



## The Identification and Phylogenetic Analysis of Tick Species in Sheep in Mosul City

### Article Info.

#### Author

Baydaa Younis Al- Iahaibi, Eman Ghanim Suleiman

Department of Microbiology, college of veterinary medicine ,university of Mosul ,Mosul, Iraq.

**Corresponding Author Email Address:**  
[baydaaum18@uomosul.edu.iq](mailto:baydaaum18@uomosul.edu.iq)

#### Article History

Received: 28 January 2026

Revised: 17 March 2026

Accepted: 22 March 2026

e Published: 30 June 2026

**Article type:** Research Article

<https://doi.org/10.23975/bjvr.2026.169045.1278>

#### Abstract

Identify of the two types of ticks (*Hyalomma* and *Rhipicephalus*) was confirmed using the 16S rRNA and the COX1 gene, with molecular weights of 460 base pairs and 700 base pairs, respectively. There were four novel tick isolates discovered in sheep in the Mosul district in this study: *Rhipicephalus turanicus* (PV174207.1, PV174208.1) and *H. anatolicum anatolicum* (PV174205.1, PV174206.1). *Hyalomma anatolicum anatolicum* and *Rhipicephalus turanicus* that infest sheep in the Mosul district were discovered using DNA research and sequencing. Our isolates of *Hyalomma* were comparable to strains from India, Iraq, China, the United Arab Emirates, and Egypt, whereas *Rh. turanicus* and strains from China and Kazakhstan had 100% genetic similarity.

**Keywords:** Hard ticks , Diagnosis , Morphology , phylogenetic. Prevalence.

## Introduction

Ticks are obligatory ectoparasites that consume blood from mammals and disseminate a variety of illnesses worldwide (1). Numerous diseases, such as bacteria, viruses, and hemoprotozoa, are carried by ticks (2). The family Ixodidae, which includes numerous significant genera, (3). It directly affects animals by causing skin lesions (redness and irritation), anemia, paralysis, weight loss, and a reduction in milk supply (4).

Ixodidae classification and evolutionary conclusions have depended on morphometric features showing host specialization as the main contributing factor (5). The identification of tick species is now frequently done using molecular methods and DNA markers (6). To confirm tick species diagnosis, molecular techniques have been developed (7). DNA's ITS 2 region is a helpful method for molecular analysis, gene identification of tick types (8,9). The mitochondrial genes 12SrRNA, 16SrRNA, and COX1 have been widely used in animal phylogenetic studies. It is also known that at least one variable-length section of the mitochondrial genome, which does not encode any genes, contains components that regulate and trigger transcription and mtDNA replication in vertebrates and insects (10). Using microscopic diagnosis based on morphological criteria, it can occasionally be challenging to identify and distinguish between tick species, especially females of ticks that are damaged or engorged. Additionally,

## Materials and Methods

### collection of hard ticks

Ticks were taken from sheep of all ages and sexes in five areas of the Mosul district: Gogjali, Badoush, Al-Shura, College of Agriculture and Forestry, and Hammam AL Alil.

The ticks were affixed to various bodily parts of the animal, including the head, neck, ears, hind limbs, udder, etc. A piece of cotton soaked in 70% ethyl alcohol was used to remove the ticks using forceps with a pointed end.

### Extracting DNA from a tick sample

Sheep tick samples were used to extract DNA using a pre-made extraction kit (Qiagen). To analyze their genetic sequence using the polymerase chain reaction technique, thirty tick samples were chosen, fifteen of which were from the genus *Hyalomma* (The base of the capitulum is round in shape, two subanal plates that protrude outside the body, The scutum is ornate and festoons are present, the spiracles are comma in shape) and fifteen of which were from the genus *Rhipicephalus* (The body consists of the hexagonal capitulum with a clear waist at its junction with the trunk, The end of the body, especially in the middle is characterized by the presence of a caudal process). The primer listed in the table(1) was used to carry out the PCR reaction according to (11,12).

**Table (1) : The tick primers utilized in this study**

| Target gene | Primer                     | bp  | Reference |
|-------------|----------------------------|-----|-----------|
| 16SrRNA     | CCGGTCTGAACTCAGATCAAGT     | 460 | 11        |
|             | GCTCAATGATTTTTTAAATTGCTGT  |     |           |
| COX1        | GGTCAACAAATCATAAAGATATTGG  | 700 | 12        |
|             | TAAACTTCAGGGTGACCAAAAAATCA |     |           |

PCR reaction mixes were made with Master Mix. PCR mixes were done in 25 µl with the total concentration as given in the table (2).

**Table 2: PCR cycling settings for tick COX1 and 16SrRNA gene amplification**

| Phases                                 | Temp °C                | Time   | Cycle number |
|--|------------------------|--------|--------------|
| <b>Polymerase activation</b>           | 95                     | 10 min | 1X           |
| <b>Denature</b>                        | 95                     | 45 sec | 35X          |
| <b>Annealing* used for each primer</b> | 16SrRNA gene = 55 °C   | 45 sec |              |
| <b>Extension</b>                       | COX1 gene= 60 °C<br>72 | 1 min  |              |
| <b>Final Extension</b>                 | 72                     | 5 min  | 1X           |
| <b>Hold</b>                            | 4                      | 4 °C   | ∞            |

The agarose gel wells were filled with 5 µl of each PCR product. A 300 Am power source and the electrophoresis was conducted for an hour at 75 V using an electrophoresis tank filled with 1X TBE buffer. The conventional molecular weight marker was a 100 bp DNA marker in 6 µl.

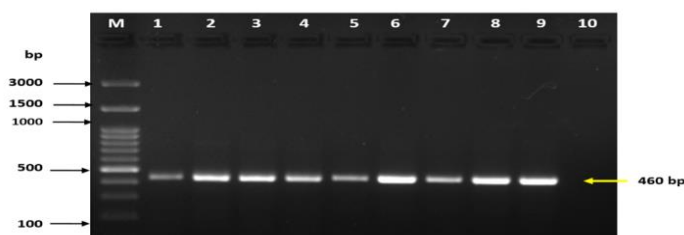
#### **DNA analysis of ticks**

In order to find the sequence of the target gene for the ten tick samples that tested positive, the PCR product using particular primers was analyzed for sequences in Macrogen, Korea. To

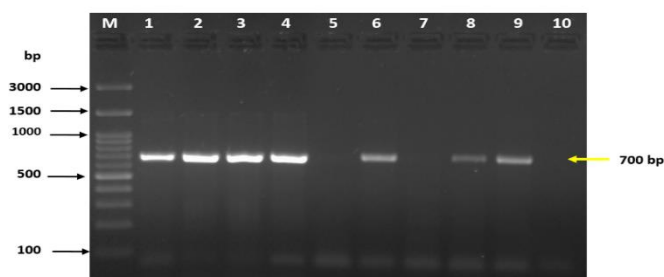
determine the phylogenetic relationship, particular bioinformatics software was used to evaluate the text-based genomic sequence files that were obtained.

## Results

Thirty tick samples, fifteen from the genus *Rhipicephalus* and fifteen from the genus *Hyalomma* were used to extract DNA. To validate the microscopic diagnosis of ticks, these samples underwent amplification using COX1 and 16S rRNA genes. According to the results, all tick samples showed positive DNA bands with a response rate of 460 base pairs when the 16SrRNA primer was employed, as shown in Figure (1). When the COX1 primer was employed, 26 extracted DNA samples yielded positive results for the tick DNA bands at a response rate of 700, as shown in Figure 2.



**Figure 1: PCR for the 16SrRNA gene of the tick genus Lane M: A 100-base pair DNA ladder. Samples in lanes 1–9 are positive. Negative control lane 10.**



**Figure 2: COX1 gene of tick genera using polymerase chain reaction (PCR). Positive samples in lanes (1-4, 6, 8, 9). Negative samples are found in lanes 5 and 7. Lane 10 is the negative control.**

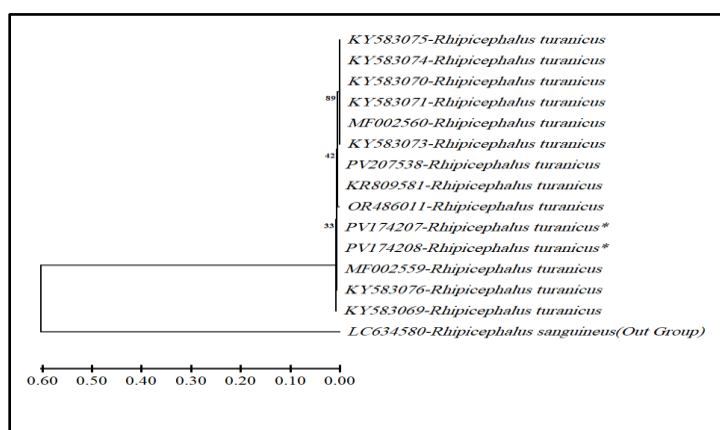
### Sequencing of 16SrRNA gene fragment

*Rhipicephalus turanicus* and *Hyalomma anatolicum anatolicum*, two species of hard ticks that infest sheep in the Mosul district, were identified through sequencing at GenBank. *R. turanicus* appears more commonly in our study. Four tick isolates were discovered, as indicated in Table (3).

**Table 3: Ticks isolated from sheep found using the BLAST software at the NCBI**

| NCBI Accession Number | Isolate Name | Tick species and Strain               |
|-----------------------|--------------|---------------------------------------|
| PV174205.1            | BE-H1        | <i>Hyalomma anatolicum anatolicum</i> |
| PV174206.1            | BE-H2        | <i>Hyalomma anatolicum anatolicum</i> |
| PV174207.1            | BE-R1        | <i>Rhipicephalus turanicus</i>        |
| PV174208.1            | BE-R2        | <i>Rhipicephalus turanicus</i>        |

*Rhipicephalus turanicus*, which diagnosed in this study, has a 100% genetic match with isolates isolated in China and Kazakhstan was discovered during Phylogenetic study of our isolates of *Rh. turanicus* and *H. anatolicum anatolicum* as indicated in table (4) and figure (3). According to Table (5) and Figure (4), our *H. anatolicum anatolicum* isolates were completely identical to those discovered in Iraq, the United Arab Emirates, Egypt, India, and China.



**Figure 3: *Rhipicephalus turanicus* phylogenetic tree from Mosul, Iraq (\*).**

Table 4 :Shows the percentage identity of *Rhipicephalus turanicus* using blast results from Genbank (NCBI) based on incomplete 16SrRNA gene sequence.

| Sample Accession Number | Ticks                          | Query Cover % | Identic Number % | The accession number for Genbank | Identification of the country |
|-------------------------|--------------------------------|---------------|------------------|----------------------------------|-------------------------------|
| PV174207                | <i>Rhipicephalus turanicus</i> | 100           | 100              | MF002559                         | China                         |
|                         |                                | 100           | 100              | KY583076                         | China                         |
| PV174208                |                                | 100           | 99.77            | PV207538                         | China                         |
|                         |                                | 100           | 99.77            | KR809581                         | China                         |
|                         |                                | 100           | 99.53            | KY583069                         | China                         |
|                         |                                | 100           | 99.53            | OR486011                         | Kazakhstan                    |
|                         |                                | 100           | 99.30            | MF002560                         | China                         |
|                         |                                | 100           | 99.30            | KY583071                         | China                         |
|                         |                                | 100           | 99.30            | KY583070                         | China                         |
|                         |                                | 100           | 99.30            | KY583075                         | China                         |
|                         |                                | 100           | 99.30            | KY583073                         | China                         |
|                         |                                | 100           | 99.30            | KY583074                         | China                         |

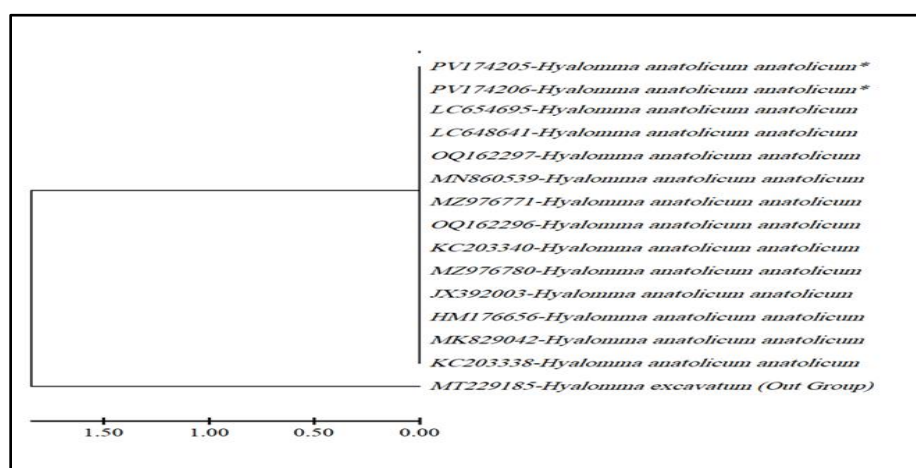


Figure 4: *Hyalomma anatolicum anatolicum* phylogenetic tree from Mosul- (\*).

**Table 5: Shows percentage identity of *Hyalomma anatolicum anatolicum* utilizing blast results from Genbank (NCBI) based on incomplete 16SrRNA gene sequences.**

| Sample Accession Number | Ticks discovered                      | Coverage of queries % | identical number % | The accession number for Genbank | Identification of the country |
|-------------------------|---------------------------------------|-----------------------|--------------------|----------------------------------|-------------------------------|
| PV174205                | <i>Hyalomma anatolicum anatolicum</i> | 100                   | 100                | LC654695                         | India                         |
| PV174206                | <i>Hyalomma anatolicum anatolicum</i> | 100                   | 100                | LC648641                         | India                         |
|                         |                                       | 100                   | 100                | OQ162297                         | Iraq                          |
|                         |                                       | 100                   | 100                | MN860539                         | China                         |
|                         |                                       | 100                   | 100                | MZ976771                         | United Arab Emirates          |
|                         |                                       | 100                   | 100                | OQ162296                         | Iraq                          |
|                         |                                       | 100                   | 100                | KC203340                         | China                         |
|                         |                                       | 100                   | 100                | MZ976780                         | United Arab Emirates          |
|                         |                                       | 100                   | 100                | JX392003                         | India                         |
|                         |                                       | 100                   | 100                | HM176656                         | India                         |
|                         |                                       | 100                   | 100                | MK829042                         | Egypt                         |
|                         |                                       | 100                   | 100                | KC203338                         | China                         |

## Discussion

Training and experience are necessary for the microscopic diagnosis of ticks (13). According to (14), it was challenging to identify species of the genera *Rhipicephalus* and *Hyalomma* using morphological characterization. Mitochondrial cytochrome oxidase subunit 1 (COX1) and ribosomal ribonucleic acid (16SrRNA) were the two types of genes employed in this study to differentiate the *Hyalomma* and *Rhipicephalus* of hard ticks identified in sheep in the Mosul district.

When utilized to differentiate the tick species, these genera were adequate and successful. This outcome was in line with findings in Australia (15) and in China, (16), in Egypt (17), in Al-Najaf \Iraq (18), in Texas (19), in the Duhok governorate(20).

In Al-Najaf Province, Iraq, *Rh. sanguineus* and *H. dromedarii* were identified in ruminants using COX1, 18SrRNA genes (21). According to (22), genetic approaches will become a mainstream technique for tick identification, supplementing microscopical identification of ticks.

*Rhipicephalus* , *Hyalomma* species are the most common tick genera found in ruminants in the majority of Iraqi provinces (22,23) , While (2) indicated that the 16SrRNA is best used for genus level identification, while the (COX1) is the most useful primer for tick diagnosis at the species level,(11) claimed that molecular analysis will become the standard tool for tick detection, suggesting that the morphological identification and mitochondrial 16SrRNA gene appear to be an effective primer for detecting genetic linkages between closely related tick species.

In the current study, we used 16SrRNA genes for hard tick species detection to diagnose *Rhipicephalus* spp. and *Hyalomma* spp. in order to address issues with morphological tick diagnosis. Additionally, (24,25) employed that 16SrRNA used to identify tick species in Egypt and to discover *Rhipicephalus turanicus* in Albania and China . 16SrRNA sequences were used to create the phylogenetic tree for this investigation. Phylogenetic analysis and trees are useful tools for determining the genetic links of closely related species in several biological study domains (26). Although it doesn't seem to help compare far related taxa, the mitochondrial 16SrRNA gene seems to be an effective marker for determining genetic relationships among tick species that are closely related (27). (25) identified *Rhipicephalus turanicus* in Albania and China, (24) identified tick species in Egypt using the same identifier,(28) used 16SrRNA to identify tick species in ruminants in Iraq's Duhok Governorate. In An Najaf Province, Iraq, (21) used 18S rRNA gene markers and cytochrome oxidase 1 (COX1) to identify several tick species. These studies all showed that these genetic markers are capable of distinguishing between several tick species, especially those belonging to the genus *Rhipicephalus*, *Hyalomma*.

## Conclusion

Two dominant hard tick species infesting sheep were identified in Mosul district, *Hyalomma anatolicum anatolicum* and *Rhipicephalus turanicus* and Molecular markers, particularly 16SrRNA and (COX1), prove to be reliable and effective tools for the confirmation of tick species

## Conflict of Interest

The authors declare that there is no conflict of interest associated with this study.

## Ethical Approval

The research Ethics Committee approved this work.

## References

- 1-Chhillar, S., Chhilar, J.S., and Kaur, H.(2014). Investigation on some hard ticks (Acari: Ixodidae)infesting domestic buffalo and cattle from Haryana, India. *Journal of Entomology and Zoology Studies*.2(4):99-104.
- 2- Guglielmone, A. A., Apanaskevich, D. A., Estrada-Peña, A., Robbins, R. G., Petney, T. N., and Horak, I. G. (2014). The hard ticks of the world: (Acari: Ixodida: Ixodidae). In *The Hard Ticks of the World: (Acari: Ixodida: Ixodidae)*. Springer, Dordrecht 10 : 978-994. doi:[10.1007/978-94-007-7497-1](https://doi.org/10.1007/978-94-007-7497-1).
- 3-Barker, S. C., and Murrell, A. (2004). Systematics and evolution of ticks with a list of valid genus and species names. *Parasitology*. 129(S1):S15-S36. doi: [10.1017/s0031182004005207](https://doi.org/10.1017/s0031182004005207).
- 4-Sen, P. C., Farjana, T., Khatun, F., Yasin, M. G., Rahman, M. A.,Aktar, M. T. D., Mondal, M. M. H., and Alim, M. A. (2012). A Cross Sectional Study on the Tick Infestation in Cattle in Faridpur District of Bangladesh. *Bangladesh Vet J*. 46 (1-4):19-30.
- 5-Nava, S., Caparros, J. A., Mangold, A. J., and Guglielmone, A. A. (2006). Ticks (Acari : Ixodida : Argasidae, Ixodidae) Infesting Humans in Northwestern Cordoba Province, Argentina. *Medicina (Buenos Aires)*. 66: 225-228.
- 6-Goul, H., Xuel, H., Yin, H., Luo, M .J., and Sun , X.(2018).Molecular characterization of hard ticks by cytochrome oxidase subunit 1 sequences .*Korean J Parasitol* . 56(6) :583-588. doi: [10.3347/kjp.2018.56.6.583](https://doi.org/10.3347/kjp.2018.56.6.583).
- 7-Murrell, A., Campbell, N. J., and Barker, S. C. (2001). Phylogenetic analyses of rhipicephaline ticks indicate that the genus *Rhipicephalus* is paraphyletic. *Mol Phylogenet Evol*. 16: 1- 7. doi: [10.1006/mpev.2000.0762](https://doi.org/10.1006/mpev.2000.0762).
- 8-Rees, D., Dioli, M., and Kirkendall, R. (2003). Molecular and morphology: evidence for cryptic hybridization in Africa *Hyalomma* (Acari: Ixodidae). *J. Molecul. Phylogenetic Evolution*.27:131-142. doi: [10.1007/s10493-021-00652-0](https://doi.org/10.1007/s10493-021-00652-0).
- 9-Abdigoudarzi, M., Ahmed, J., Seitzer, U., and Noureddine, R. (2011). rDNA ITS 2 identification of *Hyalomma*, *Rhipicephalus*, *Dermacentor* collected from different regions in Iran. *Adv. Stud. Biol*. 3: 221-238.
- 10-Hwang, U. W., Kim, W., Tautz , D., and Friedrich, M. (1998). Molecular phylogenetics at the Felsenstein zone: approaching the Strepsiptera problem using 5.8 S and 28S rDNA sequences. *Molecular phylogenetics and evolution*. 9(3): 470-480. doi: [10.1006/mpev.1998.0518](https://doi.org/10.1006/mpev.1998.0518) .
- 11- Mangold, A. J. ,and Bargues, M .D. (1998). Mitochondrial 16SrDNA sequences and phylogenetic relationships of species of *Rhipicephalus* and other tick genera among Metastriata ( Acari : Ixodidae ). *Parasitol Res*. 84: 478-484. doi: [10.1007/s004360050433](https://doi.org/10.1007/s004360050433).

- 12- Fallatah, S. A.; Ghallab, E.H. and Khater, E.I.(2019). Phylogenetic diversity and DNA barcoding of the camel tick *Hyalomma dromedarii* (Acari: Ixodidae) of the Eastern region of Saudi Arabia. *Tropical Biomedicine Vol. 36 (2)*: 390–401.
- 13- Ganjali, M., Haddadzadeh, H., and Shayan, P. (2011). Nucleotide sequence analysis of the second Internal Transcribe Spacer 2 in *Hyalomma anatolicum anatolicum* in Iran. *Inter. J. Vet. Res. 5*: 89-93.
- 14- Rumer, L., Sheshukove, O., Dautel, H., Mantke, O., and Niedrig, M. (2011). Differentiation of medically important Euro-Asian tick species *ixodes ricinus*, *ixodes persulcatus*, *ixodes hexagonus*, and *dermacentor reticulatus* by polymerase chain reaction. *Vector-Borne and Zoonotic Diseases. 11*: 899-905. doi: [10.1089/vbz.2009.0191](https://doi.org/10.1089/vbz.2009.0191).
- 15- Erster, O., Roth, A., Wolkomirsky, R., Leibovich, B., and Shkap, V. (2013). Comparative analysis of mitochondrial markers from four species of *Rhipicephalus* (Acari: Ixodidae). *Vet. Parasitol. 198(3-4)*:364-70. doi: [10.1016/j.vetpar.2013.09.005](https://doi.org/10.1016/j.vetpar.2013.09.005)
- 16- Lv, J., Wu, S., Zhang, Y., Chen, Y., Feng, C., Yuan, X., Jia, G., Deng, J., Wang, C., Wang, Q., Mei, L., and Lin, X. (2014 ): Assessment of four DNA fragments (COX1, 16SrDNA, ITS2, 12SrDNA) for species identification of the Ixodida (Acari: Ixodida). *Parasites and Vectors. 7*:1-11. doi: [10.1186/1756-3305-7-93](https://doi.org/10.1186/1756-3305-7-93).
- 17- Alsarraf, M., Mierzejewska, E.J., Mohallal, E.M.E., Behnke, J.M., and Bajer, A. (2017). Genetic and phylogenetic analysis of the ticks from the Sinai Massif, Egypt, and their possible role in the transmission of *Babesia behnkei*. *Exp Appl Acarol. 72(4)*:415-427. doi: [10.1007/s10493-017-0164-4](https://doi.org/10.1007/s10493-017-0164-4).
- 18- AL-Fatlawi, M. A.A., Ali, M. J., and Albayati, H. H. (2018). Morphological and phylogenetic study of *Hyalomma anatolicum* in Al-Najaf, Iraq. *Iraqi Journal of Veterinary Sciences.32(2)*: 261-266.
- 19- Abouel hassan, E.M., El-Gawady, H.M., AbdelAal1, A.A., El -Gayar, A.K., and Esteve, M.D. (2019). Comparison of some molecular markers for tick species identification. *J Arthropod-Borne Dis. 13(2)*:153-164.
- 20- Ismael , S.S., and Omer, L.T. (2020). Morphological and molecular study of hard ticks species that infested small ruminants in Duhok governorate , Kurdistan region, Iraq. *Basrah Journal of Veterinary Research. 19 (1)*:88-108. doi:[10.23975/bjvetr.2020.170615](https://doi.org/10.23975/bjvetr.2020.170615).
- 21- Al-Husseini , M.T. (2021). Molecular identification of three species of hard ticks (Acari: Ixodidae) collected on Al-Najaf Province, Iraq. *Annals of R.S.C.B. 25(4)*: 361 – 370.
- 22- Mustafa, B.H., and Faraj, H. (2013). Resistance of Hard ticks (Ixodidae) with some acaricide in cattle (naturally infestation) in Sulaimani governorate fields –Kurdistan regional Iraq. *J. Agr. Sci. Tech. 3 (11)*: 927-934 .

- 23- Dobson, S.J., and Barker, S.C. (1999). Phylogeny of the hard ticks (Ixodidae) inferred from 18SrRNA indicates that the genus Aponomma is paraphyletic. *Mol Phylogenet Evol.* 11(2): 288-295. doi: [10.1006/mpev.1998.0565](https://doi.org/10.1006/mpev.1998.0565).
- 24- Abdullah, H.A., El-Molla , A., Salib, F.A., Allam, N.T., Ghazy, A.A., Abdel, S.S.(2016). Morphological and molecular identification of the brown dog tick *Rhipicephalus sanguineus* and the camel tick *Hyalomma dromedarii* (Acari: Ixodidae) vectors of Rickettsioses in Egypt. *Vet World.* (10):1087-1101. doi: [10.14202/vetworld.2016.1087-1101](https://doi.org/10.14202/vetworld.2016.1087-1101).
- 25- Li ,H.Y., Zhao, S.S., Hornok, S., Farkas, R., Guo, L.P., Chen, C.F., Shao, R.F., Lv, J.Z., and Wang, Y.Z.(2017) Morphological and molecular divergence of *Rhipicephalus turanicus* tick from Albania and China. *Exp Appl Acarol.* 73:493-499. doi: [10.1007/s10493-017-0189-8](https://doi.org/10.1007/s10493-017-0189-8).
- 26- Yang, Z., and Rannala, B.(2012). Molecular phylogenetics: Principles and practice. *Nat Rev Genet.* 13:303-314. doi: [10.1038/nrg3186](https://doi.org/10.1038/nrg3186) .
- 27- Norris, D.E., Klompen, J., Keirans, J.E., Black ,W.C.(1996). Population genetics of *Ixodes scapularis* (Acari: Ixodidae) based on mitochondrial 16S and 12S genes. *J Med Entomol.* 33:78-89. doi: [10.1093/jmedent/33.1.78](https://doi.org/10.1093/jmedent/33.1.78).
- 28- Ismael , S.S., and Omer, L.T. (2021).Molecular identification of new circulating *Hyalomma asiaticum asiaticum* from sheep and goats in Duhok governorate, Iraq. *Iraqi Journal of Veterinary Sciences.*35 (1):79-83.doi:[10.33899/ijvs.2020.126330.1298](https://doi.org/10.33899/ijvs.2020.126330.1298).

## تحديد وتحليل السلالات الوراثية لأنواع القراد في الأغنام في مدينة الموصل

بيداء يونس محمود وإيمان غانم سليمان

فرع الاحياء المجهرية, كلية الطب البيطري , جامعة الموصل , موصل , العراق.

### الخلاصة

استخدم كل من جين 16SrRNA وجين COX1 اللذين يبلغ وزنهما الجزيئي 460 و700 زوجا قاعديا لتأكيد تشخيص كل من *Rhipicephalus* و *Hyalomma* في هذه الدراسة و تم تصنيف نوعين من القراد الصلب من خلال الدراسة الجزيئية والتسلسل الجيني، وهما *Hyalomma anatolicum anatolicum* و *Rhipicephalus turanicus* اللذان يصيبان الأغنام في قضاء الموصل، وكان النوع *Rhipicephalus turanicus* أكثر تكراراً في هذه الدراسة، وتم تسجيل أربع عزلات جديدة من القراد في الأغنام في قضاء الموصل: وهي (PV174206.1, PV174205.1) *Hyalomma anatolicum anatolicum* و (PV174207.1, PV174208.1) *Rhipicephalus turanicus* بين (100%) كان هناك تشابه وراثي بين *Hyalomma anatolicum anatolicum* مع العزلات المسجلة في الصين وكازاخستان، بينما كانت عزلتنا *Hyalomma anatolicum anatolicum* (PV174205.1, PV174206.1) قريبة من العزلات المسجلة في العراق والإمارات العربية المتحدة ومصر والهند والصين بنسبة تشابه 100%.

الكلمات المفتاحية: القراد الصلب ، التشخيص، الصفات الشكلية، النشوء والتطور ،انتشار.