



First record and molecular detection of *Ornithodoros maritimus* Vermeil & Marguet, 1967 in Türkiye with notes on other tick species collected on the Gull Island, Sinop

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Abstract

Ticks play an important role in the ecology of zoonotic diseases, however their diversity and host associations in insular ecosystems remain insufficiently documented in Türkiye. We investigated tick occurrence on yellow-legged Gulls (*Larus michahellis*) and within their nesting environment on Gull Island (Sinop, Türkiye) between March and June 2025. A total of 574 gull chicks and 833 nests were examined, yielding eight tick specimens. Morphological examination and molecular analyses revealed three noteworthy observations: (i) the detection of an adult *Ixodes ricinus* female attached to a yellow-legged gull chick, representing a rare avian host record, (ii) the presence of a questing male *Hyalomma marginatum* on the island floor, and (iii) the first record of *Ornithodoros maritimus* in Türkiye, confirmed by mitochondrial 16 S rRNA sequencing and phylogenetic analysis. The findings suggest that small insular habitats can be intermittently colonized by tick species of medical relevance, likely through host-mediated dispersal, while also highlighting ecological constraints that may limit long-term population establishment. These observations contribute to the faunistic knowledge of ticks in Türkiye and underscore the need for targeted surveillance of seabird-associated soft ticks along coastal ecosystems.

Keywords *Ornithodoros maritimus* · *Ixodes ricinus* · *Hyalomma marginatum* · Yellow-legged gull (*Larus michahellis*) · Ticks · Türkiye

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Introduction

A total of 56 hard and soft tick species have been reported from Türkiye, including the recent addition of *Haemaphysalis longicornis* (Bursali et al. 2012; Bursali et al. 2020; Kar et al. 2017; Keskin and Doi 2025; Keskin and Erciyas-Yavuz 2018; Keskin et al. 2014; Keskin and Selçuk 2021; Orkun and Karaer 2018; Orkun and Vatansever 2021). However, this list also contains species considered *nomen neglectum*, rare records, synonyms, or accidental findings. Based on consolidated and reliable records, approximately 40 tick species are currently recognized as established in Türkiye. In Türkiye, limited monitoring studies suggest that some tick species are relatively abundant, including *Hyalomma marginatum*, *Ixodes ricinus* s.l., *Haemaphysalis parva*, *Rhipicephalus sanguineus* s.l., and *Dermacentor marginatus*, whereas others, such as *Hyalomma rufipes*, *Dermacentor niveus*, and *Ixodes hexagonus*, appear to be rare (Estrada-Peña et al. 2017).

Ixodes ricinus s.l. Linnaeus, 1758 is one of the most widespread tick species complex in Europe and serves as a significant vector of various pathogens affecting both humans and animals (Černý et al. naeus 2020). In Türkiye, *I. ricinus* has been reported in several regions, particularly in the Black Sea and Marmara provinces (Hekimoğlu 2022). Due to its ability to transmit a range of disease agents, *I. ricinus* poses a substantial public health concern. This tick species plays an active role not only in the transmission of pathogens but also in their natural maintenance in the environment. Notably, *I. ricinus* is recognized as the principal vector of Lyme disease in Europe. Furthermore, it is capable of transmitting rickettsial and viral pathogens responsible for diseases such as spotted fever and tick-borne encephalitis (Kahl and Gray 2023; Lindsø et al. 2024; Pedersen et al. 2020). Although the genome of Crimean-Congo Hemorrhagic Fever (CCHF) virus has been detected in questing *I. ricinus* ticks in multiple studies, the species' potential role in the natural transmission cycle of CCHF remains unclear (Cuadrado-Matías et al. 2024; Hoogstraal 1979; Sultankulova et al. 2022; Zarrabi-Ahrabi et al. 2023). This species is a three-host tick capable of infesting a wide range of hosts, including birds, mammals, and humans. This characteristic enables the tick to obtain blood meals from diverse host species, thereby facilitating the transmission of a broad spectrum of pathogens to a wide range of hosts living in far or nearby habitats (Gray et al. 2021; Kahl and Gray 2023).

Hyalomma marginatum Koch, 1844 is considered the most important tick species in terms of public health in Türkiye (Tavassoli et al. 2024). It is the primary vector of Crimean-Congo Hemorrhagic Fever (CCHF) in the region (Hekimoğlu and Sağlam 2024). *H. marginatum* is widely distributed across Türkiye; however, the Central Anatolia region, where CCHF is endemic, has the highest tick population density (Hekimoğlu et al. 2020). This species is a two-host tick, with larvae preferring ground-dwelling and/or feeding birds, leporids, and insectivores, while adults primarily prefer cattle as their host. Nevertheless, *H. marginatum* can occasionally infest humans and other mammals. Its ecological preference includes dry climates and areas dominated by pasture-based farming (Celina and Černý 2025). In addition to its local life cycle, like *I. ricinus*, also *H. marginatum* poses further risk due to the presence of migratory birds. Türkiye lies along one of the major bird migration routes, and the tick's larvae and nymphs can be transported by these birds to new regions, potentially increasing the risk of CCHF and other tick-borne diseases transmission (Bacak et al. 2024; Celina and Černý 2025).

Ornithodoros maritimus Vermeil & Marguet, 1967 (syn. *Carios maritimus*, *Alectorobius maritimus*) is a soft tick belonging to the *Ornithodoros capensis* species complex (Dupraz et al. 2017). In this study, we follow the nomenclature proposed in the last comprehensive global checklist of valid tick species (Guglielmone et al. 2010), which recognizes *O. maritimus* as the valid species name; this usage is also consistent with the Global Biodiversity Information Facility (GBIF), World Register of Marine Species (WoRMS), and Ocean Biodiversity Information System (OBIS). This species parasitizes a wide range of seabirds, particularly gulls and is generally reported from the Palearctic, especially the UK, France, Italy, Spain, Portugal, Tunisia, and Morocco (Dietrich et al. 2011; Dupraz et al. 2016). Although widely distributed in these regions, *O. maritimus* has not previously been documented in Türkiye. The tick exhibits feeding behaviour similar to that of other soft ticks, with minor differences. Its entire life cycle takes place within the host's nest, and it generally feeds on the host during quiet nighttime periods when the host is at rest (Duffy and Dautri 1987). Several pathogenic agents have been reported from *O. maritimus*, including Meaban and Soldado viruses, as well as *Borrelia* species such as *B. turicatae* and rickettsial agents. Notably, West Nile virus, a pathogen of zoonotic importance, has also been detected in this tick species (Mans et al. 2022; Sanz-Aguilar et al. 2020).

Larus michahellis Naumann, 1840 (Yellow-legged gull) is among the most widespread and abundant gull species across the Mediterranean (Olsen 2010). This large-bodied gull, weighing between 420 and 1,600 g, is also the dominant gull species in the Mediterranean, the Marmara Sea, and the Black Sea in Türkiye (Karaardic et al. 2022; Ramos et al. 2009). Over the past 50–60 years, its populations have increased, and its distribution expanded, primarily northwards and inland, colonizing various areas across Central Europe. This expansion is likely facilitated by post-breeding movements, during which yellow-legged gulls of most age classes migrate north from their traditional Mediterranean colonies, sometimes reaching as far as the North and Baltic Seas. The population increase appears to result not only from the species' ability to utilize inland habitats resembling the rocky cliffs it naturally nests on, but also from its adaptation to man-made structures, such as rooftops in major cities like Istanbul (Kirwan et al. 2024).

Sinop is a province located in northern Türkiye, within the Black Sea region, characterized by a humid climate. To date, several tick species have been reported from this area, including *Ixodes* spp., *Dermacentor* spp., *Rhipicephalus* spp., and *Hyalomma* spp. Moreover, various pathogenic agents have been detected in these ticks, particularly *Borrelia burgdorferi* sensu lato (Gunes and Atas 2020; Güneş et al. 2007).

In the present study, we report the first infestation of the yellow-legged gull with *Ixodes ricinus*, the first occurrence of *Hyalomma marginatum* on Sinop Gull Island, and the first record of *Ornithodoros maritimus* in Türkiye.

Materials and methods

Geographical location and sampling

The sampling site, Gull Island, has a circumference of 486 m, a surface area of 7,838 m², and is located 87.7 m from the mainland (42°02'53.29"N, 35°02'57.93"E). The site was mapped in QGIS 3.36 using OpenStreetMap as the base layer, with distances and areas mea-

sured directly in QGIS. Approximately 47% of the island's surface area consists of arboreal and shrubby vegetation. The dominant and most widespread species is the Bay Laurel (*Laurus nobilis*). Other woody and shrubby species, including the holm oak (*Quercus ilex*), dog rose (*Rosa canina*), elm (*Ulmus* spp.), and common hawthorn (*Crataegus monogyna*), exhibit lower frequency and distribution levels across the island. Annual herbaceous plants occupy roughly 11% of the island, primarily distributed within the transition zones between bare rocky areas and shrublands. Although seasonal dominance levels fluctuate, nitrophilous (nitrogen-loving) annual herbs are the prevalent taxa due to intensive seagull guano deposition. Within this niche, the dominant species include common nettle (*Urtica dioica*), lords-and-ladies (*Arum* spp.), cleavers or sticky willy (*Galium aparine*), common mallow (*Malva sylvestris*), ribwort plantain (*Plantago lanceolata*), white campion (*Silene latifolia*), and milk thistle (*Silybum marianum*). Notably, yellow-legged gull nesting sites are densely concentrated beneath the canopy of these herbaceous plants. Rocky terrain constitutes 42% of the island's total area, hosting sparse populations of marine algae (Figs. 1 and 2) (Supplementary Fig. S1). During the sampling period, the island was occupied by a dense breeding colony of yellow-legged gulls (*Larus michahellis*), and gull nests were distributed across much of the available surface area. Sampling was conducted twice per month between March and June 2025. Tick specimens were collected by systematically examining yellow-legged gull chicks, gull nests, and the island floor. Each chick was inspected thoroughly, with all body regions (including the head, neck, wings, legs, and cloacal area) examined for the presence of ticks, which were removed using fine-tipped forceps. All gull nests present on the island were manually inspected, and any ticks encountered were collected using forceps. In addition, the island floor surrounding nesting areas was inspected for questing ticks. All collected specimens were preserved in screw-cap tubes containing 70% ethanol, and each tube was labeled with the collection date, number of specimens, and sampling location.



Fig. 1 Geographical location of the sampling site. The red star indicates Gull Island (Sinop, Türkiye). Insets show its position within Sinop Province and the Black Sea, and a photograph of the island. Map created in QGIS 3.36 using OpenStreetMap data (© OpenStreetMap contributors)

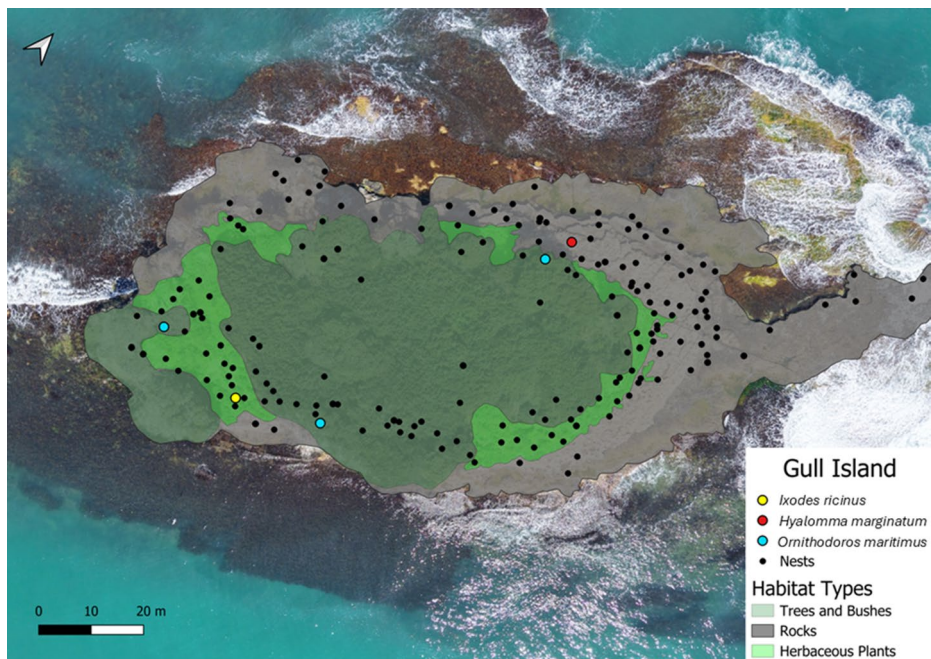


Fig. 2 Aerial view of Gull Island showing the spatial distribution of seabird nests and tick collection sites. The base image is an orthophoto edited in QGIS 3.36. Black dots indicate yellow-legged gull (*Larus michahellis*) nests. Colored points represent locations where ticks were collected: *Ixodes ricinus* (yellow), *Hyalomma marginatum* (red), and *Ornithodoros maritimus* (blue). Habitat types are overlaid and classified as areas dominated by trees and bushes, herbaceous vegetation, and rocky substrates. Scale bar shown in meters

Microscopic examination

All tick specimens were examined morphologically under a stereomicroscope. Species identification was performed using standard taxonomic keys (Estrada-Peña et al. 2017; Hoogstraal et al. 1976). For morphometric analyses of argasid ticks, the following characters were measured: body length (BL), body width (BW), capitulum length (CL), hypostome length (HL), palp length (PL), coxa I length (CIL), coxa IV length (CIVL), tarsus I length (TIL), and genital aperture width (GAW). Measurements were taken using MAGUS-View software with a MAGUS Stereo 8T microscope equipped with a 2FA100 1× C-mount adapter and a CBF70 camera and were recorded according to sex and developmental stage.

DNA extraction and PCR

To confirm the suspected *Ornithodoros* spp.—difficult to identify morphologically and representing a first record in Türkiye—molecular methods were used. A single leg was excised from each of three male argasid ticks and placed individually into sterile 1.5 mL microcentrifuge tubes. Samples were frozen in liquid nitrogen and homogenized with sterile, tube-compatible pestles. The homogenates were suspended in 200 µL sterile DPBS and processed for DNA extraction using the E.Z.N.A.[®] Tissue DNA Kit (Omega Bio-Tek, USA),

following the manufacturer's instructions. Extracted DNA was used as template in PCR reactions consisting of 25 µL 2× Taq PCR Master Mix (Biomatik, Canada), 1 µL of each primer (10 µM), 8 µL DNA, and nuclease-free water to a final volume of 50 µL. A fragment of the mitochondrial 16 S rRNA gene was amplified using primers designed by Black and Piesman (1994): forward 5'-CTGCTCAATGATTTTTTAAATTGC-3' and reverse 5'-CCG GTCTGAACTCAGATCATGTA-3'. PCR cycling conditions included an initial denaturation at 94 °C for 2 min, followed by 35 cycles of denaturation at 94 °C for 45 s, annealing at 50 °C for 45 s, and extension at 72 °C for 45 s, with a final extension at 72 °C for 10 min. Amplicons were visualized on 2% agarose gels, purified with the PCR and Gel Extraction Mini Prep Kit (Genaxxon Bioscience, Germany), and sequenced bidirectionally by Sanger sequencing.

Phylogeny

DNA sequences were aligned and inspected using BioEdit Sequence Alignment Editor (Hall 1999). Each sequence was queried against the NCBI database using BLAST to identify the closest matches for the targeted gene region. The resulting sequences were deposited in GenBank under the accession numbers PX106412, PX106413, and PX106414.

To infer the phylogenetic relationships of the argasid ticks identified in this study, we conducted phylogenetic analyses using 129 publicly available *Ornithodoros* spp. 16 S mitochondrial rRNA gene sequences from GenBank, together with the sequences obtained. In phylogenetic analyses, the focal species was designated as *Alectorobius maritimus* to maintain consistency with NCBI Taxonomy and GenBank records. Likewise, several reference sequences appear under *Alectorobius* spp. in the phylogenetic tree, reflecting the nomenclature used in NCBI Taxonomy rather than taxonomic revision by the authors. The 16 S mitochondrial rRNA sequences of *Argas persicus* (GU355920) and *Argas monachus* (EU283344) were included as outgroups. The complete dataset is provided in Supplementary Material 1.

First, all sequences were aligned with the reference sequences using BioEdit Sequence Alignment Editor. The best substitution model for the sequences was determined by testing the compatibility of the data set to 286 different substitution models using the Maximum Likelihood statistical method by ModelFinder program implemented in the IQ-TREE web server (Kalyaanamoorthy et al. 2017; Trifinopoulos et al. 2016). The best-fit model automatically chosen by IQ-TREE web server according to Bayesian Information Criterion (BIC) was used to infer the evolutionary history based on the Transition (TIM) model. To model evolutionary rate differences between sites, FreeRate model was used (Yang 1994). To validate the phylogenetic trees, 1000 replicates of Hasegawa approximate likelihood ratio test (SH-aLRT) and Ultrafast bootstrap (UFBoot) were used, which produce less false positive and less biased results when compared to other methods such as normal bootstrap (Guindon et al. 2010; Minh et al. 2013). The tree was drawn to scale. Furthermore, branch lengths were measured regarding the number of substitutions per site.

Results

Sampling and morphological examination of ticks

For the purpose of tick collection, 574 yellow-legged gull chicks and 833 yellow-legged gull nests were screened. A total of 8 tick specimens was collected from a yellow-legged gull chick ($n=1$), yellow-legged gull nests ($n=6$) and island floor ($n=1$) (Fig. 2). The tick, collected from a yellow-legged gull chick in April 2025 was described via morphological characteristics as a female *I. ricinus*. The tick was attached to chick's tibia (Supplementary Fig. S2). The morphological keys, including an elongated internal spur and a short external spur on coxa I, relatively long palpi, a basis capituli without lateral projections, and a slightly longer than wide scutum with small and homogenously distributed punctations, were observed on the specimen (Fig. 3).

One of the other tick specimens was described as a male *H. marginatum*, the CCHF tick, based on morphological characteristics. The questing tick was collected from the island floor directly in May 2025. Deeply incised coxa I with contiguous and unequal spurs, rare large punctations and dense small punctations especially caudal side of conscutum, long lateral grooves almost reaching eyes, absence of parma, less than six setae on palpal segment I and a complete longitudinal dorsal, ivory strip of enamelling on each leg segment, particularly distinct on the hind legs, were observed on the specimen as morphological keys (Fig. 4).

All the tick specimens, collected from yellow-legged gull nests in May and June 2025, were described as *O. maritimus* via morphological features. A total of 6 specimens were a nymph, a female, and 4 males. With the presence of pre-anal and transverse postanal groove, presence of cheeks, and absence of dorsoventral groove characteristics, the ticks

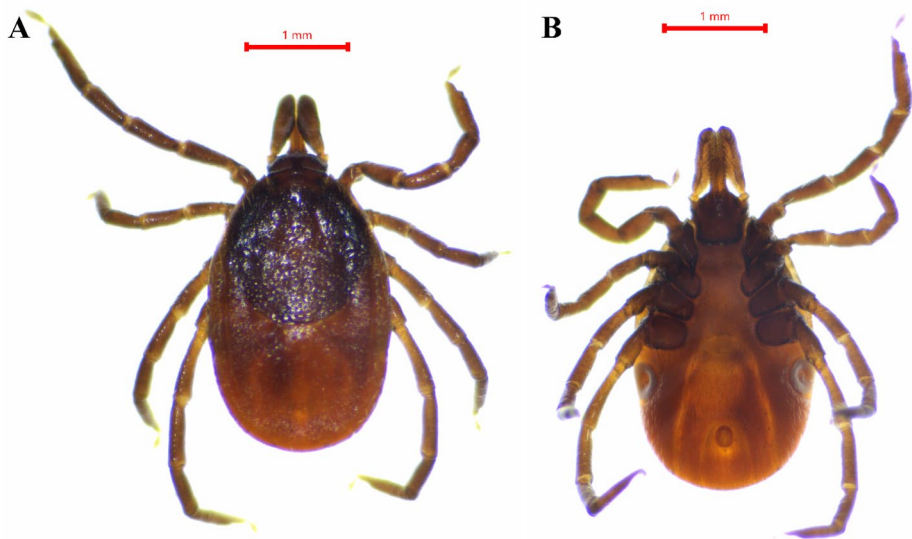


Fig. 3 Stereo micrographs of *Ixodes ricinus*, female. Dorsal side (A), Ventral side (B) Scale bar indicates 1 mm



Fig. 4 Stereo micrographs of *Hyalomma marginatum*, male. Dorsal side (A), Ventral side (B). Scale bar indicates 2 mm

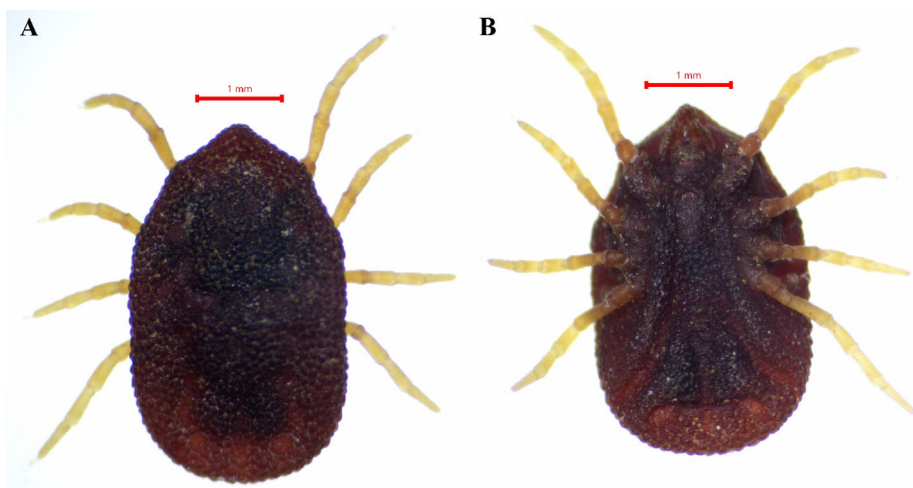


Fig. 5 Stereo micrographs of *Ornithodoros maritimus*, male. Dorsal side (A), Ventral side (B). Scale bar indicates 1 mm

were identified in the *Alectorobius* subgenus. Observation of evenly distributed mammillae of the posteromedian area, and discs of the posterolateral quadrant on the dorsum in several compartments shows us the ticks were *O. maritimus* (Figs. 5 and 6).

Morphometric measurements of male *O. maritimus* ticks ($n=4$) were as follows (mean $\pm$ SD; range, in mm): body length (BL) 4.128 ± 0.142 (4.34–4.04), body width (BW) 2.400 ± 0.087 (2.45–2.27), BL/BW ratio 1.721 ± 0.063 (1.78–1.661), capitulum length (CL) 0.420 ± 0.029 (0.45–0.38), CL/BL ratio 0.102 ± 0.008 (0.111–0.093), hypostome length (HL) 0.163 ± 0.005 (0.17–0.16), palp length (PL) 0.285 ± 0.019 (0.30–0.26), coxa I length (CIL) 0.568 ± 0.054 (0.62–0.50), coxa IV length (CIVL) 0.365 ± 0.030 (0.41–0.35), tarsus I length (TIL) 0.495 ± 0.061 (0.58–0.45), and genital aperture width (GAW) 0.238 ± 0.010 (0.25–0.23). In female sample, measurements (mm) were: BL 5.08, BW 2.90, BL/BW ratio 1.752, CL 0.63, CL/BL ratio 0.124, HL 0.19, PL 0.38, CIL 0.56, CIVL 0.43, TIL 0.55, and GAW 0.43. In nymph, values (mm) were: BL 3.34, BW 2.02, BL/BW ratio 1.653, CL 0.43,

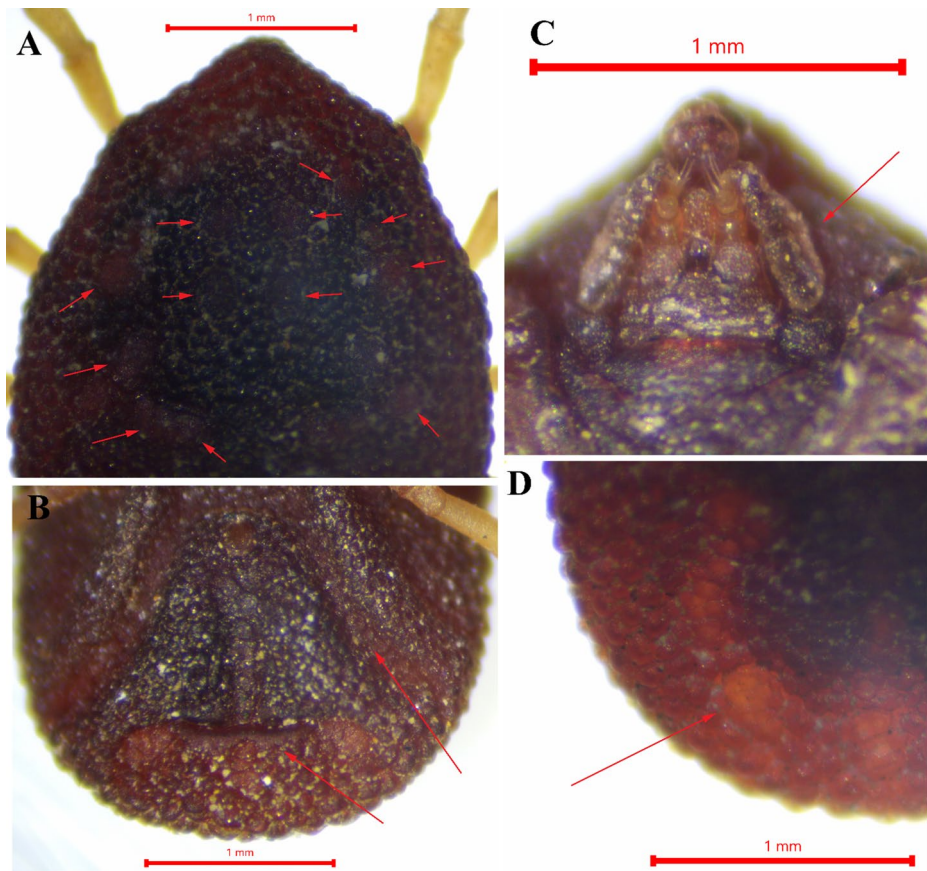


Fig. 6 Morphological characteristics of *Ornithodoros maritimus*, male. All scale bars indicate 1 mm. Arrows indicates anterodorsal discs (A), pre- and post-anal grooves (B), cheek specific to *Alectorobius* sub-genus, covering capitulum (C) and a disc of posterolateral quadrant includes multiple compartments (D)

CL/BL ratio 0.129, HL 0.15, PL 0.23, CIL 0.45, CIVL 0.28, and TIL 0.29. All detailed morphometric measurements are provided in Supplementary Material 2.

Sequencing and phylogeny

PCR amplification of the mitochondrial 16 S rRNA gene from *O. maritimus* samples yielded products of approximately 480 bp, as visualized on a 2% agarose gel. Bidirectional Sanger sequencing of these amplicons revealed 99.76% similarity to *Alectorobius maritimus* isolate CRETAV-OMAS006 (GenBank accession no. PV826764). Phylogenetic analysis, based on 129 publicly available *Ornithodoros* spp. 16 S rRNA sequences, two outgroup sequences, and the sequences obtained in this study, placed our samples within the Capensis group, clustering closely with previously reported *O. maritimus* isolates (Fig. 7; Supplementary Fig. S3).

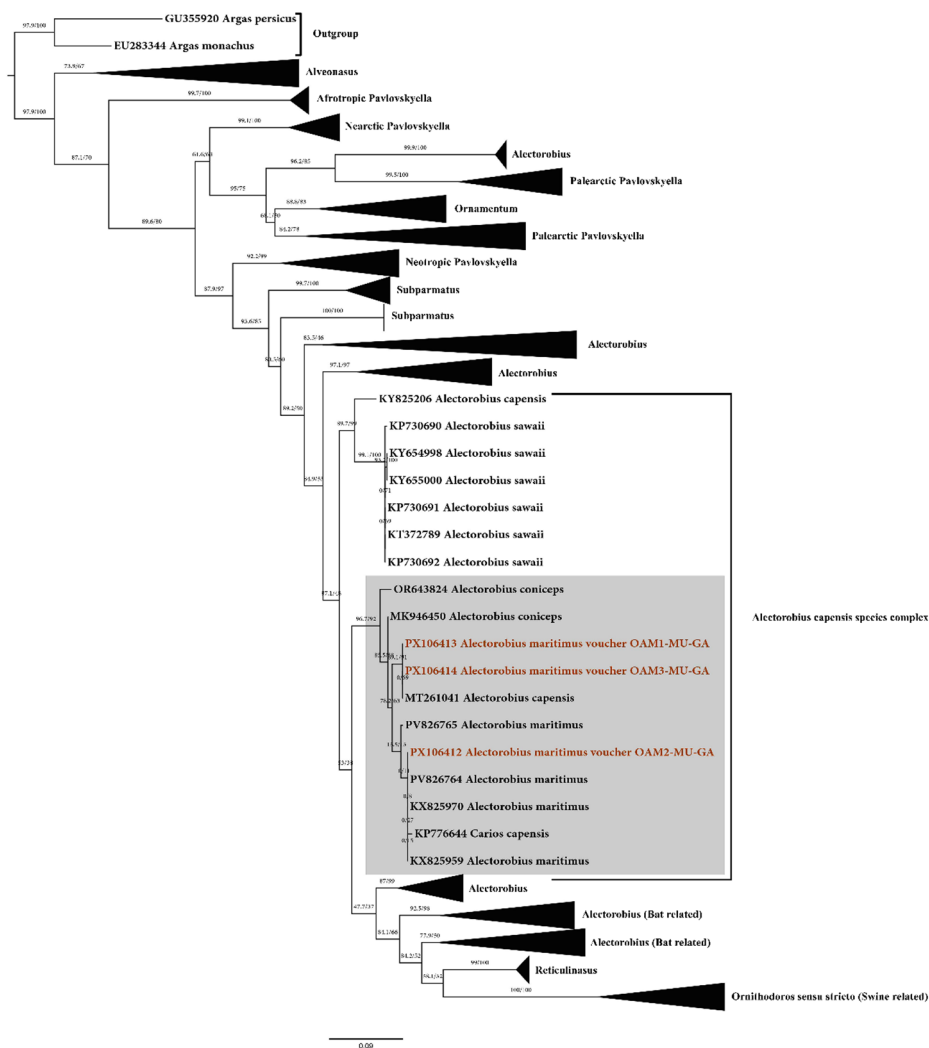


Fig. 7 Maximum likelihood phylogenetic tree of mitochondrial 16S rRNA gene sequences of *Ornithodoros maritimus* (syn. *Alectorobius maritimus*) and related argasid ticks. The analysis was performed under the Transition (TIM) substitution model with variance estimation and 1,000 bootstrap replicates. Ultrafast bootstrap (UFBoot) and SH-aLRT support values are shown next to the branches. *Argas persicus* and *Argas monachus* were included as outgroups. Sequences generated in this study are shown in red, with the corresponding cluster highlighted in grey. Taxon names in the tree follow NCBI Taxonomy and therefore include *Alectorobius* spp. labels for some sequences. Clades outside the *Ornithodoros capensis* species complex are collapsed. The tree was visualized using FigTree v1.4.4

Discussion

Ticks and tick-borne diseases have long been a major public health concern in Türkiye, which continues to report the highest number of CCHF outbreaks worldwide. Consequently, ticks attract considerable scientific and public attention (Zarrabi-Ahrabi et al. 2025). In this

study, we describe three interesting observations from Gull Island (Sinop, Türkiye), a very small and ecologically constrained area in Türkiye where tick-borne diseases are of significant importance. While our findings are qualitative rather than quantitative, they provide valuable insights into host–parasite interactions in insular ecosystems with limited host diversity.

The first observation involves the attachment of an adult female *I. ricinus* female to yellow-legged gull chick. By successfully feeding on a wide range of hosts, *I. ricinus* can parasitize birds, reptiles, and mammals (Bacak et al. 2024; Eren and Açııcı 2025; Kar et al. 2021). This tick has been reported from several regions of Türkiye, particularly the Marmara and Black Sea regions, and is among the most frequently documented tick species on humans. To our knowledge, there are no previous records of *I. ricinus* attached to the yellow-legged gull. Occasional records exist of this tick feeding on seabirds such as the Northern Gannet (*Morus bassanus*), Common Gull (*Larus canus*), and European Herring Gull (*Larus argentatus*) in the Faroe Islands, the island of Texel (the Netherlands), and Sweden, respectively (Garben et al. 1982; Jaenson et al. 1994; Medlock et al. 2017). These seabird species also occur in Türkiye (eBird 2025a, b, c). Taken together, previous records and our observations suggest that *I. ricinus* may attach to the Yellow-legged gull as well as its other accidental hosts, especially when tick populations are limited to small and isolated habitats with inadequate host possibilities. In the present case, the attached female did not appear engorged, further supporting the interpretation of an accidental host record. A plausible explanation is that the limited availability of conventional mammalian hosts on Gull Island may increase the likelihood of atypical tick–host encounters. Accordingly, rather than indicating established use of seabirds as hosts, this finding highlights how ecological constraints in small and isolated habitats may promote occasional attachment to non-preferred hosts.

The second observation was the discovery of a male *H. marginatum* actively searching for a host on the island floor. *Hyalomma marginatum* is a medically important tick species in Türkiye, primarily due to its role as the main vector of CCHF virus and its predominance among *Hyalomma* species in the region (Estrada-Peña et al. 2017). This species is widely distributed across Türkiye, particularly in the Kelkit Valley (Akyildiz et al. 2021; Bursali et al. 2012; Kar et al. 2021), and has also been reported from the Sinop region (Albayrak et al. 2010). However, population densities in this region are relatively low, likely reflecting climatic and habitat conditions that are less favorable for the expansion of this predominantly xerophilic species. *Hyalomma marginatum* typically inhabits arid open habitats such as steppe, savannah, and scrubland valleys and hills, and is rarely associated with deciduous or mixed forests. Adult ticks usually feed on cattle, whereas immature stages parasitize ground-dwelling or ground-feeding birds, insectivores, and lagomorphs (Valcárcel et al. 2020). The presence of an adult *H. marginatum* on the island may reflect passive introduction via avian hosts, such as migratory passerines known to host immature stages (e.g., European Robin, *Erithacus rubecula*), with nymphs transported during stopovers and subsequently molting into adults (Bacak et al. 2024). However, according to regional ornithological observations, European Robins are rarely recorded on Gull Island. In contrast, the island is dominated by breeding yellow-legged gulls, which aggressively exclude other vertebrates from their nesting areas, further limiting opportunities for host availability. This observation is ecologically informative in that it illustrates the potential for *H. marginatum* to be passively dispersed by birds into atypical and spatially constrained habitats, while simultaneously underscoring the environmental limitations that restrict its

persistence and population establishment in insular ecosystems. Given the short distance between Gull Island and the mainland (87.7 m), the occurrence of *H. marginatum* on the island is not unexpected per se; however, it provides useful context for understanding how even very small landmasses can intermittently receive ticks from surrounding landscapes. In such confined environments, spatial compression may transiently increase the likelihood of host–tick encounters, despite the absence of ecological conditions required for long-term survival or establishment.

The third unexpected finding was the first report of *O. maritimus* in Türkiye. As shown in previous studies, this tick has been found in yellow-legged gull nests (Dupraz et al. 2017; Gomard et al. 2021; Khan et al. 2019). The species was redescribed by Hoogstraal et al. (1976). *O. maritimus* is a member of the Capensis group of *Ornithodoros* and is closely associated with marine birds and coastal ecosystems (Estrada-Peña et al. 2017; Hoogstraal et al. 1976). Because of this host and habitat preference, human bites are rare and usually occur in researchers, although the species has been linked to the human pathogen *Ortho-flavivirus nilense* (West Nile virus) (Sanz-Aguilar et al. 2020). It also serves as a vector for seabird-associated viruses such as *Orthonairovirus soldadoense* (Soldado virus), *Ortho-flavivirus meabanense* (Meaban virus), and piroplasms such as *Babesia* sp. YLG, whose pathogenic features remain poorly understood (Bonsergent et al. 2022, 2023; Chastel et al. 1979, 1985; Hubálek et al. 2014; Yu and Park 2024). However, with the adaptation of the yellow-legged gull to urban habitats, the risk of *O. maritimus* bites in pedestrians may increase.

Ornithodoros maritimus and *O. capensis* can be misidentified due to their morphological similarities, which may result in the deposition of misleading sequences in GenBank. We observed that many *O. capensis* sequences (KY825206, KR907245, AB076082, MT261041) were obtained from ticks collected from marine birds. Accordingly, in our phylogenetic tree, two of our three samples did not cluster directly with *O. maritimus* but instead grouped with *O. capensis* sequences (MT261041), despite the fact that these ticks were collected from a yellow-legged gull (*Larus michahellis*).

Only a limited number of *O. maritimus* specimens were recovered during the study period. As with the other tick species reported here, this pattern is best interpreted in an ecological and biogeographical context. Argasid ticks associated with seabirds typically reach high local densities only after prolonged persistence within stable nesting environments, where repeated host use allows populations to accumulate over successive breeding seasons. Demographic and dispersal models suggest that soft tick populations are subject to strong Allee effects during early colonization, resulting in slow local population growth at low densities and a lag in establishment before a viable breeding population is achieved (Kada et al. 2017). In this respect, the absence of previous records of *O. maritimus* from Türkiye—despite extensive acarological studies focused mainly on hard ticks (Mumcuoğlu et al. 2024)—is noteworthy. These observations are consistent with a scenario in which *O. maritimus* represents a recently established or newly introduced component of the Turkish tick fauna, for which population build-up within local seabird colonies may still be in an early phase, particularly in small and dynamic breeding sites such as Gull Island.

In conclusion, the observation of three different tick species on a small and isolated landmass with a surface area of only 7,838 m² demonstrates that there is no completely safe environment free from ticks and the diseases they may transmit. This situation poses a potential risk not only for animal health but also for human health. Our findings also empha-

size another important point: birds have a remarkable ability to spread ticks, including medically important species, to new areas beyond their original habitats. Such movements create opportunities for the introduction and establishment of ticks and tick-borne pathogens in previously unaffected ecosystems. In this context, expanding and intensifying research on tick fauna in atypical and unexpected locations will be critical for uncovering findings that may otherwise remain unnoticed.

The yellow-legged gull typically breeds in colonies on remote islands and inaccessible cliffs. However, over the past five decades, shifts in urban housing patterns have enabled this species to establish breeding populations on high rooftops in cities along the Black Sea coast, particularly in Istanbul. Their numbers continue to increase steadily. As an opportunistic species, yellow-legged gulls readily exploit anthropogenic food sources, such as household waste and food left for stray cats and dogs, which reduces the likelihood of food limitation. Importantly, during the breeding season (March–June), when gulls nest in close association with humans and domestic animals, they may facilitate the transmission of ticks to their chicks, other animals, and even humans. This potential public health risk warrants specific attention, and targeted investigations of nests in urban populations are strongly recommended.

In Türkiye, research on ticks associated with waterbirds and seabirds is still very limited, leaving significant gaps in our understanding of the role these hosts play in maintaining and disseminating tick populations. Addressing this gap by focusing on waterbird- and seabird-associated ticks could yield important insights into both the ecology of these parasites and their potential role in disease transmission. Moreover, research on soft ticks (family Argasidae) in Türkiye remains notably scarce. Concentrating scientific efforts on this group may not only reveal new faunistic records but also provide evidence of previously undetected tick-borne pathogens. Such studies will contribute to a more comprehensive understanding of tick diversity, host associations, and the risks they pose, ultimately strengthening preparedness for the prevention and control of tick-borne diseases.

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Author contributions AGK, ACO, ES and GA conceptualized the study and designed methodology. ACO and ES examined the gulls and collected the specimens. GA and SZA morphologically identified the ticks. GA performed the molecular and phylogenetic analyses. GA and SZA evaluated the results and wrote the manuscript. All authors contributed to editing and gave final approval for publication.

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Data availability The sequence data obtained from this study are freely available within the NCBI GenBank database under accession numbers PX106412, PX106413, and PX106414. The datasets generated during the current study are available in the Results and Supplementary files repository.

Declarations

Competing interests The authors declare no competing interests.

Ethical approval Ethical approval does not apply to for this study. The sampling of birds was approved by the General Directorate of Nature Conservation and National Parks, Ministry of Agriculture and Forestry, Republic of Turkey (protocol number: E-72784983-288.04-19026603).

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References

- Akyildiz G, Bente D, Gargili-Keles A, Vatansever Z, Kar S (2021) High prevalence and different genotypes of Crimean-Congo hemorrhagic fever virus genome in questing unfed adult *Hyalomma marginatum* in Thrace, Turkey. Ticks and Tick-borne diseases. 12:101622. <https://doi.org/10.1016/j.ttbdis.2020.101622>
- Albayrak H, Ozan E, Kurt M (2010) Molecular detection of Crimean-Congo haemorrhagic fever virus (CCHFV) but not West Nile virus (WNV) in hard ticks from provinces in Northern Turkey. Zoonoses Public Health 57:e156–e160. <https://doi.org/10.1111/j.1863-2378.2009.01316.x>
- Bacak E, Ozsemir AC, Akyildiz G, Gungor U, Bente D, Gargili-Keles A, Beskardes V, Kar S (2024) Bidirectional tick transport by migratory birds of the African-Western Palearctic flyway over Turkish thrace: observation of the current situation and future projection. Parasitol Res 123:37. <https://doi.org/10.1007/s00436-023-08069-x>
- Black WC, Piesman J (1994) Phylogeny of hard- and soft-tick taxa (Acari: Ixodida) based on mitochondrial 16S rDNA sequences. Proc Natl Acad Sci U S A 91:10034–10038. <https://doi.org/10.1073/pnas.91.21.10034>
- Bonsergent C, Vittecoq M, Leray C, Burkart L, McCoy KD, Malandrin L (2022) Characterization and diversity of *Babesia* sp. YLG, a new member of the peircei group infecting mediterranean yellow-legged gulls (*Larus michahellis*). 13:101852. Ticks and Tick-borne Diseases <https://doi.org/10.1016/j.ttbdis.2021.101852>
- Bonsergent C, Vittecoq M, Leray C, Jouglin M, Buysse M, McCoy KD, Malandrin L (2023) A soft tick vector of *Babesia* sp. YLG in Yellow-legged gull (*Larus michahellis*) nests. Peer Community J 3. <https://doi.org/10.24072/pcjournal.316>
- Bursali A, Keskin A, Tekin S (2012) A review of the ticks (Acari: Ixodida) of turkey: species diversity, hosts and geographical distribution. Exp Appl Acarol 57:91–104. <https://doi.org/10.1007/s10493-012-9530-4>
- Bursali A, Keskin A, Tekin S (2020) A contribution to the tick (Acari: Ixodidae) fauna of turkey: the first record of *Ixodes inopinatus* Estrada-Peña. Petney Acarological Stud 2:126–130. <https://doi.org/10.47121/acarolstud.706768>. Nava
- Celina SS, Černý J (2025) *Hyalomma marginatum* in Europe: The Past, Current Status, and Future Challenges—A Systematic Review. Transboundary and Emerging Diseases 2025, 7771431. <https://doi.org/10.1155/tbed/7771431>
- Černý J, Lynn G, Hrnková J, Golovchenko M, Rudenko N, Grubhoffer L (2020) Management options for *Ixodes ricinus*-associated pathogens: a review of prevention strategies. Int J Environ Res Public Health 17:1830. <https://doi.org/10.3390/ijerph17061830>
- Chastel C, Rogues G, Beaucournu JC (1979) Morphology and morphogenesis of Soldado virus (Hughes group); similarities with viruses of the Bunyaviridae family. Arch Virol 60:153–159. <https://doi.org/10.1007/BF01348031>
- Chastel C, Main AJ, Guiguen C, le Lay G, Quillien MC, Monnat JY, Beaucournu JC (1985) The isolation of Meaban virus, a new flavivirus from the seabird tick *Ornithodoros (Alectorobius) maritimus* in France. Arch Virol 83:129–140. <https://doi.org/10.1007/BF01309911>
- Cuadrado-Matías R, Moraga-Fernández A, Peralbo-Moreno A, Negro AI, Sánchez-Seco MP, Ruiz-Fons F (2024) Crimean-Congo haemorrhagic fever virus in questing non-*Hyalomma* spp. Ticks in Northwest Spain, 2021. Zoonoses Public Health 71:578–583. <https://doi.org/10.1111/zph.13130>

- Dietrich M, Gómez-Díaz E, McCoy KD (2011) Worldwide distribution and diversity of seabird ticks: implications for the ecology and epidemiology of tick-borne pathogens. *Vector Borne Zoonotic Dis* 11:453–470. <https://doi.org/10.1089/vbz.2010.0009>
- Duffy DC, Dautri A (1987) Diel rhythms of tick parasitism on incubating African Penguins. *Med Vet Entomol* 1:103–106. <https://doi.org/10.1111/j.1365-2915.1987.tb00329.x>
- Dupraz M, Toty C, Noël V, Estrada-Peña A, González-Solís J, Boulinier T, Dujardin J-P, McCoy KD (2016) Linking morphometric and genetic divergence with host use in the tick complex, *Ornithodoros capensis* sensu Lato. *Infect Genet Evol* 46:12–22. <https://doi.org/10.1016/j.meegid.2016.10.005>
- Dupraz M, Toty C, Devillers E, Blanchon T, Elguero E, Vittecoq M, Moutailler S, McCoy KD (2017) Population structure of the soft tick *Ornithodoros maritimus* and its associated infectious agents within a colony of its seabird host *Larus Michahellis*. *Int J Parasitology: Parasites Wildl* 6:122–130. <https://doi.org/10.1016/j.ijppaw.2017.05.001>
- eBird (2025a) Common Gull (*Larus canus*). eBird. <https://ebird.org/species/mewgul>. Accessed 3 September 2025
- eBird (2025b) European Herring Gull (*Larus argentatus*). eBird. <https://ebird.org/species/euhgull1>. Accessed 3 September 2025
- eBird (2025c) Northern Gannet (*Morus bassanus*). eBird. <https://ebird.org/species/norgan>. Accessed 3 September 2025
- Eren G, Açıcı M (2025) An updated checklist of ticks and mites (Acari) reported on reptiles of Türkiye: new records and new host-parasite associations. *Acarological Stud* 7:12–41. <https://doi.org/10.47121/acarolistud.1554694>
- Estrada-Peña A, Mihalca AD, Petney TN (2017) Ticks of Europe and North africa: A guide to species identification. Switzerland, Springer
- Garben AFM, Vos H, Bronswijk JEMH (1982) *Haemaphysalis punctata* Canestrini and Fanzago 1877, a tick of pastured sea dunes on the Island of Texel (The Netherlands). *Acarologia* 23:19–25
- Gomar Y, Flores O, Vittecoq M, Blanchon T, Toty C, Duron O, Mavingui P, Tortosa P, McCoy KD (2021) Changes in bacterial Diversity, composition and interactions during the development of the seabird tick *Ornithodoros maritimus* (Argasidae). *Microb Ecol* 81:770–783. <https://doi.org/10.1007/s00248-020-01611-9>
- Gray J, Kahl O, Zintl A (2021) What do we still need to know about *Ixodes ricinus*? Ticks and tick-borne diseases 12. 101682. <https://doi.org/10.1016/j.tbd.2021.101682>
- Guglielmone AA, Robbins RG, Apanaskevich DA, Petney TN, Estrada-Peña A, Horak IG, Shao RF, Barker SC (2010) The Argasidae, Ixodidae and Nuttalliellidae (Acari: Ixodida) of the world: a list of valid species names. *Zootaxa* 2528:1–28. <https://doi.org/10.11646/zootaxa.2528.1.1>
- Guindon S, Dufayard J-F, Lefort V, Anisimova M, Hordijk W, Gascuel O (2010) New algorithms and methods to estimate Maximum-Likelihood phylogenies: assessing the performance of PhyML 3.0. *Syst Biol* 59:307–321. <https://doi.org/10.1093/sysbio/syq010>
- Gunes T, Ataş M (2020) The prevalence of tick-borne pathogens in ticks collected from the northernmost Province (Sinop) of Turkey. *Vector-Borne Zoonotic Dis* 20:171–176. <https://doi.org/10.1089/vbz.2019.2513>
- Güneş T, Kaya S, Poyraz O, Engin A (2007) The prevalence of *Borrelia burgdorferi* sensu Lato in *Ixodes ricinus* ticks in the Sinop region of Turkey. *Turkish J Veterinary Anim Sci* 31:153–158
- Hall T (1999) BioEdit: a user-friendly biological sequence alignment editor and analysis program for windows 95/98/NT. *Nucleic Acids Symp Ser* 41:95–98
- Hekimoğlu O, Kuyucu AC, Ozer N (2020) Preliminary investigation on the genetic diversity and population structure of *Hyalomma marginatum* (Acari: Ixodidae) in Turkey. *Syst Appl Acarology* 25:1867–1882. <https://doi.org/10.11158/saa.25.10.10>
- Hekimoğlu O (2022) Phylogenetic placement of Turkish populations of *Ixodes ricinus* and *Ixodes inopinatus*. *Exp Appl Acarol* 88:179–189. <https://doi.org/10.1007/s10493-022-00750-7>
- Hekimoğlu O, Sağlam İK (2024) High Crimean-Congo hemorrhagic fever incidence linked to greater genetic diversity and differentiation in *Hyalomma marginatum* populations in Türkiye. *Parasites Vectors* 17:477. <https://doi.org/10.1186/s13071-024-06530-z>
- Hoogstraal H (1979) The epidemiology of tick-borne Crimean-Congo hemorrhagic fever in Asia, Europe, and Africa. *J Med Entomol* 15:307–417. <https://doi.org/10.1093/jmedent/15.4.307>
- Hoogstraal H, Clifford CM, Keirans JE, Kaiser MN, Evans DE (1976) The *Ornithodoros* (*Alectorobius*) *capensis* group (Acarina: ixodoidea: Argasidae) of the Palearctic and Oriental regions. *O.(A.) maritimus*: Identity, marine bird hosts, virus infections, and distribution in Western Europe and Northwestern Africa. *J Parasitol*, 62(5):799–810 <https://doi.org/10.2307/3278964>
- Hubálek Z, Rudolf I, Nowotny N (2014) Chapter Five - Arboviruses pathogenic for domestic and wild animals. In: Maramorosch K, Murphy FA (eds) *Advances in virus research*, vol 89. Academic, pp 201–275

- Jaenson TG, Tälleklint L, Lundqvist L, Olsen B, Chirico J, Mejlon H (1994) Geographical distribution, host associations, and vector roles of ticks (Acari: Ixodidae, Argasidae) in Sweden. *J Med Entomol* 31:240–256. <https://doi.org/10.1093/jmedent/31.2.240>
- Kada S, McCoy KD, Bouludier T (2017) Impact of life stage-dependent dispersal on the colonization dynamics of host patches by ticks and tick-borne infectious agents. *Parasites Vectors* 10:375. <https://doi.org/10.1186/s13071-017-2261-y>
- Kahl O, Gray JS (2023) The biology of *Ixodes ricinus* with emphasis on its ecology. *Ticks tick-borne Dis* 14:102114. <https://doi.org/10.1016/j.ttbdis.2022.102114>
- Kalyaanamoorthy S, Minh BQ, Wong TKF, von Haeseler A, Jermini LS (2017) ModelFinder: fast model selection for accurate phylogenetic estimates. *Nat Methods* 14:587–589. <https://doi.org/10.1038/nmeth.4285>
- Kar S, Yilmazer N, Akyildiz G, Gargili A (2017) The human infesting ticks in the City of Istanbul and its vicinity with reference to a new species for Turkey. *Syst Appl Acarology* 22:2245–2255. <https://doi.org/10.11158/saa.22.12.14>
- Kar S, Akyildiz G, Guven E, Bente D, Vatansever Z (2021) Monthly infestation characteristics of ticks on cattle in Thrace, a Crimean congo hemorrhagic fever-endemic area of Turkey. *Parasitol Res* 120:3395–3404. <https://doi.org/10.1007/s00436-021-07244-2>
- Karaardic H, Köse F, Öztürk Y (2022) Breeding biology of the Yellow-legged gull (*Larus michahellis*, Naumann, 1840): a small Island population in Southwestern Türkiye. *Commagene J Biology* 6:232–236. <https://doi.org/10.31594/commagene.1195049>
- Keskin A, Doi K (2025) Discovery of the potentially invasive Asian longhorned tick, *Haemaphysalis longicornis* neumann (Acari: Ixodidae) in Türkiye: an unexpected finding through citizen science. *Exp Appl Acarol* 94:47. <https://doi.org/10.1007/s10493-025-01015-9>
- Keskin A, Erciyas-Yavuz K (2018) Ticks (Acari: Ixodidae) parasitizing passerine birds in Turkey with new records and new Tick–Host associations. *J Med Entomol* 56:156–161. <https://doi.org/10.1093/jme/tjy151>
- Keskin A, Selçuk AY (2021) A survey for tick (Acari: Ixodidae) infestation on some wild mammals and the first record of *Ixodes trianguliceps* birula in Turkey. *Syst Appl Acarology* 26:2209–2220. <https://doi.org/10.11158/saa.26.12.1>
- Keskin A, Koprulu TK, Bursali A, Ozsemir AC, Yavuz KE, Tekin S (2014) First record of *Ixodes Arborecola* (Ixodida: Ixodidae) from Turkey with presence of *Candidatus rickettsia vini* (Rickettsiales: rickettsiaceae). *J Med Entomol* 51:864–867. <https://doi.org/10.1603/me13169>
- Khan J, Provencher J, Forbes M, Mallory M, Lebarbenchon C, McCoy K (2019) Parasites of seabirds: A survey of effects and ecological implications 82
- Kirwan GM, David TS, Pyle P, Sharpe CJ, Garcia E (2024) Yellow-legged gull (*Larus michahellis*), version 1.1. In: Keeney BK, Kirwan GM (eds) *Birds of the world*. Cornell Lab of Ornithology, Ithaca, NY, USA
- Lindsoe LK, Viljugrein H, Myrsetrud A (2024) Vector competence of *Ixodes ricinus* instars for the transmission of *Borrelia burgdorferi* sensu lato in different small mammalian hosts. *Parasites Vectors* 17:23. <https://doi.org/10.1186/s13071-023-06110-7>
- Mans BJ, Venzal JM, Munoz-Leal S (2022) Editorial: soft ticks as parasites and vectors. *Front Vet Sci* 9:1037492. <https://doi.org/10.3389/fvets.2022.1037492>
- Medlock JM, Hansford K, Vaux AGC, Simonsen W, Jensen J-K, Joensen C, Versteirt V, Hansen LJ (2017) Surveillance for *Ixodes ricinus* ticks (Acari, Ixodidae) on the Faroe Islands. *Ticks Tick-borne Dis* 8:190–195. <https://doi.org/10.1016/j.ttbdis.2016.11.001>
- Minh BQ, Nguyen MAT, von Haeseler A (2013) Ultrafast approximation for phylogenetic bootstrap. *Mol Biol Evol* 30:1188–1195. <https://doi.org/10.1093/molbev/mst024>
- Mumcuoglu KY, Bayrak N, Şenel E, Keskin A, Taşdemir A, Taylan Özkan A (2024) Bibliometric and scientometric analysis of acarological publications in Türkiye between the years 1992–2023. *Acarological Stud* 6(2):112–126. <https://doi.org/10.47121/acarolstud.1499068>
- Olsen KM (2010) *Gulls of Europe, Asia and North America*, Bloomsbury Publishing
- Orkun Ö, Karaer Z (2018) First record of the tick *Ixodes (Pholeoixodes) kaiseri* in Turkey. *Exp Appl Acarol* 74:201–205. <https://doi.org/10.1007/s10493-018-0219-1>
- Orkun Ö, Vatansever Z (2021) Rediscovery and first genetic description of some poorly known tick species: *Haemaphysalis kopetdaghica* Kerbabaev, 1962 and *Dermacentor raskemensis* Pomerantzev, 1946. *Ticks and Tick-borne Diseases* 12, 101726. <https://doi.org/10.1016/j.ttbdis.2021.101726>
- Pedersen BN, Jenkins A, Kjelland V (2020) Tick-borne pathogens in *Ixodes ricinus* ticks collected from migratory birds in Southern Norway. *PLoS ONE* 15:e0230579. <https://doi.org/10.1371/journal.pone.0230579>
- Ramos R, Ramirez F, Sanpera C, Jover L, Ruiz X (2009) Feeding ecology of yellow-legged gulls *Larus michahellis* in the Western mediterranean: a comparative assessment using conventional and isotopic methods. *Mar Ecol Prog Ser* 377:289–297. <https://doi.org/10.3354/meps07792>

- Sanz-Aguilar A, Payo-Payo A, Rotger A, Yousfi L, Moutailler S, Beck C, Dumarest M, Igual JM, Miranda MÁ, Torres MV (2020) Infestation of small seabirds by *Ornithodoros maritimus* ticks: effects on chick body condition, reproduction and associated infectious agents. Ticks and Tick-borne diseases 11. 101281. <https://doi.org/10.1016/j.ttbdis.2019.101281>
- Sultankulova KT, Shynybekova GO, Kozhabergenov NS, Mukhami NN, Chervyakova OV, Burashev YD, Zakarya KD, Nakhanov AK, Barakbayev KB, Orynbayev MB (2022) The prevalence and genetic variants of the CCHF virus Circulating among ticks in the Southern regions of Kazakhstan. Pathogens 11:841. <https://doi.org/10.3390/pathogens11080841>
- Tavassoli M, Zarrabi-Ahrabi S, Akyildiz G, Gargili-Keles A (2024) Crimean-Congo hemorrhagic fever, transfer patterns, vectors and history in Iran and neighboring countries. Veterinary Res Forum 15:575
- Trifinopoulos J, Nguyen L-T, von Haeseler A, Minh BQ (2016) W-IQ-TREE: a fast online phylogenetic tool for maximum likelihood analysis. Nucleic Acids Res 44:W232–W235. <https://doi.org/10.1093/nar/gkw256>
- Valcárcel F, González J, González MG, Sánchez M, Tercero JM, Elhachimi L, Carbonell JD, Olmeda AS (2020) Comparative ecology of *Hyalomma lusitanicum* and *Hyalomma marginatum* Koch, 1844 (Acarina: Ixodidae). <https://doi.org/10.3390/insects11050303>. Insects 11
- Yang Z (1994) Maximum likelihood phylogenetic Estimation from DNA sequences with variable rates over sites: approximate methods. J Mol Evol 39:306–314. <https://doi.org/10.1007/bf00160154>
- Yu K-M, Park S-J (2024) Tick-borne viruses: Epidemiology, pathogenesis, and animal models. One Health 19:100903. <https://doi.org/10.1016/j.onehlt.2024.100903>
- Zarrabi-Ahrabi S, Akyildiz G, Kar S, Gargili-Keles A (2023) Detection of the Crimean–Congo hemorrhagic fever virus genome In questing Ixodes spp. And haemaphysalis spp. In the Periurban forestry areas of istanbul: has a new biorisk emerged? Vector-Borne Zoonotic Dis 23:528–536. <https://doi.org/10.1089/vbz.2023.0023>
- Zarrabi-Ahrabi S, Pınarlık F, Akyıldız G, Kuşkucu M, Kar S, Ergönül Ö, Gargılı-Keleş A, on behalf of TEHV-BISG (2025) Human tick biting and tick-borne disease risk in Türkiye: systematic review. PLoS Negl Trop Dis 19:e0013092. <https://doi.org/10.1371/journal.pntd.0013092>

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