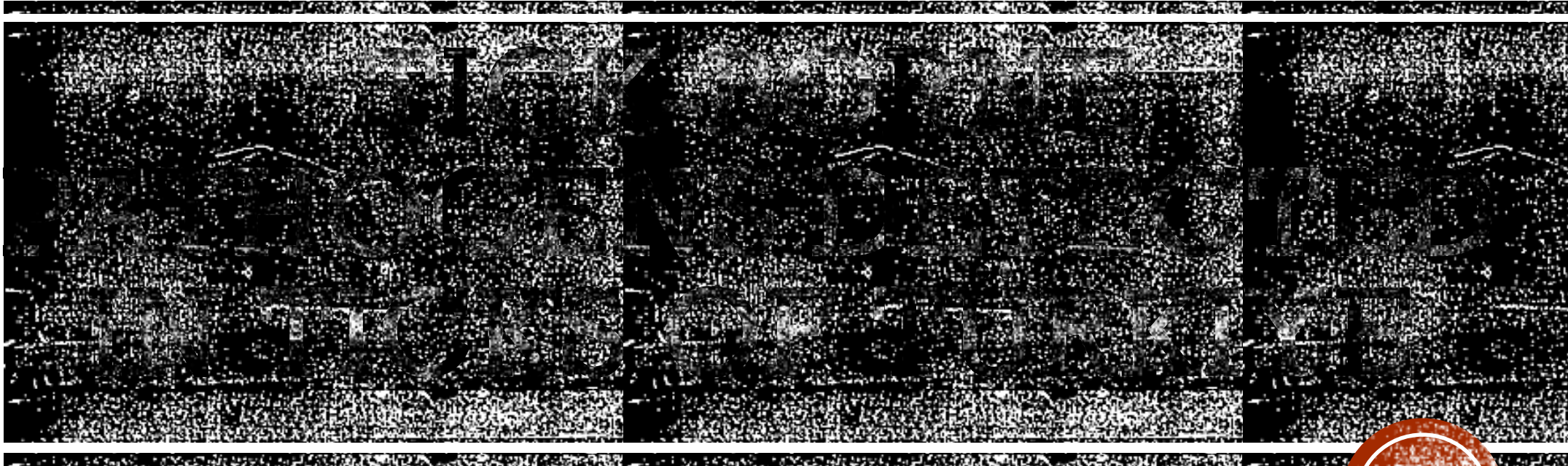


Ömer ORKUN

Ankara University Faculty of Vet. Med.,
Department of Parasitology

Ticks and Tick-Borne Diseases Lab.



Data SIO, NOAA, U.S. Navy, NGA, GEBCO
Image Landsat / Copernicus

Google Earth





- This study was conducted in the Sarıyar Anatolian wild sheep breeding area between 2014 and 2016.

Research paper

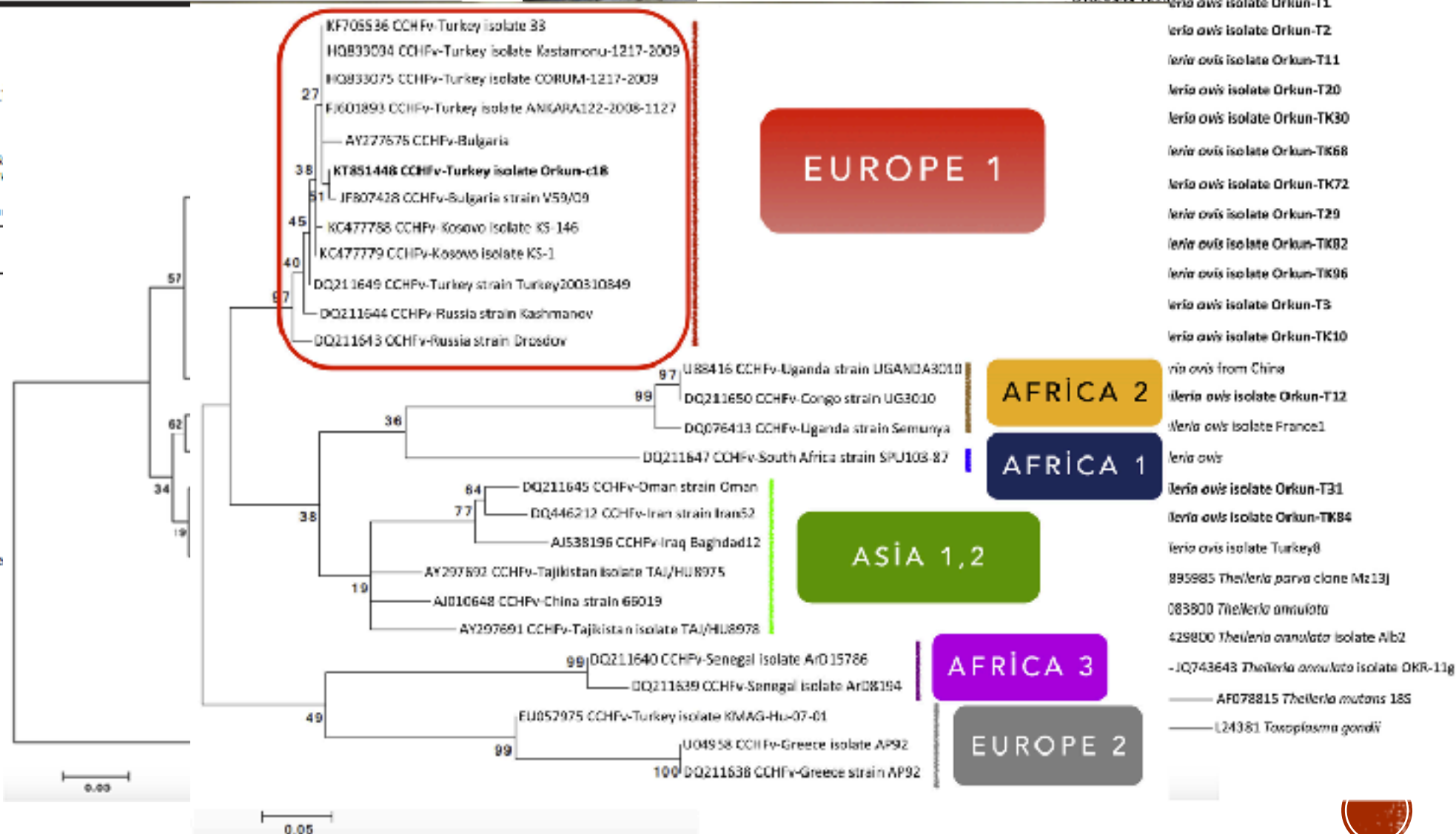
Ticks threatening lineage of Anatolian (*anatolica*) and determination of their tOmer Orkun^{a,*}, Hasan Emir^b, Zafer Karaer^a^a Department of Parasitology, Faculty of Veterinary Medicine, Ankara University, Ankara^b General Directorate of Nature Conservation and National Parks, Ministry of Forestry

Table 1

Tick species collected from different hosts in this study: PCR positivity, infection

Host	Tick Species	A/B/C/D
Anatolian Wild Sheep	<i>R. bursa</i> (adult)	9/41/268/1108
		7/41/268/1108
		8/41/268/1108
		1/41/268/1108
		3/37/137/1065
Hares	<i>R. coarctatus</i> (adult)	1/37/137/1065
		0/1/2/2
	<i>R. coarctatus</i> (nymph)	0/1/2/2
	<i>R. coarctatus</i> (nymph)	0/24/273/1002
	<i>R. coarctatus</i> (infected adult)	1/1/2/2/2/2/2
Guinea fowls	<i>R. coarctatus</i> (nymph)	0/5/42/42
	<i>R. coarctatus</i> (larvae)	0/3/17/17
Chickens	<i>R. coarctatus</i> (nymph)	0/1/1/1/1
	<i>R. coarctatus</i> (nymph)	0/1/8/8
Turkey	<i>R. coarctatus</i> (adult)	1/1/2/2/2/2
	<i>R. bursa</i> (adult)	1/1/2/2/2/2
Quagga rika (infected)	<i>R. coarctatus</i> (adult)	1/1/1/1
	<i>R. coarctatus</i> (adult)	1/1/1/1
Total	-	29/175/851/3404

A: number of positive pools; B: number of analyzed pools; C: number of analyzed positive pools.





Research paper

Crimean-Congo hemorrhagic fever virus tick surveillance study

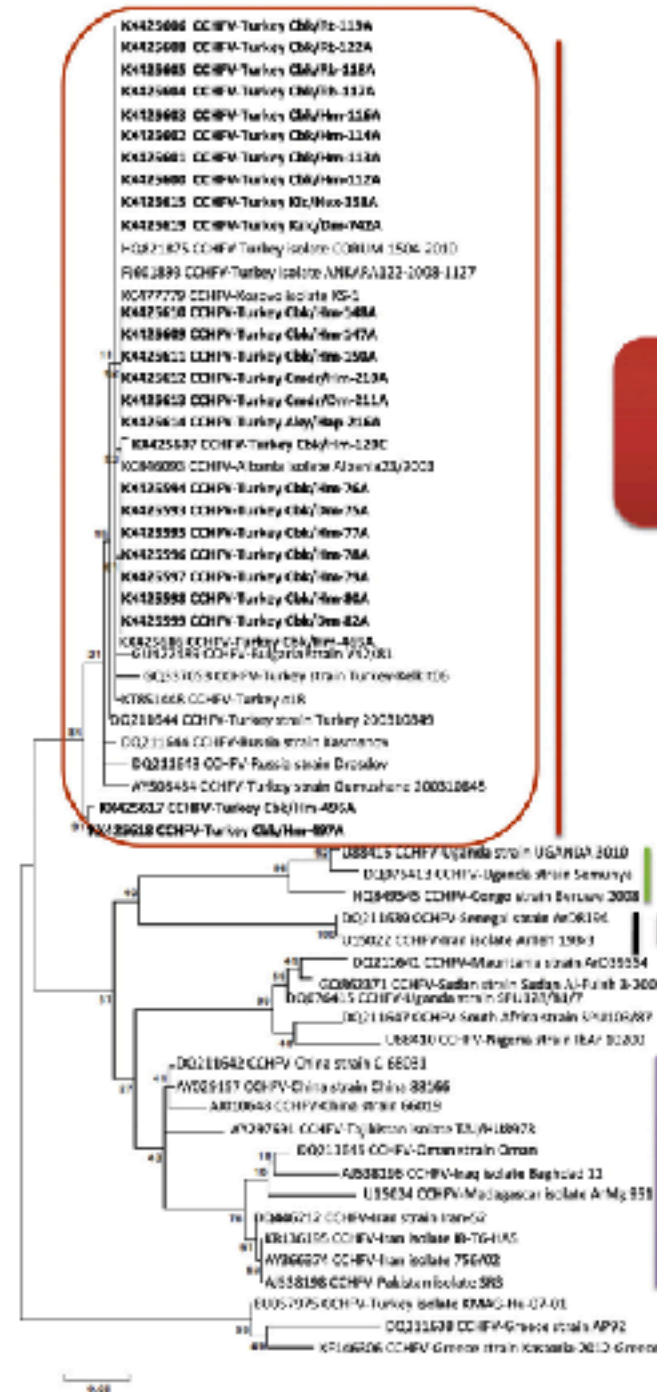
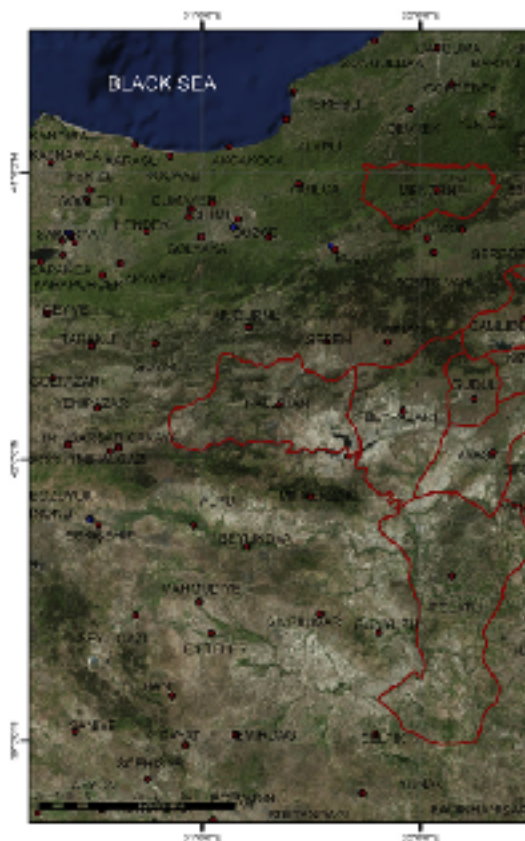
Ömer Orkun^a, Zafer Karaer, Ayşe Çakmak, Serpil N

Department of Parasitology, Faculty of Veterinary Medicine, Ankara University, Ankara, T

Table 3

CCCHV-positive tick species, their locations and GenBank accession numbers.

CCCHV-positive tick species	Locations (village/district)
<i>Hyalomma marginatum</i>	Ovacık/Çubuk Ovacık/Çubuk Ovacık/Çubuk Aydıncık/Çubuk Yeşilkent/Çubuk Yeşilkent/Çubuk Yeşilkent/Çubuk Yeşilkent/Çubuk Yeşilkent/Çubuk Karadana/Çubuk Karadana/Çubuk Karadana/Çubuk Karadana/Çubuk Kışlacık/Çubuk Kışlacık/Çubuk Kışlacık/Çubuk Akkuş/Çubuk Ruşn/Kalecik Yeşilkent/Çubuk Yeşilkent/Çubuk Aydıncık/Çubuk Uğurlu/Kızılcahamam
<i>Hyalomma excavatum</i>	Karayatak/Akyurt
<i>Dermacentor marginatus</i>	Karadana/Çubuk Karadana/Çubuk
<i>Haemaphysalis parva</i>	Karadana/Çubuk
<i>Rhipicephalus bursa</i>	Karadana/Çubuk
<i>Rhipicephalus turanicus</i>	Karadana/Çubuk

^a Crimean-Congo hemorrhagic fever virus isolate Burgas-tick10/2014 access^b Crimean-Congo hemorrhagic fever virus strain Turkey/Corum123-2011 ac^c Crimean-Congo hemorrhagic fever virus strain Turkey/Kastamonu27-2011^d Crimean-Congo hemorrhagic fever virus strain Corum1094-2011 accession

EUROPE 1

AFRICA 2

AFRICA 3

AFRICA 1

ASIA 1,2

EUROPE 2

Research paper

Molecular characterization of *Babesia* species in wild animals and their ticks in Turkey

Ömer Orkun^a, Zafer Karar^a

^aDepartment of Parasitology, Faculty of Veterinary Medicine, Ankara University, Ankara, Turkey



MF379311 *Rickettsia slovaca* isolate Ro-d10
KJ306733 *Rickettsia slovaca* isolate Ruqa01
MF379305 *Rickettsia slovaca* isolate Ro-715

Molecular identification of tick-borne bacteria in wild animals and their ticks in Central Anatolia, Turkey

Ömer Orkun^a, Ayşe Çakmak

^aDepartment of Parasitology, Faculty of Veterinary Medicine, Ankara University, Ankara, Turkey



Table 2

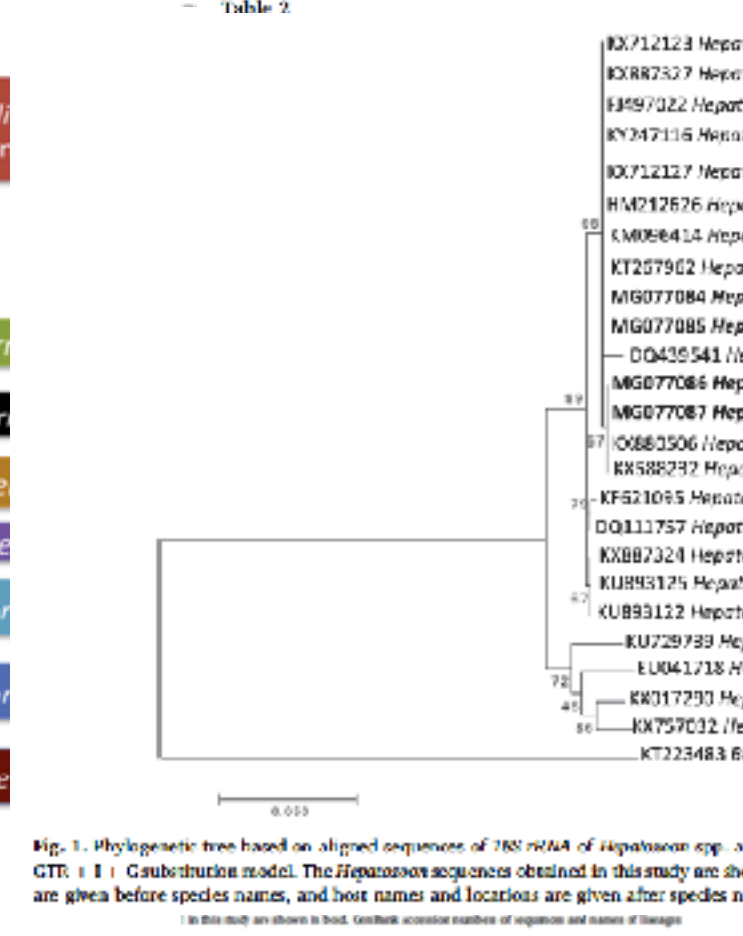
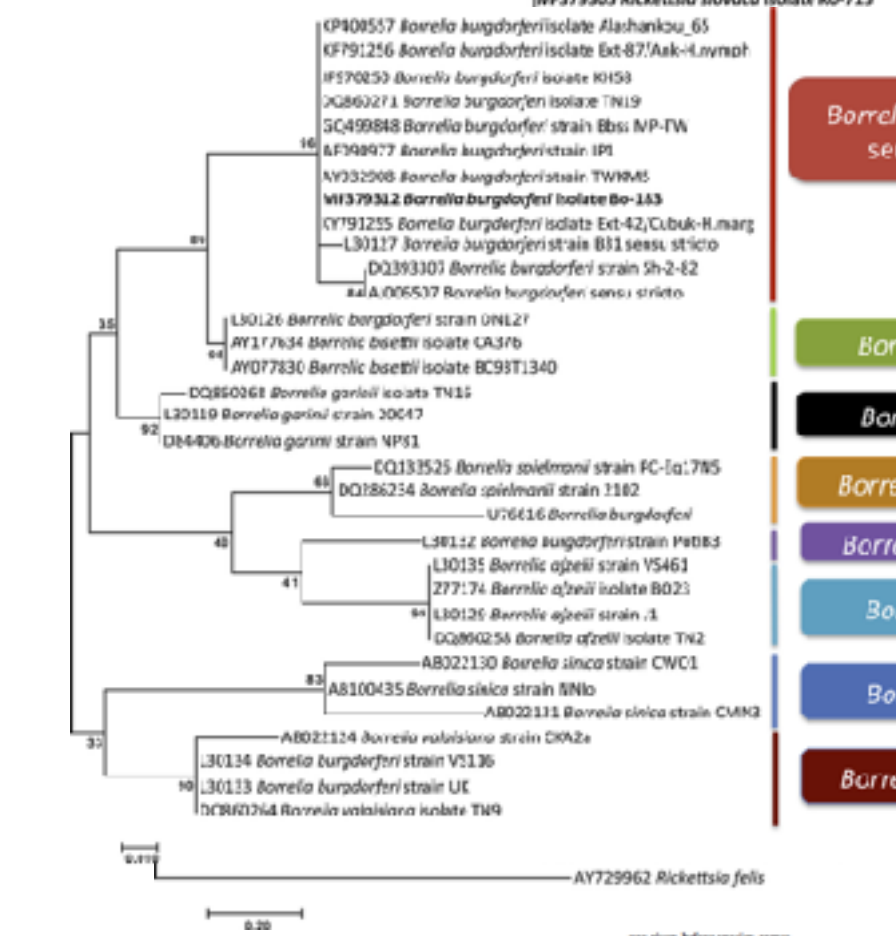
Short communication

Hepatozoon canis in Turkish red foxes and their ticks

Ömer Orkun^a, Serpil Nalbantoğlu

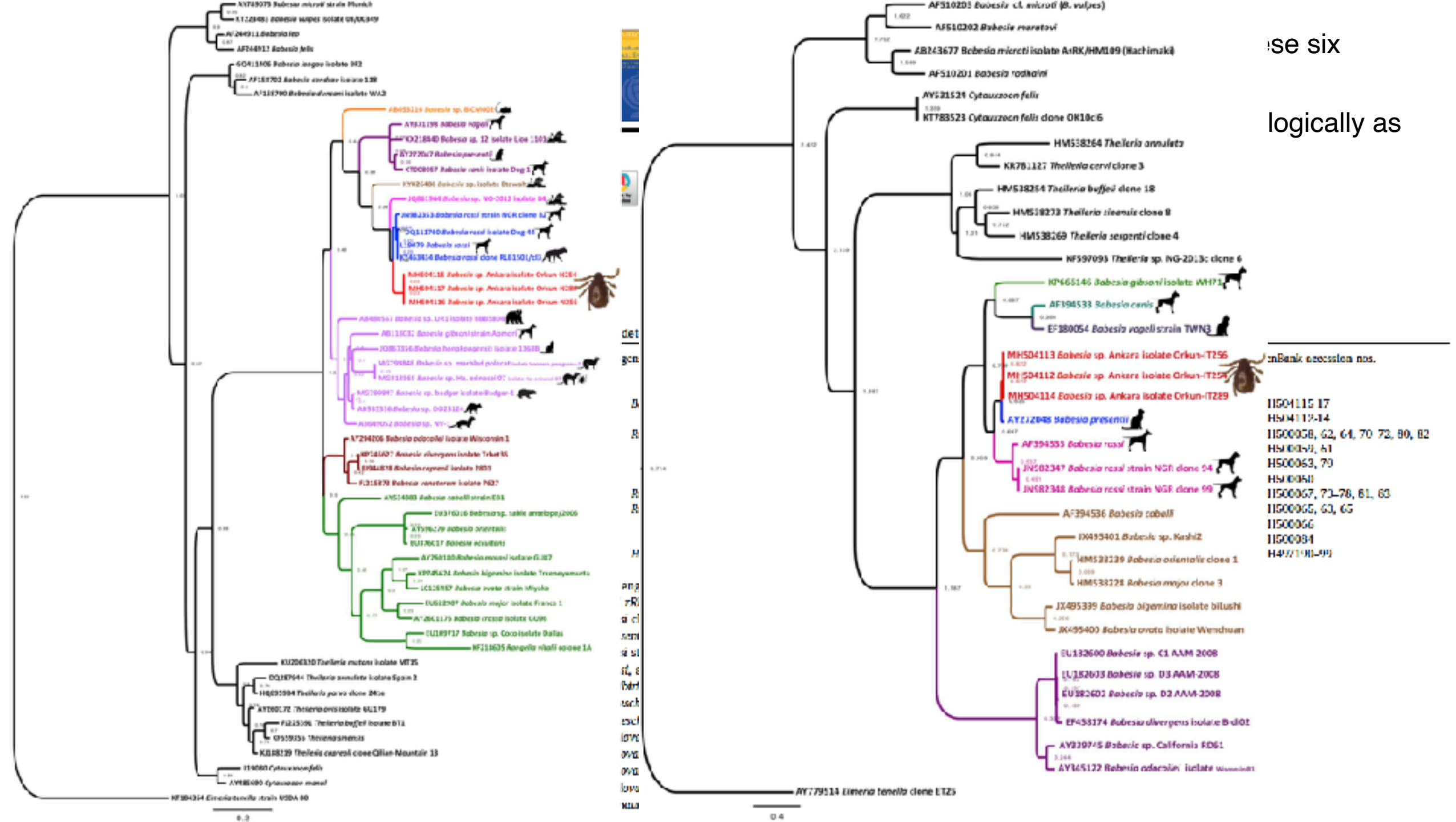
^aDepartment of Parasitology, Faculty of Veterinary Medicine, Ankara University, Ankara, Turkey

Table 2
Babesia spp. detected in this study and their level of nucleotide similarity with other isolates.



<i>Hepatozoon canis</i> isolate	Host	Location	GenBank accession no.
KX712123	<i>Hepatozoon canis</i> isolate 939-golden jackal	Austria	MF379258-74
KX887327	<i>Hepatozoon canis</i> isolate Fox P052-fox	Slovakia	MF379276-87
FJ497022	<i>Hepatozoon canis</i> isolate Dog 165	Cro-dog-Croatia	MF379275
KY347116	<i>Hepatozoon canis</i> isolate Fox5-dog	Turkey	MF379280-90
KX712127	<i>Hepatozoon canis</i> isolate 2734-golden jackal	Romania	MF379292
HM212626	<i>Hepatozoon canis</i> isolate Fox Hep2-fox	Croatia	MF379294-98
KM066414	<i>Hepatozoon canis</i> isolate ROPax109-fox	Romania	MF379300
KT257902	<i>Hepatozoon canis</i> strain Sarawak clone-17-dog	Malaysia	MF379303-05
MG077084	<i>Hepatozoon canis</i> isolate M-799-Ha.	pona-Turkey	MF379308
MG077085	<i>Hepatozoon canis</i> isolate TL1-fox	Turkey	MF379311
DQ436541	<i>Hepatozoon canis</i> isolate Spain 4-fox	Spain	MF379312
MG077086	<i>Hepatozoon canis</i> isolate TL2-fox	Turkey	MF379313
MG077087	<i>Hepatozoon canis</i> isolate TL4-fox	Turkey	MF379314
KX887328	<i>Hepatozoon canis</i> isolate 89-dog	Iran	MF379315
KX887329	<i>Hepatozoon canis</i> isolate Samsun-dog	Turkey	MF379316
KF521065	<i>Hepatozoon canis</i> strain BK 47-dog	Thailand	MF379317
DQ111757	<i>Hepatozoon canis</i> isolate Dog 78-dog	Sudan	MF379318
KX887324	<i>Hepatozoon canis</i> isolate Fox015-fox	Slovakia	MF379319
KU893125	<i>Hepatozoon canis</i> isolate fox 33-fox	Czech Republic	MF379320
KU893122	<i>Hepatozoon canis</i> isolate fox 5-2-fox	Czech Republic	MF379321
KU729739	<i>Hepatozoon americanum</i> isolate Bolom 03-dog	Brazil	MF379322
EU041718	<i>Hepatozoon ursi</i> isolate Gifu 2-black bear	Japan	MF379323
KX017290	<i>Hepatozoon felis</i> isolate Elanvalh-lion	India	MF379324
KX757032	<i>Hepatozoon silvestris</i> isolate 152/15-wildcat	Belarus and Kazakhstan	MF379325
KT223483	<i>Babesia vulpus</i> isolate CB-00349-fox	Spain	MF379326

Fig. 1. Phylogenetic tree based on aligned sequences of 18S rRNA of *Hepatozoon* spp. and constructed by using Maximum Likelihood method calculated under the GTR + I + G substitution model. The *Hepatozoon* sequences obtained in this study are shown in bold. GenBank accession numbers of sequences and names of lineages are given before species names, and host names and locations are given after species name.





original article

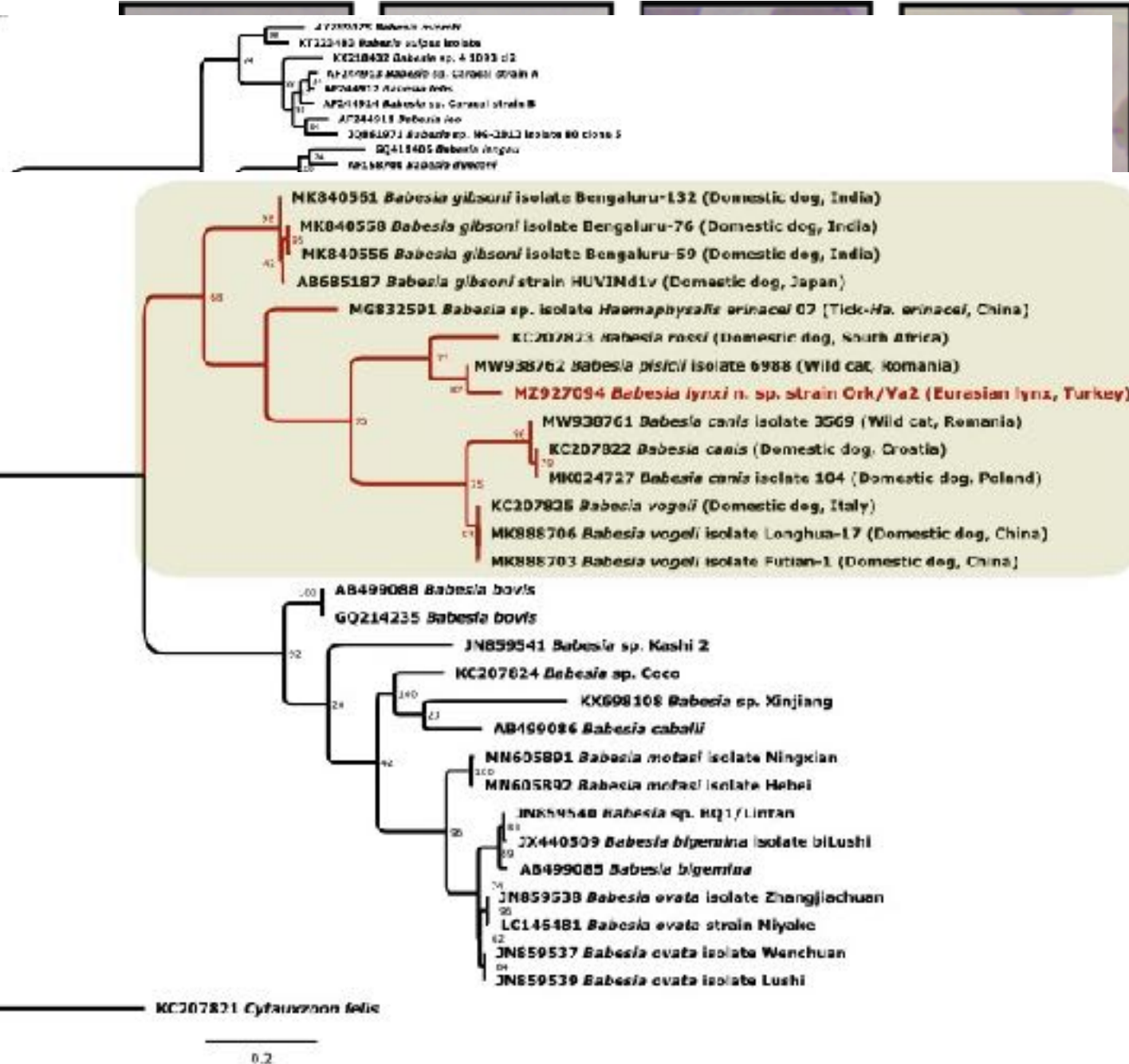
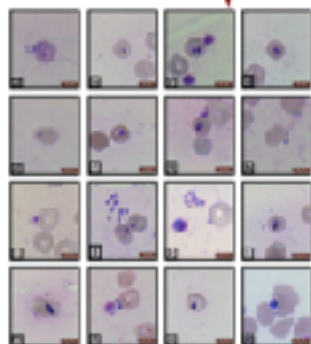
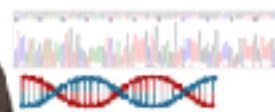
Description of a novel *Babesia* sp. genotype from a naturally infected Eurasian lynx (*Lynx lynx*) in Anatolia, Turkey, with remarks on its morphology and phylogenetic relation to other piroplasmid species

Ömer Özkün

Nilgün and Fikriye Bıkmaz Research Laboratory, Department of Perinatology, Faculty of Veterinary Medicine, Ankara University, Ankara 06112, Turkey

- A free-living, juvenile, female Eurasian lynx was found wounded, most likely due to being hit by a car, on a road located in the Yozgat province (Sorgun district, 39°55' 05" N, 35°18' 47" E, ~1360 m) of Turkey by national park officers in August 2020

***Babesia lynxi* n. sp.**





Short communication

Molecular investigation of the natural transovarial transmission of tick-borne pathogens in Turkey

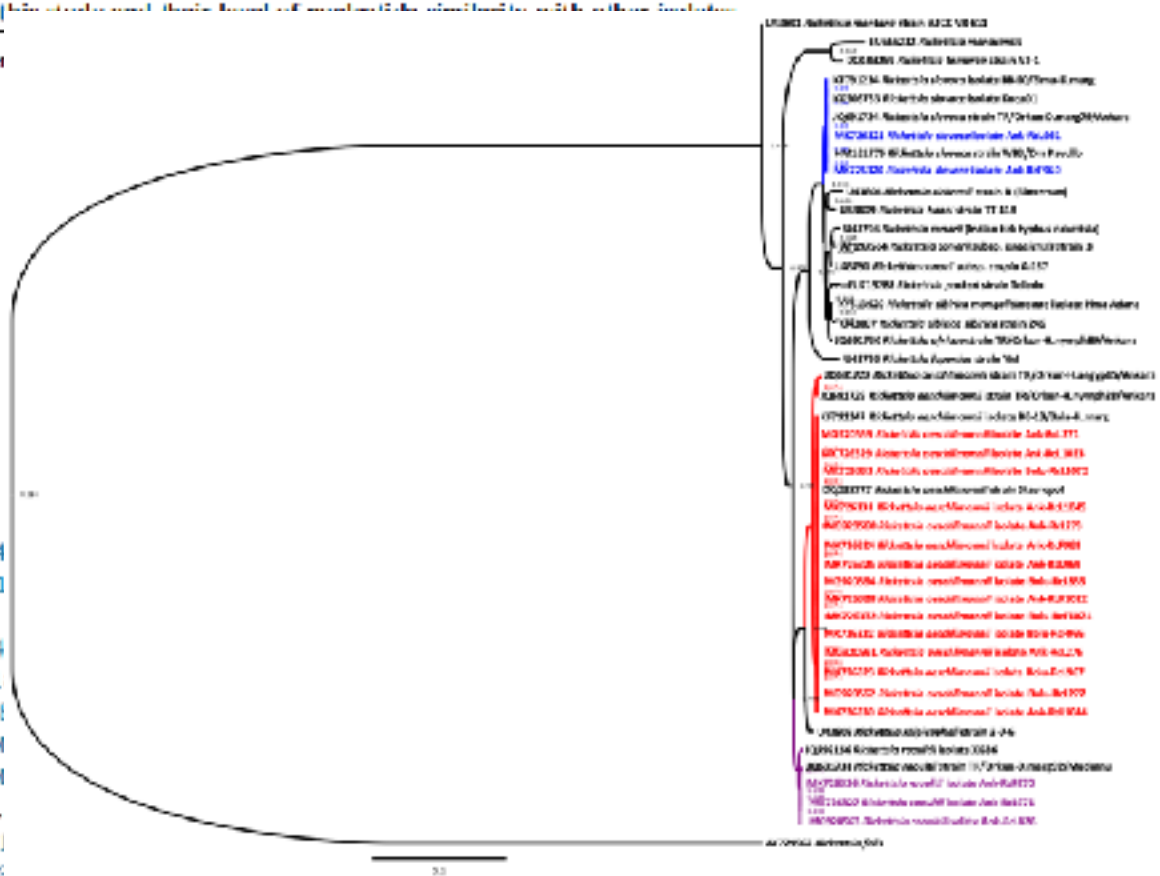
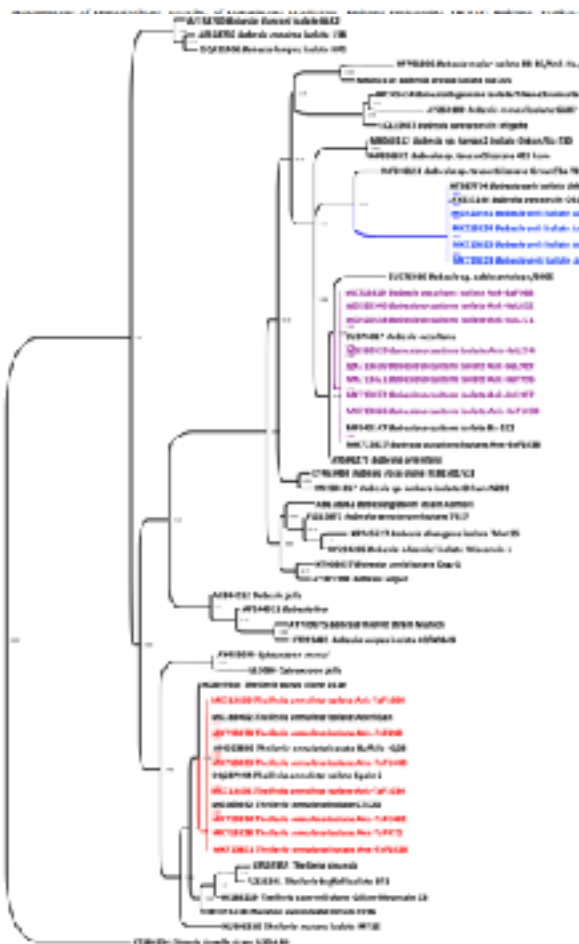
Ömer Orkun



Table 3

Babesia spp., *Rickettsia* spp., and *Theileria* spp. detected in 1458 ticks and 1458 larvae found on pastures in the districts of Adana, Hatay, Kilis, Kahramanmaraş, Mardin, Şanlıurfa, Gaziantep, and Adana, Turkey.

Detected pathogens		Tick species (No. positive for larvae pools)
<i>Babesia</i> spp.	<i>Ba. occultaans</i>	<i>Hy. marginatus</i> (1 - 2) <i>Hy. marginatum</i> (1 - 2) <i>Hy. excavatum</i> (1 - 2)
	<i>Ba. ovis</i>	<i>Rh. bursa</i> (1 - 3)
<i>Theileria</i> spp.	<i>Th. annulata</i>	<i>Hy. excavatum</i> (5 - 0) <i>Rh. bursa</i> (1 - 0)
<i>Rickettsia</i> spp.	<i>Ri. aeschlimannii</i>	<i>Hy. marginatum</i> (2 - 4)
		<i>Hy. marginatum</i> (2 - 4)
	<i>Ri. rasilii</i>	<i>De. marginatus</i> (1 - 2)
	<i>Ri. slovaca</i>	<i>De. marginatus</i> (1 - 1)

^a *Babesia occultaans* isolate Trender 1, accession no. KP74^b *Babesia occultaans* isolate Ba-212, accession no. MF0401^c *Babesia occultaans* isolate 58, accession no. HQ331478.^d *Babesia ovis* isolate tick20.3D, accession no. KT587794^e *Theileria annulata* isolate Azerbaijan, accession no. MK1^f *Theileria annulata* isolate CER20, accession no. MG5691^g *Rickettsia aeschlimannii* isolate Ro-775, accession no. M^h *Rickettsia aeschlimannii* isolate Ro-718, accession no. Mⁱ *Rickettsia raoultii* strain IM16, accession no. CP019435.^j *Rickettsia raoultii* strain Khabarovsk, accession no. CP01^k *Rickettsia slovaca* isolate Ro-714, accession no. MF3796...^l *Rickettsia slovaca* isolate BB-131/Polat-D.marg, accession no. KF791246.

Babesia spp. and *Theileria* spp. were detected in 1458 ticks and 1458 larvae found on pastures in the districts of Adana, Hatay, Kilis, Kahramanmaraş, Mardin, Şanlıurfa, Gaziantep, and Adana, Turkey.

^c The 0.6% difference is due to the number of the examined larvae pool in *Rh. bursa*, so it can be ignored.



Identification of tick animals in Turkey

Ömer Orkun¹ · Hasan Emir²

Table 1 Ticks collected from wild

Host	Location (District/ province)
Red deer	Nalihan/Ankara
Brown bear	Kazanköyü/Ankara
	Kayseri
Gray wolf	Gerede/Ikiz
Dunstan lynx	Çamlıdere/Ankara
Red fox	Nalihan/Ankara
	Ankara
European hare	Ankara
Tortoise	Mucur/Kırşehir
Total	

♂ male, ♀ female, L larva
^a All (three) *Rickettsia*-positive tick
^b Two of *Rickettsia*-positive ticks
^c One fully engorged female tick
^d All (two) of *Babesia*-positive tick
^e The *Rickettsia*-positive tick was 6

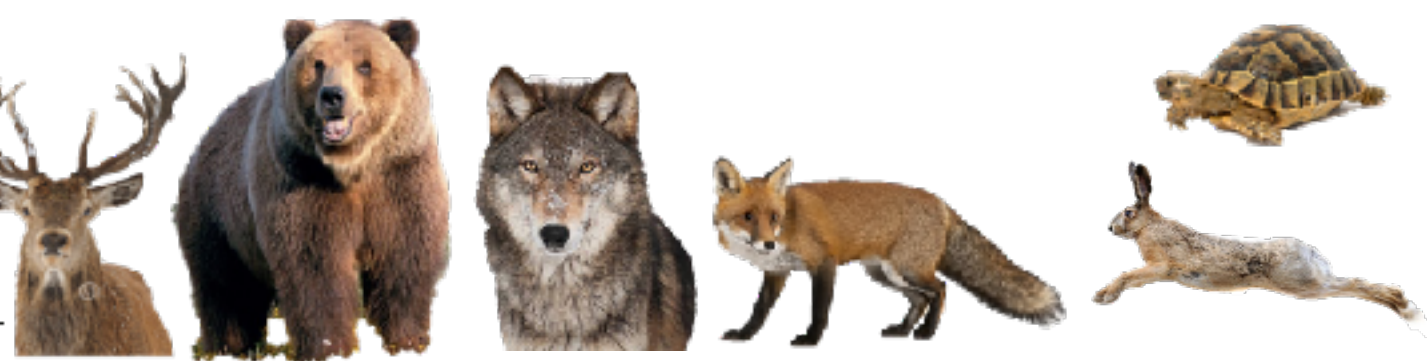
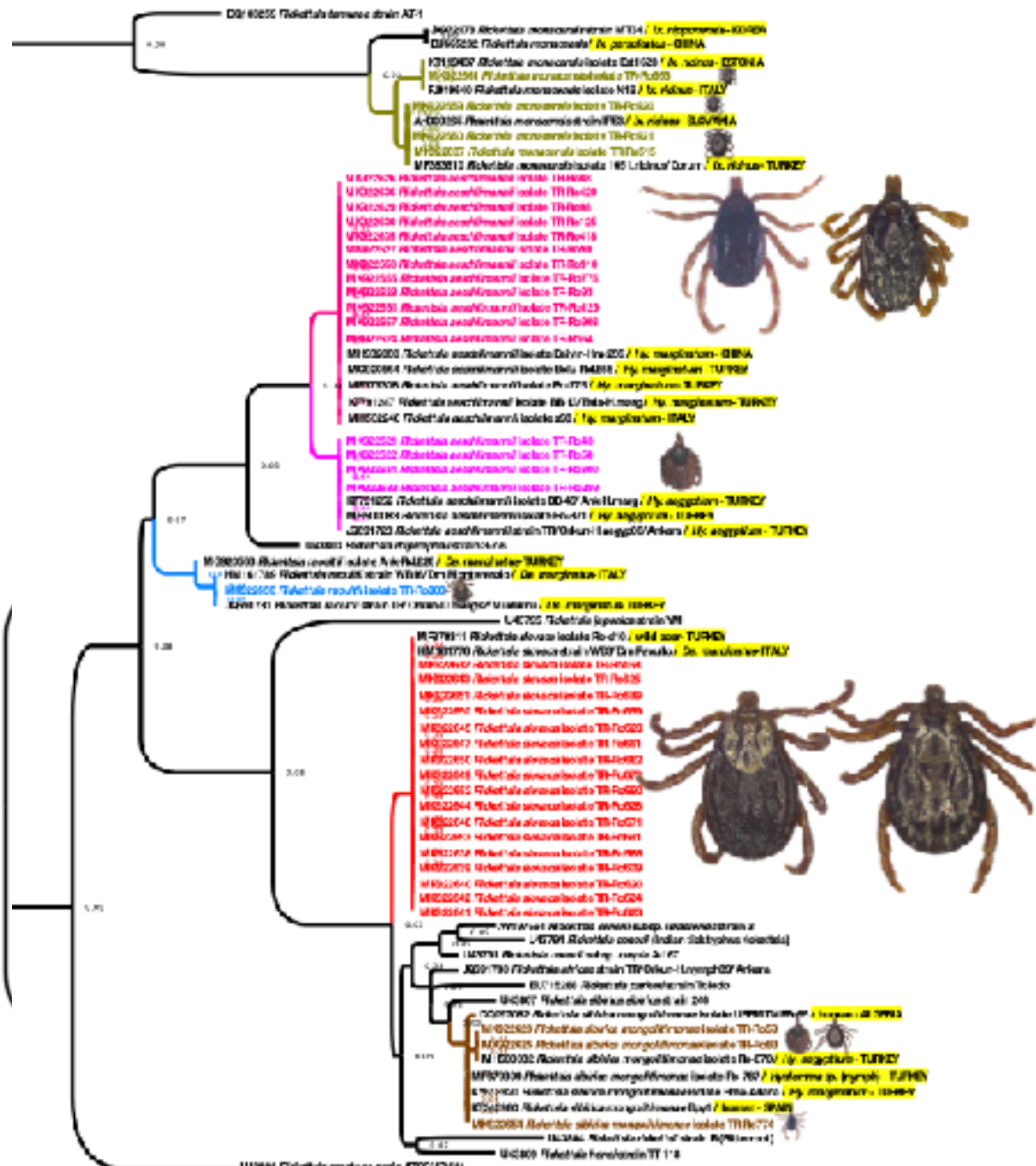


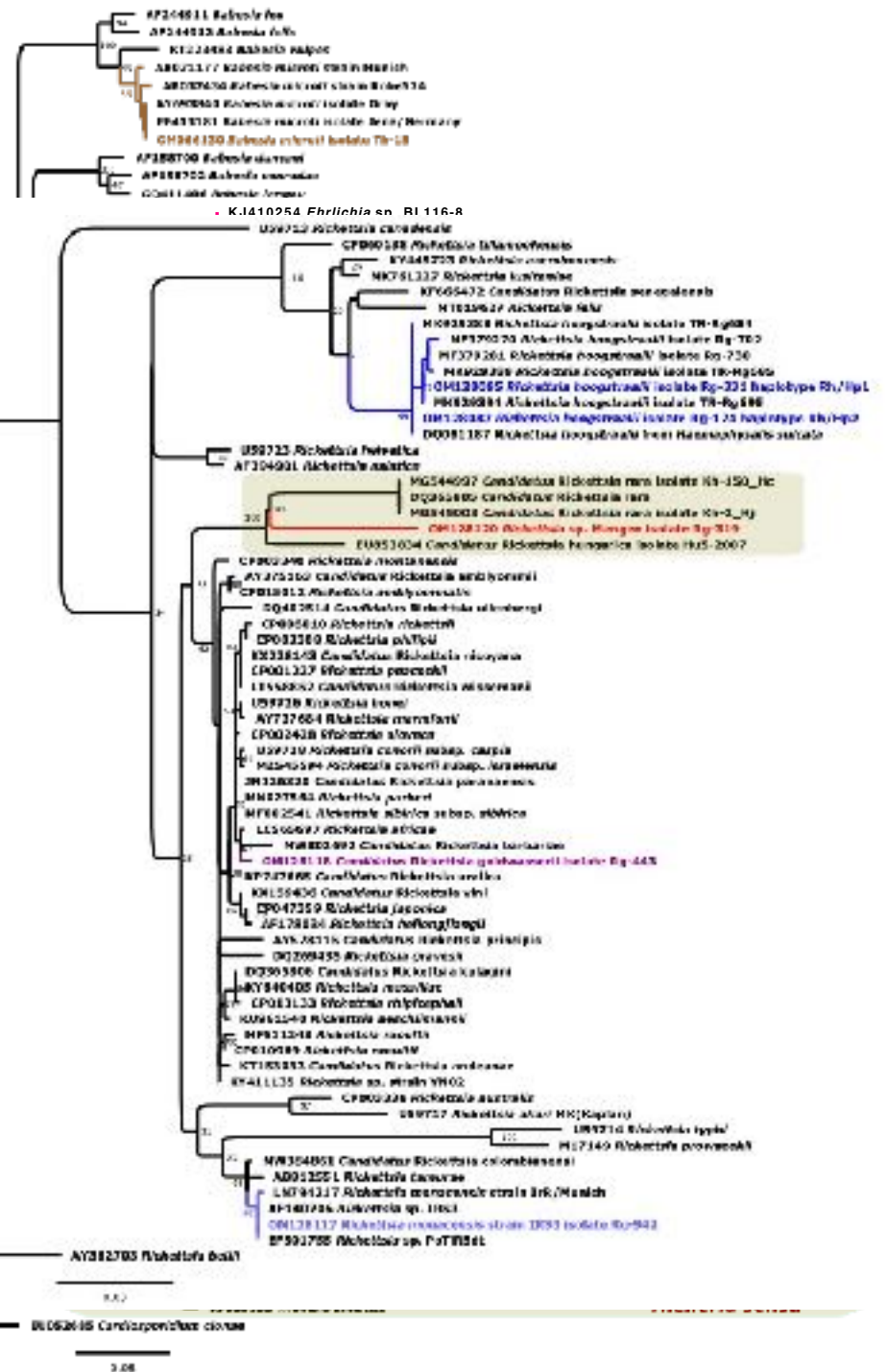
Table 2 Detected pathogens in the collected ticks and their levels of nucleotide similarity with other sequences

Detected pathogens	Host	Tick species (no. of positive ticks)	Sequenced gene	Nucleotide identity percentage (%)	GenBank accession nos.
<i>Rickettsia</i> spp.	Red Fox	<i>Rhipicephalus turanicus</i> (2)	18S rRNA	100 ^a	MN463016, 17
	European Hare	<i>Rhipicephalus turanicus</i> (1)	18S rRNA	100 ^a	MN463018
<i>Theileria</i> spp.	Red Deer	<i>Theileria capreoli</i> (1)	18S rRNA	100 ^{b, c}	MN463019
		<i>Rhipicephalus turanicus</i> (1)	18S rRNA	100 ^{b, c}	MN463020
<i>Hepatozoon</i> spp.	Brown Bear	<i>Hyalomma marginatum</i> (1)	18S rRNA	100 ^d	MN463021
		<i>Rhipicephalus turanicus</i> (1)	18S rRNA	100 ^d	MN463022
		<i>Ixodes ricinus</i> (1)	18S rRNA	100 ^d	MN905073
	Red Fox	<i>Rhipicephalus turanicus</i> (4)	18S rRNA	99.4–99.7 ^{–f}	MN463023–26
		<i>Haemaphysalis parva</i> (1)	18S rRNA	99.8 ^g	MN463027
	Finnish Lynx	<i>Haemaphysalis parva</i> (2)	18S rRNA	100 ^h	MN905024, 25
	Gray Wolf	<i>Haemaphysalis parva</i> (3)	18S rRNA	100 ^{–i}	MN463028–30
<i>Hemolivia</i> spp.	Turkish	<i>Hyalomma ascarum</i> (2)	18S rRNA	100 ^e	MN463031, 32
<i>Rickettsia</i> spp.	European Hare	<i>Rhipicephalus turanicus</i> (1)	ompA	99.8 ^j	MN482129
	Eurasian Lynx	<i>Haemaphysalis parva</i> (1)	ompA	99.8 ^m	MN911187
	Gray Wolf	<i>Haemaphysalis parva</i> (3)	gltA	100 ⁿ	MN496082–84
	Red Fox	<i>Haemaphysalis parva</i> (1)	gltA	100 ⁿ	MN496085
	European Hare	<i>Haemaphysalis parva</i> (1)	gltA	100 ⁿ	MN496086
	Finnish Lynx	<i>Haemaphysalis parva</i> (2)	gltA	100 ⁿ	MN911188, 89



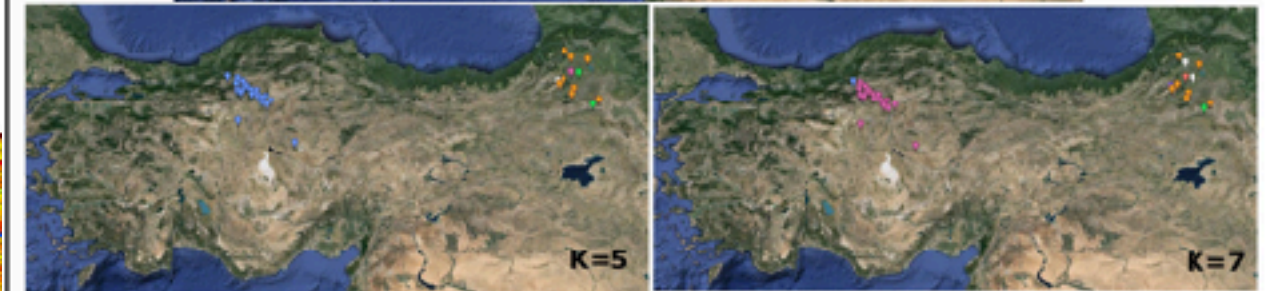
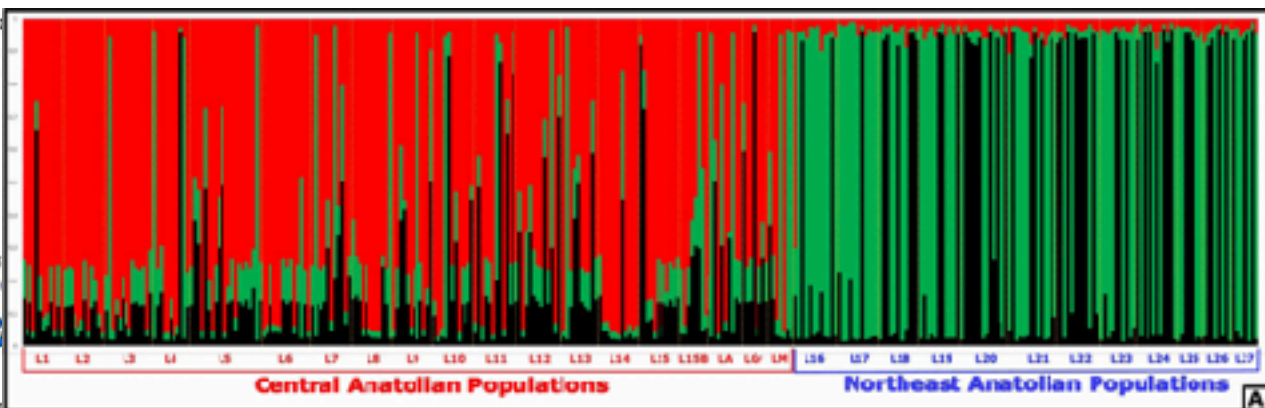
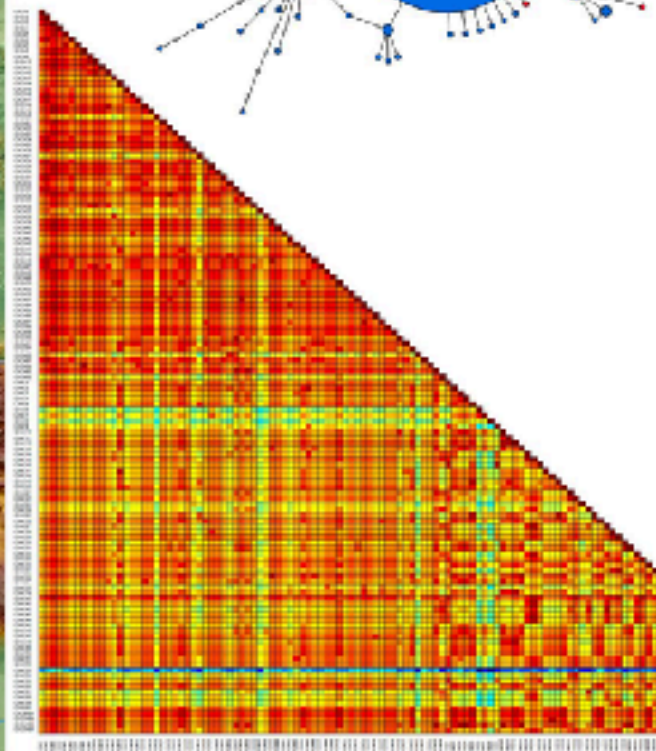
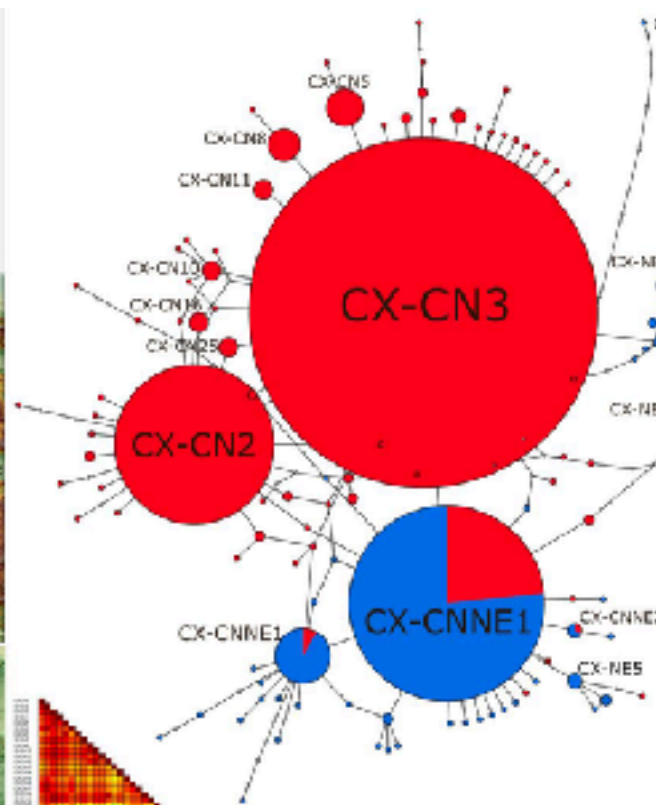
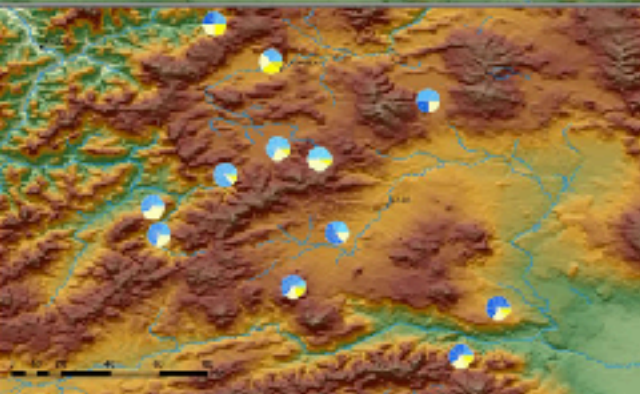
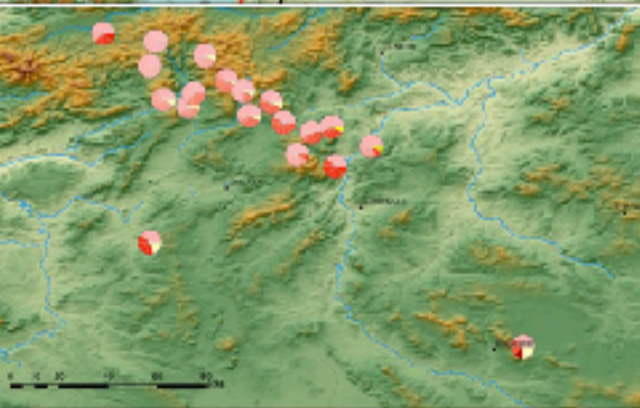
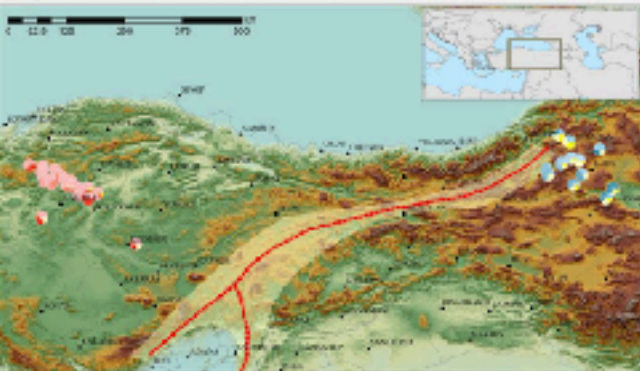
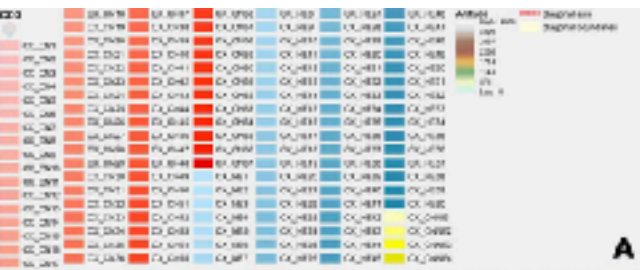
pathogens in host-seeking ticks and their levels of nucleotide identity with other sequences.

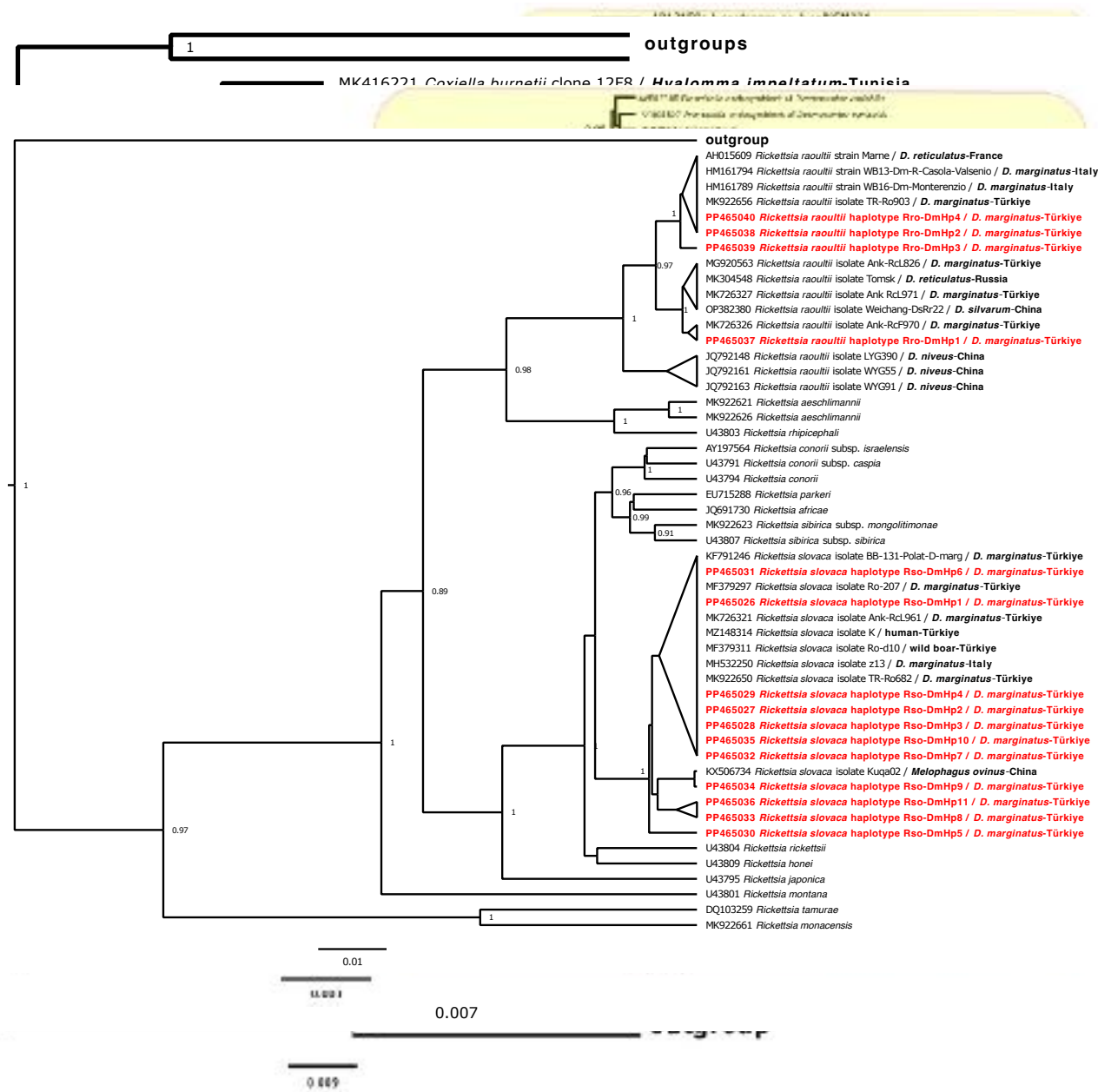
pathogens	Tick species (no. of positive ticks)	Locations-district/province (no. of positive ticks)	Sequenced gene	Nucleotide identity percentage (%)
<i>Babesia ooculans</i>	<i>Hyalomma marginatum</i> (12)	Kizilirmak/Ankara (8)	18S rRNA ^a	100 ^a
<i>Babesia crassa</i>	<i>Haemaphysalis parva</i> (9)	Çubuk/Ankara (1)	18S rRNA ^a	100 ^a
<i>Babesia microti</i>	<i>Haemaphysalis parva</i> (4)	Mucur/Kırsehir (3)	18S rRNA ^a	100 ^a
		Kizilirmak/Ankara (3)	18S rRNA ^a	100 ^a
			18S rRNA ^a	99.2-99.3 ^d
		Akyurt/Ankara (1)	18S rRNA ^a	100 ^c
			18S rRNA ^a	99.3 ^c
<i>Babesia</i> sp. tavsan1	<i>Hyalomma marginatum</i> (1)	Kizilirmak/Ankara	18S rRNA ^a	100 ^c
<i>Babesia</i> sp. tavsan2	<i>Rhipicephalus sanguineus</i> (1)	Kahramankazan/Ankara	18S rRNA ^a	97.6 ^f
			18S rRNA ^a	99.7-100 ^{a,b}
<i>Babesia</i> sp. Urdus (sp. nov.)	<i>Haemaphysalis parva</i> (1)	Kizilirmak/Ankara	18S rRNA ^a	98.3 ^f , 97.8 ^f
			18S rRNA ^a	95.4 ^g , 94.6 ^h
<i>Theileria annulata</i>	<i>Hyalomma excavatum</i> (1)	Kalecik/Ankara	18S rRNA ^a	97.2 ^g , 97.05 ^h
<i>Hepatozoon</i> sp.	<i>Haemaphysalis subeola</i> (1)	Kizilirmak/Ankara	18S rRNA	100 ⁱ
<i>Hepatozoon</i> sp.	<i>Haemaphysalis parva</i> (1)	Kizilirmak/Ankara	18S rRNA	99.8 ^g , 99.5 ⁱ
<i>Hyalomma marginatum</i>	<i>Hyalomma marginatum</i> (3)	Central Ankara (3)	18S rRNA	100 ^a
		Mucur/Kırsehir (1)	18S rRNA	100 ^a
			18S rRNA	100 ^a
<i>Borrelia burgdorferi</i>	<i>Ixodes ricinus</i> (2)	Mengen/Bolu	fla	100 ^a
<i>Borrelia lusitanae</i>	<i>Ixodes ricinus</i> (1)	Mengen/Bolu	fla	100 ^a
<i>Rickettsia sibirica</i>	<i>Dermacentor marginatus</i> (17)	Kizilirmak/Ankara (13)	ompA	100 ^a
		Çubuk/Ankara (3)	ompA	100 ^a
		Ayas/Ankara (1)	ompA	100 ^a
<i>Rickettsia aeschlimannii</i>	<i>Hyalomma marginatum</i> (12)	Kizilirmak/Ankara (11)	ompA	100 ^a
		Mucur/Kırsehir (1)	ompA	100 ^a
		Central Ankara (2)	ompA	100 ^a
		Kizilirmak/Ankara (1)	ompA	100 ^a
		Kahramankazan/Ankara (1)	ompA	100 ^a
<i>Rickettsia sibirica mongolotimonae</i>	<i>Hyalomma marginatum</i> (2)	Akyurt/Ankara (1)	ompA	100 ^a
		Kahramankazan/Ankara (1)	ompA	100 ^a
		Mucur/Kırsehir	ompA	100 ^a
<i>Rickettsia monacensis</i>	<i>Ixodes ricinus</i> (4)	Mengen/Bolu	ompA	98.8-99.6 ^f
<i>Rickettsia raoultii</i>	<i>Dermacentor marginatus</i> (1)	Mucur/Kırsehir	ompA	100 ^a



Detect(ed) pathogens in tick samples and their levels of nucleotide similarity with other sequences recorded in GenBank

[illegible]





Prevalence

- *Babesia* spp. – 1.72%(12/696)
 - *B. occultans* – 1.29% (9/696)
 - *B. vulpes* – 0.28% (2/696)
 - *B. bigemina* – 0.14% (1/696)
- *Theileria ovis* – 0.71% (5/696)
- *Hepatozoon* spp. – 1.01% (7/696)
 - *Hepatozoon* sp.-rodent related– 0.71% (5/696)
 - *Hepatozoon* sp.-mustelid related– 0.14% (1/696)
 - *H. canis* – 0.14% (1/696)
- *Coxiella* spp.
 - *C. burnetii* – 2.72% (19/696)
- *Francisella* spp.
 - *F. tularensis* subsp. *holarctica* – 0.43% (3/696)
 - *Francisella*-like endosymbiont – 1.72% (12/696)
- *Rickettsia* spp. – 56.32% (392/696)
 - *R. slovaca* – 32.9% (229/696)
 - *R. raoultii* – 23.42% (163/696)



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Thank you



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ResearchGate

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