10. Di Domenico M, Pascucci I, Curini V, Cocco A, Dall'Acqua F, Pompili C, Cammà C. Detection
214 of *Anaplasma phagocytophilum* genotypes that are potentially virulent for human in wild ruminants
215 and *Ixodes ricinus* in Central Italy. *Ticks Tick Borne Dis*. 2016;7:782-787. doi:
216 10.1016/j.ttbdis.2016.03.012.
- 217 11. García-Pérez AL, Oporto B, Espí A, del Cerro A, Barral M, Povedano I, Barandika JF, Hurtado
218 A. Anaplasmataceae in wild ungulates and carnivores in northern Spain. *Ticks Tick Borne Dis*.
219 2016;7(2):264-9. doi: 10.1016/j.ttbdis.2015.10.019.
- 220 12. Kazimírová M, Hamšíková Z, Špitalská E, Minichová L, Mahríková L, Caban R, et al. Diverse
221 tick-borne microorganisms identified in free-living ungulates in Slovakia. *Parasit Vectors*.
222 2018;11:495. doi: 10.1186/s13071-018-3068-1.
- 223 13. Hornok S, Sugár L, Fernández de Mera IG, de la Fuente J, Horváth G, Kovács T, et al. Tick- and
224 fly-borne bacteria in ungulates: the prevalence of *Anaplasma phagocytophilum*, haemoplasmas and
225 rickettsiae in water buffalo and deer species in Central Europe, Hungary. *BMC Vet Res*.
226 2018;14:98. doi: 10.1186/s12917-018-1403-6.
- 227 14. Inokuma H, Terada Y, Kamio T, Raoult D, Brouqui P. Analysis of the 16S rRNA gene sequence
228 of *Anaplasma centrale* and its phylogenetic relatedness to other *Ehrlichiae*. *Clin Diagn Lab*
229 *Immunol*. 2001;8:241-4.
- 230 15. Kawahara M, Rikihisa Y, Lin Q, Isogai E, Tahara K, Itagaki A, et al. Novel genetic variants of
231 *Anaplasma phagocytophilum*, *Anaplasma bovis*, *Anaplasma centrale*, and a novel *Ehrlichia* sp. in
232 wild deer and ticks on two major islands in Japan. *Appl Environ Microbiol*. 2006;72:1102-9.

- 233 16. Sato M, Nishizawa I, Fujihara M, Nishimura T, Matsubara K, Harasawa R. Phylogenetic
234 analysis of the 16S rRNA gene of *Anaplasma* species detected from Japanese serows (*Capricornis*
235 *crispus*). J Vet Med Sci. 2009;71:1677-9.
- 236 17. Yang J, Liu Z, Niu Q, Liu J, Han R, Guan G, Hassan MA, Liu G, Luo J, Yin H. A novel zoonotic
237 *Anaplasma* species is prevalent in small ruminants: potential public health implications. Parasit
238 Vectors. 2017;10:264. doi: 10.1186/s13071-017-2182-9.
- 239 18. Clarridge JE III. Impact of 16S rRNA gene sequence analysis for identification of bacteria on
240 clinical microbiology and infectious diseases. Clin Microbiol Rev. 2004;17:840-862.
- 241 19. Lu M, Tian JH, Yu B, Guo WP, Holmes EC, Zhang YZ. Extensive diversity of rickettsiales
242 bacteria in ticks from Wuhan, China. Ticks Tick Borne Dis. 2017;8:574-580. doi:
243 10.1016/j.ttbdis.2017.03.006.
- 244 20. Sun XF, Zhao L, Wen HL, Luo LM, Yu XJ. *Anaplasma* species in China. Lancet Infect Dis.
245 2015;15:1263-4. doi: 10.1016/S1473-3099(15)00377-1.
- 246 21. Yang J, Liu Z, Niu Q, Liu J, Han R, Liu G, et al. Molecular survey and characterization of a
247 novel *Anaplasma* species closely related to *Anaplasma capra* in ticks, northwestern China. Parasit
248 Vectors. 2016;9:603.
- 249

250 **Table 1**

251 Nucleotide sequence of primers used in the study

Target gene	Primer name	Sequence (5'-3')	Amplicon length	Reference
23S rRNA	Ana23S-212F	ATAAGCTGCGGGGAATTGTC	696 bp	[4]
	Ana23S-908R	TGGAGGACCGAACCTGTTAC		[4]
	Ana23S-212F	ATAAGCTGCGGGGAATTGTC	541 bp	[4]
	Ana23S-753R	GTGACAGCGTACCTTTTGCA		[4]
16S rRNA	Ana16Sup1	CGGGTGAGTAATGCATAGGA	1089 bp	This study
	Ana16Sdo3	TAGCACGTGTGTAGCCCAC		This study
	Ana16sIntup1	AACTCCGTGCCAGCAGCCGCG	581 bp	This study
	Ana16Sdo1	CCCAACATCTCACGACAC		This study
<i>gltA</i>	Outer-F	GCGATTTTAGAGTGYGGAGATTG	1077 bp	[2]
	Outer-R	TACAATACCGGAGTAAAAGTCAA		[2]
	Inner-F	GGGTTCTGTCC <u>ACT</u> GCTGCGTG	793 bp	[2]*
	Inner-R	TTGGATCGTA <u>ATT</u> CTTGTAGACC		[2]*
<i>groEL</i>	Ac-groEL-F1	GCGAGGCGTTAGACAAGTCCATT	1264 bp	[2]
	Ac-groEL-R3	TCCAGAGATGCGAGCGTGTATAG		[2]
	Ac-groEL-F2	TGCACTGCTGGTCCAAAGGGGCT	1087 bp	This study
	Ac-groEL-R2	CAACTTCGCTAGAGCCGCCAACC		This study

253 • Modified from [2]*, in accordance to GenBank accession number KM206274 sequence

254

255 **Table 2**

256

257 Sequence lengths and identity rates with *Anaplasma spp.* sequences

258

Gene	Sequence lengths	GenBank accession numbers	Reference organisms and sequences	Identity rate
23S rRNA	CEL15 - 367 bp CEL17 - 506 bp DVC 17 - 515 bp	MH084724 MH084723	<i>Cand. A. mediterraneum</i> KY498330 <i>A. ovis</i> KM021411 <i>A. centrale</i> NR-076686 <i>A. marginale</i> KY498332 <i>A. platys</i> KM021412 <i>A. phagocytophilum</i> KM021418	99.6 % 95.0% 94.6% 93.8% 91.6% 90.8%
16S rRNA	CEL17 - 531 bp DVC 17 - 518 bp	MH084721 MH084722	<i>A. capra</i> KM206273 - MF066917 <i>A. marginale</i> AF414874 <i>A. centrale</i> AF318944 <i>A. ovis</i> AJ633049 <i>A. phagocytophilum</i> NR-044762 <i>A. platys</i> AY077619	99.6% - 99.8% 98.7% 98.5% 98.3% 96.4% 96.2%
<i>groEL</i>	CEL15 - 559 bp CEL17 - 1008 bp DVC 17 - 1087 bp	MH084718 MH084717	<i>A. capra</i> KM206275 - AB454078 <i>A. marginale</i> AF414864 <i>A. centrale</i> EF520691 <i>A. ovis</i> AF441131 <i>A. platys</i> AY044161 <i>A. phagocytophilum</i> JF494833	91.4% - 97.7% 83.2% 83.2% 83.2% 77.5% 76.2%
<i>gltA</i>	CEL15 - 729 bp CEL17 - 707 bp DVC 17 - 725 bp	MH084720 MH084719	<i>A. capra</i> KM206274 - MG940872 <i>A. marginale</i> AF304139 <i>A. ovis</i> PKOE01000003 <i>A. centrale</i> CP001759 <i>A. phagocytophilum</i> AY464132 <i>A. platys</i> EU516387	87.9% - 98% 74.6% 74.2% 73.3% 65.4% 61.4%

259 CEL : *Cervus elaphus*

260 DVC : *Rucervus duvaucelii*

261