



Hematological, Biochemical, and Pathological Study of Hemomycoplasmosis in One-Humped Camels in Basrah Governorate, Iraq



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THE objectives of our study were to investigate Hemomycoplasmosis in camels of Basrah, Iraq using blood smears stained with Giemsa and the final diagnosis was confirmed with PCR. The study was conducted to examine 100 local camel breeds (8 months – to 5 years old) of both sexes. Results indicated that diseased camels showed different clinical manifestations. The phylogenetic tree genetic relationship analysis showed that the local *Mycoplasma hemolamae* isolates showed closed genetics related to NCBI BLAST *Mycoplasma hemolamae* UK isolate (JF495171.1). Results also indicated macrocytic hypochromic anemia with a significant increase in ESR. Leucocytosis with lymphocytosis was also indicated with a significant difference in clotting factor indices, Furthermore, a significant rise in ALT, AST, Total bilirubin, Blood urea nitrogen (BUN), and Icteric indices in addition to low protein values as well as a substantial difference in acute phase response in diseased camels than in controls was registered. paleness of internal organs, splenomegaly, and enlargement of kidneys with hepatomegaly was detected on post-mortem changes, However, severe white pulp atrophy, as well as a hemosiderin-laden macrophage in the spleen beside degenerated renal tubuleepithelial cells and atrophy of glomeruli with a dilated central vein and pericentral vein in the kidney, infiltration of inflammatory cells which could refer to an area of necrosis in the central hepatic region in the liver was also indicated in the histopathological examinations. It has been concluded that Hemomycoplasmosis was still circulating in the Iraq environment; therefore, strictly applying the control measures is advised.

Keywords: Camels, Diagnosis, Hemomycoplasmosis, PCR.

Introduction

Camels are versatile animals that have been used for transportation and the production of milk, wool, and meat in arid and semi-arid regions of the world since ancient times. Those animals have lost their former importance as a result of industry progress and technology in all fields, However, camel breeding is now mostly for meat production. These types of animals are subjected to a variety of diseases, however, some of which are zoonotic and inflict significant economic losses [1-3].

Hemomycoplasma spp. causes haemotropic mycoplasmosis in animals. It is an important infectious disease characterized by anemia, weakness and emaciation, and mostly death of infected animals [4]. Moreover, *Mycoplasma haemolamae*, the causative species in camelids, which was previously recognized as eperythrozoon [5,6].

The disease is extremely common in different places of the world including Africa, America, southern Europe, and central Asia, and

transmitted mechanically by different species of ticks [4,7]. Furthermore, the disease was circulated in different rejoin of Iraq [8-11].

According to DNA sequence analysis of the 16 S small subunit ribosomal RNA gene, *Mycoplasma haemolamae* resembled other Hemomycoplasma spp. such as *Mycoplasma wenyonii*, *Mycoplasma suis*, and *Mycoplasma haemofelis*, and were thus classed as Haemotrophic mycoplasmas within the Mycoplasmagenus (Haemoplasmas) [12,13]. Moreover, Depending on the specific organism, dose, and host susceptibility, the effects of infection could be ranged from subclinical to fatal anemia, However, individuals who are immunocompromised or have a simultaneous condition are more likely to get hemoplasmas [5].

The disease was registered in cows, buffaloes, and sheep in Basrah Governorate and tested positive for hemomycoplasmosis [10,11,14]. Nevertheless, no Information's concerning Hemomycoplasmosis in camels at Basrah governorate was encountered and little knowledge was provided, Therefore, This study was aimed to hematological, biochemical, and pathological studies of Hemomycoplasmosis in one-humped camels at Basrah, Iraq.

Material and Methods

The current work conducted to examine 100 local camel breeds. Eighty local camel breeds of different ages ranging between (8 months to 5 years old) and of both sexes showing signs of lethargy, anemia as well as emaciation and Twenty (20) clinically normal camels served as control group. Clinical and laboratory examinations was applied to both animal groups and parasitic load was screened according to standard methods. Twelve (12) milliliters of jugular vein blood were aspirated from each camel which was separated as follow, 3 milliliter of blood mixed with

Ethylene diamine tetra acetic acid (EDTA) were used to measure, Total erythrocyte count (RBC), The concentration of hemoglobin (Hb), Packed cell volume (PCV), Total platelet count, Mean volume of platelets and its distribution width, and Total leukocytes count, (HEMATOLOGICAL ANALYZER, GENEX, USA), Moreover, Clotting time was estimated according to (Dayyal, 2016) [15]. Giemsa stain blood smears were used to calculate Differential leukocytes count (DLC) [16]. In addition, 3 milliliter of the blood was mixed with the Trisodium citrate (using plasma) for estimation of Prothrombin time and activated partial thromboplastin time according to (BIOLABO / FRANCE). Furthermore, ESR is estimated according to Harvey, 2012[16] using the Wintrobe method.

Serum was extracted for spectrophotometric biochemical analysis (using commercial kits) for estimation of ALT, AST, Total protein, Blood urea nitrogen (BUN) and Icteric index according the manufacture instructions of (ROCHE DIAGNOSTICS, INDIANAPOLIS, GMBH, GERMANY).

In the present study determination of Acute phase response was done by determination of Haptoglobin (Haptoglobin Serum ELISA Technique) was applied following the manufacturer instructions of (BIOTECHNOLOGY CO -CHINA), However, estimation of the Fibrinogen time was done by using plasma following the manufacturer's instructions of (BIOLABO, FRANCE).

The Real-Time PCR and PCR primer for direct detection of *Mycoplasma haemolamae* were designed in this study using NCBI Genbank sequence database (JF495171.1) and Primer 3 plus primer design online software and obtained from (MACROGEN/ KOREA) as the following Table 1:

TABLE 1. qPCR primers and probe.

| Primers | | Sequence (5'-3') | Product size |
|--|---|-------------------------------|--------------|
| <i>16S ribosomal RNA gene</i> qPCR primer | F | CGCAATGGGATTGAGATATGGC | 87bp |
| | R | ATTGCTCCATCAGGCTTTTCG | |
| <i>16S ribosomal RNA gene</i> qPCR probe | | FAM-ACGGGAAGCAGCAGTGAGGA-BHQ1 | |

Real-Time PCR (qPCR)

The qPCR technique was performed for direct detection of *Mycoplasma haemolamae* based 16S ribosomal RNA gene and the technique was carried out according to the following steps:

Real-Time PCR master mix preparation

With 20µL final volume the master mix was prepared using (GoTaq® qPCR Master Mix) according to company instructions (Table 3):

The PCR micro tube transfer into the Exispin vortex centrifuge at 3000rpm for 3 minutes. Then placed in Real-time PCR Thermocycler (BioRad, USA).

Real-Time PCR Thermocycler procedure

Real-Time PCR thermocycler procedure were set according to primer annealing temperature and qPCR master mix kit instructions as the following (Table 4):

The DNA sequencing was carried out to identify genetic relationship analysis in 16S ribosomal RNA gene of local *Mycoplasma haemolamae* isolates (IQ-Basrah-No.1 and IQ-Basrah-No.5) related to NCBI-Blast related country *Mycoplasma haemolamae* isolate.

Post mortem macroscopic examination of the of hemomycoplasmosis includes an examination of the spleen, kidney, and liver, Moreover, Specimens for the histopathology were taken from the mentioned organs, All the manufacturing tissues will be stained with the standard hematoxylin and eosin stain and examined under a light microscope [17].

Statistical analysis

Statistics in the current study were calculated according to the SPSS program, However,

TABLE 2. Specific primer used for detection of *Mycoplasma haemolamae* in PCR technique.

| Primers | | Sequence (5'-3') | Product size |
|-------------------------------|---|----------------------|--------------|
| <i>16S ribosomal RNA gene</i> | F | CTAAATTAAAGGGGCGCCGC | 546bp |
| <i>PCR primer</i> | R | TACTCGCCTTAGCCTCTGGT | |

TABLE 3. Real-Time PCR master mix preparation:

| qPCR Master mix | Volume |
|---|--------|
| DNA template 5-50ng | 5µL |
| qPCR 16SrRNA gene Forward primer (10pmol) | 1µL |
| qPCR 16SrRNA gene Reverse primer (10pmol) | 1µL |
| TaqMan probe (20pmol) | 1µL |
| qPCR master mix | 10 µL |
| Nuclease free water | 2 µL |
| Total volume | 20µL |

TABLE 4. qPCR Thermocycler procedure.

| Step | Condition | Cycle |
|---------------------|--------------|-------|
| Pre-Denaturation | 95 °C 5 min | 1 |
| Denaturation- | 95 °C 20 sec | |
| Annealing/Extension | 60 °C 1min. | 40 |
| Scan or Detection | | |

the comparison between the two groups (The diseased and control group) analyzed using the student *t*. test. Moreover, the Mean and standard error of the mean was also calculated, and $P < 0.05$ is the statistical value used between the study groups [18].

Results

Results indicated that diseased camels exhibited signs of, paleness of mucus membranes, loss of appetite, emaciation, diarrhea and/or constipation, rough hair coat, lacrimation, enlargement of superficial lymph nodes, coughing, recumbency and increased body temperature, respiratory and heart rates.

On stained blood smears, The causative organism *Mycoplasma hemolamae* has been seen in its rod shape, However, it also appears as a small coccoid form as a single or in form of chains on the cell membranes of infected, However, parasitemia was more than 100% (Fig.1).

Diagnosis of *Mycoplasma hemolamae* was confirmed by PCR technique and results showed that the Agarose gel electrophoresis image that exhibited the polymerase chain product analysis of 16S ribosomal RNA gene in *Mycoplasma hemolamae* from extracted DNA of blood samples was found in all blood samples that examined, However, the positive samples were indicated at 546bp (Fig.2).

The phylogenetic tree genetic relationship analysis showed that the local *Mycoplasma*

hemolamae isolates (IQ-Basrah-No.1 and IQ-Basrah-No.5) showed closed genetics related to NCBI BLAST *Mycoplasma hemolamae* UK isolate (JF495171.1) at total genetic change (0.03-0.01%). (Fig.3, Table 5).

Concerning the blood changes, results indicated a significant decrease in RBC count, Hb concentration, PCV, in diseased camels than in controls which reflected macrocytic hypochromic anemia. ESR was significantly increased ($P < 0.05$) in diseased camels compared with control group (Table 6).

Moreover, an increase values significantly has been detected in total leukocytes count in infected camels with Hemomycoplasmosis than in the control group, Furthermore, lymphocytosis ($P < 0.05$) was detected in diseased camels than in the control group (Table 7).

Concerning the indices of clotting factors, the results of the current study indicated a significant decrease in total platelet count in diseased camels than in controls, Whereas, a significant rise has been encountered in the values of Mean volume of platelets and its distribution width, Clotting time, Prothrombin time and the Activated partial thromboplastin time in diseased camels than in controls (Table 8).

The results of the biochemical changes of diseased camels and controls revealed a significant increase ($P < 0.05$) detected in ALT, AST, Total bilirubin, BUN, and Icteric index values in

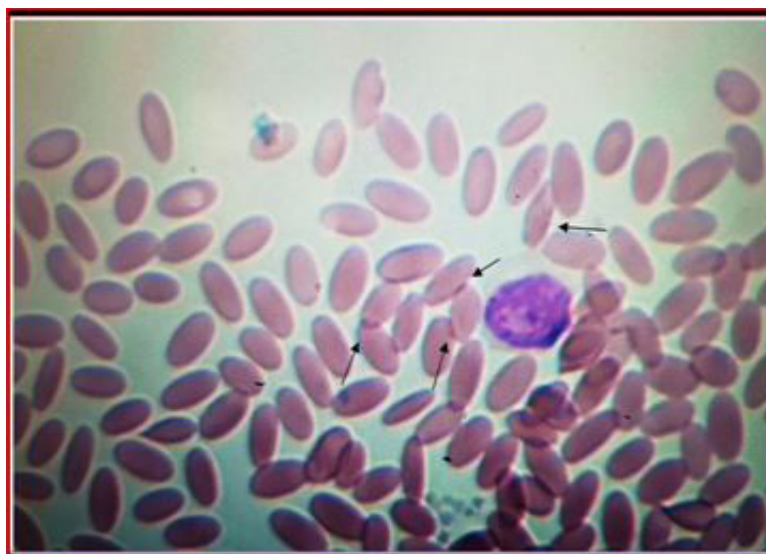


Fig. 1. Giemsa stained blood smear, *Mycoplasma hemolamae* (black arrows)

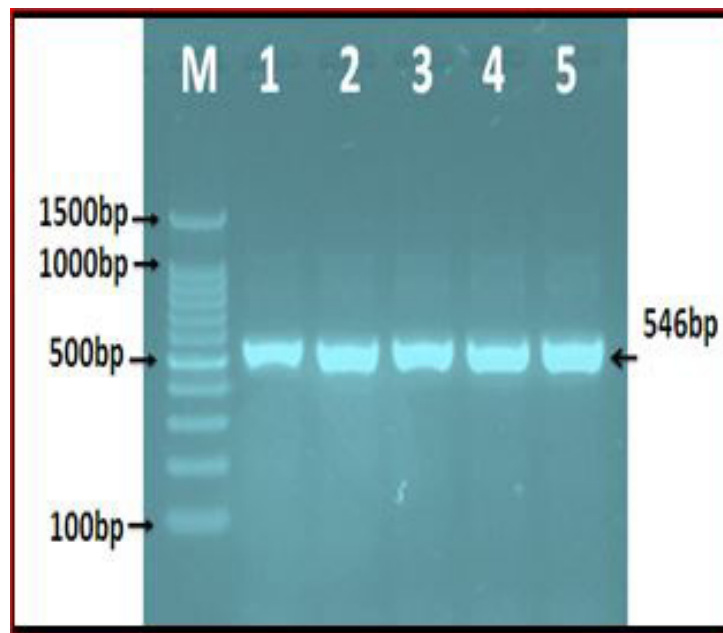


Fig. 2. Agarose gel electrophoresis image that exhibited the PCR product analysis of 16S ribosomal RNA gene in *Mycoplasma hemolamae* from extracted DNA of blood samples. Where M: marker (1500-100bp) and the Lane (1-5) some positive *Mycoplasma hemolamae* samples at (546bp) PCR product

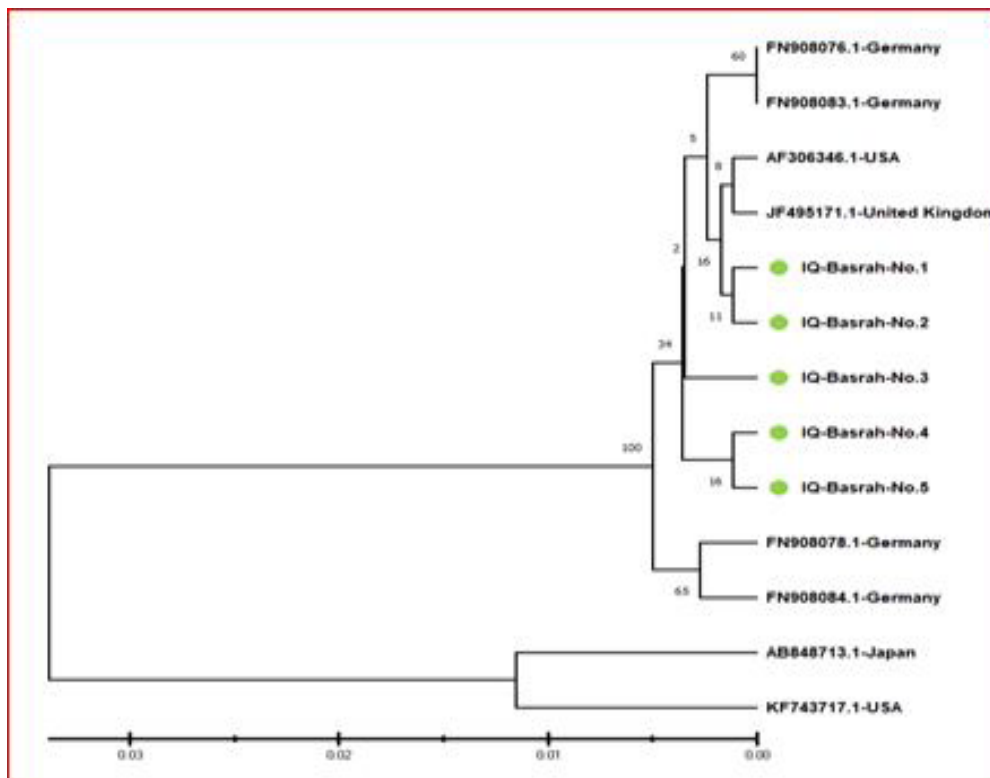


Fig. 3. A tree of phylogenetic analysis which based on 16S ribosomal RNA gene partial sequence of the local *Mycoplasma hemolamae* isolates used for genetic relation analysis, using the Un-weighted Pair Group Method in (the MEGA 6.0 version)

TABLE 5. The NCBI-BLAST Homology Sequence identity percentage between local *Mycoplasma hemolamae* and NCBI-BLAST closed-related *Mycoplasma hemolamae* isolate:

| local <i>Mycoplasma hemolamae</i> isolate | Accession number | Homology sequence identity (%) | | |
|---|------------------|--------------------------------|------------------|--------------|
| | | Country related NCBI | Accession number | Identity (%) |
| IQ-Basrah-No.1 | ON600995.1 | UK | JF495171.1 | 99.77% |
| IQ-Basrah-No.2 | ON600996.1 | UK | JF495171.1 | 99.77% |
| IQ-Basrah-No.3 | ON600997.1 | UK | JF495171.1 | 99.54% |
| IQ-Basrah-No.4 | ON600998.1 | UK | JF495171.1 | 99.77% |
| IQ-Basrah-No.5 | ON600999.1 | UK | JF495171.1 | 99.77% |

TABLE 6. Blood parameters of infected camels with *Mycoplasma hemolamae* and healthy group

| Blood parameters | Controls n=20 | Diseased n=80 |
|-------------------|------------------|--------------------|
| RBC $\times 10^6$ | 7.76 \pm 1.21 | 4.91 \pm 1.77 * |
| Hb g/dl | 12.63 \pm 1.82 | 8.78 \pm 2.31 * |
| PCV % | 28.3 \pm 3.87 | 23.6 \pm 2.54 * |
| MCV /fl | 36.46 \pm 4.52 | 48.06 \pm 3.36 * |
| MCHC/dl | 44.62 \pm 7.81 | 37.2 \pm 6.11 * |
| ESR mm/8h | 12.57 \pm 2.72 | 22.82 \pm 4.25 * |

Mean significant at P<0.05

TABLE 7. The leukocytes count (Total and absolute Differential) of infected camels with *Mycoplasma hemolamae* and healthy group

| Parameters | Controls n=20 | Diseased n=80 |
|-------------------|--------------------|-----------------------|
| WBC $\times 10^3$ | 11.67 \pm 1.45 | 13.94 \pm 1.87 * |
| Lymphocytes | 5142.67 \pm 7.31 | 7234.54 \pm 22.76 * |
| Neutrophils | 5787.56 \pm 9.22 | 5872.45 \pm 32.81 |
| Monocytes | 340 \pm 1.11 | 342 \pm 1.45 |
| Eosinophils | 206 \pm 1.91 | 201 \pm 5.65 |
| Basophils | 91 \pm 2.30 | 90 \pm 1.21 |

Mean significant at P<0.05

TABLE 8. The indices of clotting factors of infected camels with *Mycoplasma hemolamae* and healthy group

| Parameters | Controls n=20 | Diseased n=80 |
|---|-----------------|-------------------|
| Platelets count (Plt) $\times 10^3$ | 413 \pm 27.41 | 312 \pm 24.12* |
| Mean platelets volume (MPV) /fl | 3.16 \pm 0.79 | 10.38 \pm 1.34* |
| Platelets distribution width (PDW) % | 14.2 \pm 1.2 | 18.91 \pm 2.3* |
| Clotting time (CT) / mint | 3.2 \pm 0.62 | 5.2 \pm 1.43* |
| Prothrombin time (Prt) / sec | 107 \pm 2.6 | 147 \pm 3.6* |
| Activated partial thromboplastin time (Aptt) /sec | 12.42 \pm 1.2 | 18.72 \pm 2.17* |

Mean significant at P<0.05

infected camels with Hemomycoplasmosis than in the control animal group. However, a significant low level ($P < 0.05$) was detected in total protein in infected camels compared with the control group (Table 9).

Diseased camels show a significant difference in acute phase response. As results indicated a significant increase ($P < 0.05$) in both haptoglobin values and also in Fibrinogen time in diseased animals than in control group (Table 10).

It has been noted that dead camels due to Hemomycoplasmosis show signs of emaciation, paleness of internal organs splenomegaly, and enlargement of kidneys. Moreover, histopathological changes were characterized by severe white pulp atrophy as well as a hemosiderin-laden macrophage beside an increase of giant cell in the splenic parenchyma. Nevertheless, a degree of central arteriole hyperplasia was also detected. Figures (4,5). Furthermore, a vacuolated and degenerated renal tubules and atrophy of glomerulus with vacuolation of mesangial cells, as well as a dilation of renal tubules and Bowman capsule basement membrane thickness have been indicated too. Fig. (6,7).

As for histopathological changes in the liver, the results of the study showed a dilated central vein contains mononuclear inflammatory cells

with pericentral vein infiltration of inflammatory cells which could refer to an area of necrosis in the central hepatic region as well as a degree of diffuse degenerative changes of the hepatocytes in the central hepatic zone. Moreover, diffuse degenerative changes and vacuolation of the hepatocytes in the central hepatic zone has been indicated too. Furthermore, diffuse periportal region fibrosis was also seen in the histopathological sections. In addition to subcapsular region fibrosis with degenerative changes and vacuolation of the hepatocytes in the subcapsular region Fig. (8,9).

Discussion

Hemomycoplasma is considered an important infectious pathogen infected domestic animals causing harmful effects which could be terminated with the death of the diseased animals. Nevertheless, it has been mentioned that Hemomycoplasma could silently infect animals and lead to disease mostly in stressed conditions [12].

It has been shown that the disease was detected and diagnosed in cattle, buffaloes, and sheep in the south part of Iraq [10,11,14], moreover, Nineveh province [8].

Diseased camels show several clinical manifestations which were mentioned also by

TABLE 9. Biochemical changes in infected camels with *Mycoplasma hemolamae* and healthy group

| Parameters | Controls n=20 | Diseased n=80 |
|-----------------------|---------------|---------------|
| AST U/L | 111 ± 11.31 | 192 ± 10.74* |
| ALT U/L | 15 ± 2.65 | 47.7 ± 8.32* |
| Total bilirubin mg/dl | 0.34 ± 0.22 | 0.72 ± 0.21* |
| BUN mg/dl | 12.54 ± 1.61 | 33.56 ± 8.23* |
| Icteric index mg/dl | 3.43 ± 0.65 | 6.43 ± 2.4* |
| Total protein g/dl | 6.4 ± 1.43 | 4.6 ± 0.78* |

Mean significant at $P < 0.05$

TABLE 10. Haptoglobin and Fibrinogen values (The Acute phase response) of infected camels with *Mycoplasma hemolamae* and healthy group

| Parameters | Controls n=20 | Diseased n=80 |
|-----------------------|-----------------|---------------|
| Haptoglobin g/100mL | 0.15 ± 0.022 | 0.072 ± 0.07* |
| Fibrinogen time / sec | 27.18 ± 10.23 ± | 38.71 ± 4.87* |

Mean significant at $P < 0.05$

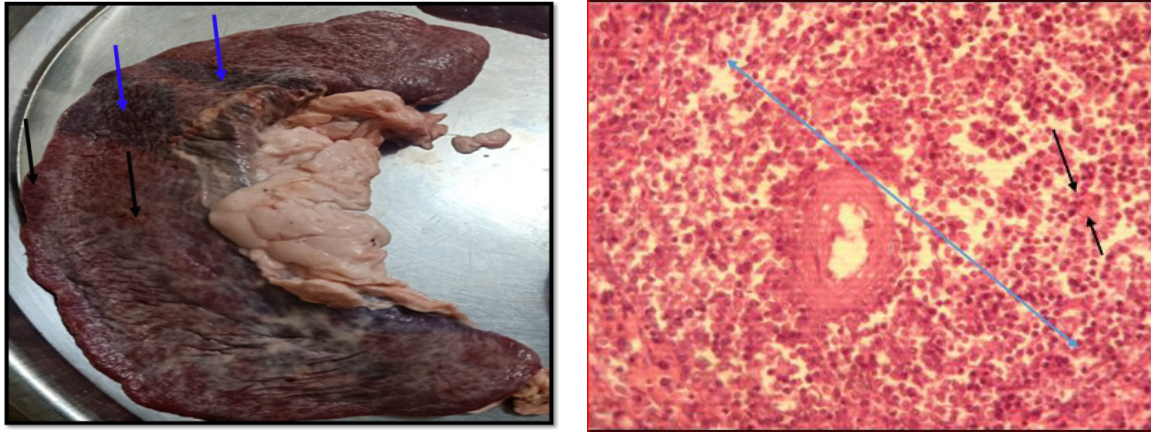


Fig. 4,5. Photographic view of the spleen of a dead camel with Hemomycoplasmosis revealed splenomegaly with hemorrhagic spots (black arrows), hemosiderin-laden macrophage and thickening of the blood vessel wall (black arrow) (Right). H & E stain. 400X.

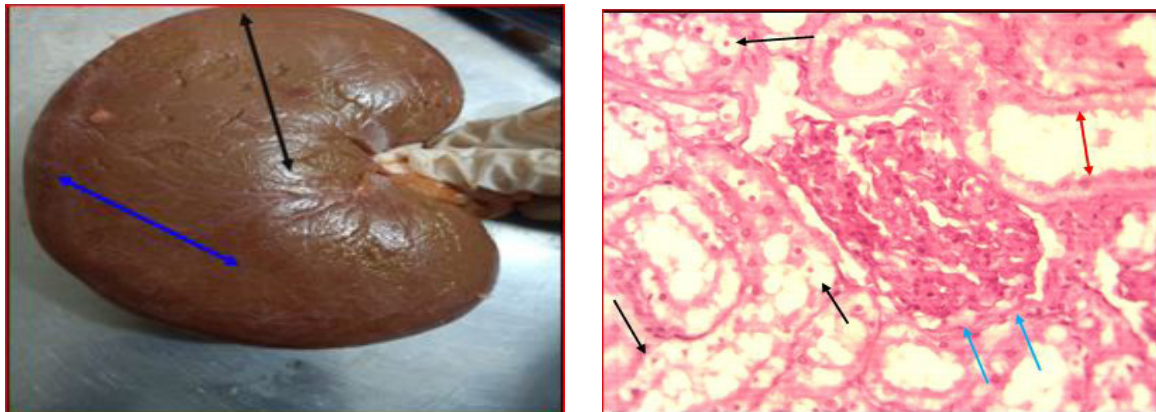


Fig. 6,7. Macroscopic view of kidney of a dead camel with Hemomycoplasmosis revealed enlargement of kidney with diffuse paleness of the pelvic region of the kidney (double-headed black arrow), severe vacuolated and necrotic renal tubules (black arrows), dilation of renal tubules (red arrows), and degree of bowman capsule basement membrane thickness (Hyalinization of the glomerulus) (Right). H & E stain. 400X.

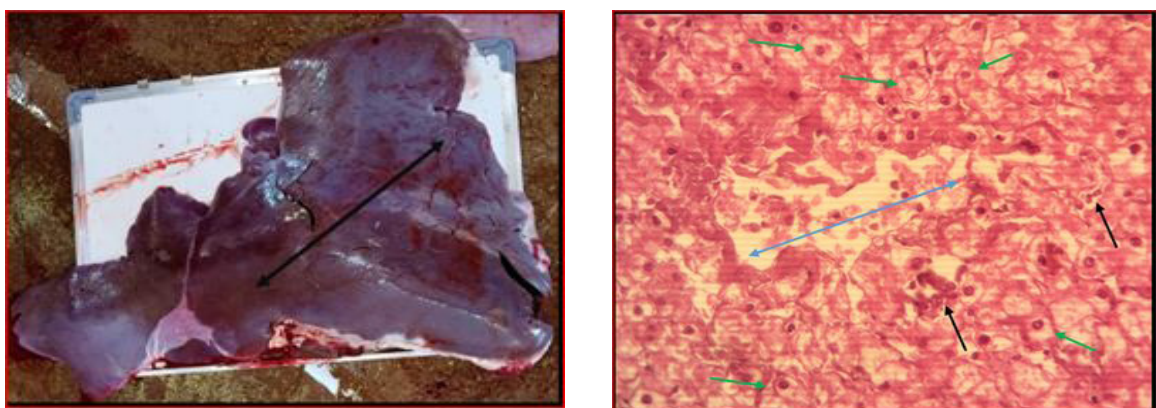


Fig. 8,9. Macroscopic view revealed hepatomegaly which is represented by the hypertrophied liver with diffuse congestion of the parietal region (double-headed black arrow) (Left), dilated central vein contains mononuclear inflammatory cells (double-headed blue arrow), pericentral vein infiltration of inflammatory cells may refer to an area of necrosis in the central hepatic region (black arrows), also there are diffuse degenerative changes and necrosis of the hepatocytes in the central hepatic zone (Green arrows) (Right). H & E stain. 400X.

others [4,7,19,20]. On blood smears stained with Giemsa, *Mycoplasma hemolamaea* rod shape, or as a single small coccoid or in form of long or short chains located on the erythrocyte cell walls, same results were mentioned by many researchers [5,21,22].

Diagnosis of *Mycoplasma hemolamae* was confirmed by PCR technique and results show that the electrophoresis image of the Agarose gel which visualized the PCR product, the positive samples were indicated at 546bp. The same results were also documented by several authors [7,22-25].

The phylogenetic tree genetic relationship analysis showed that the local *Mycoplasma hemolamae* isolates (IQ-Basrah-No.1 to IQ-Basrah-No.5) showed closed genetics related to NCBI BLAST *Mycoplasma hemolamae* UK isolate (JF495171.1) at total genetic change (0.03-0.01%). The sequencing of the gene (16S rDNA) presented approximately 99.8% homology with *Mycoplasma haemolamae* sequences deposited in GenBank. On the other hand, it has been documented that the genome of the organism *Mycoplasma haemolamae* is the same which belongs to the *Mycoplasma* and consists of single and round chromosome [26].

Results of the current study indicated a macrocytic hypochromic type of anemia affected the diseased camels, results are consistent with some authors [27,28]. Anemia which demonstrated in the current work was defiantly happen due to a significant low amount of total erythrocyte count, hemoglobin concentration, and the packed cell volume, where erythrocytes hemolytic effect induced by causative Hemomycoplasma infections is regularly extravascular and results mostly in regenerative anemia with erythrocyte clumping which could appear. However, the increase in mean corpuscular volume could indicate the presence of immature erythrocytes which considered as an index of regenerative type of anemia [27,29,30]. On the other hand, Mahran, and Jamwalet al. [31,32], stated that the main causes of anemia during any blood parasitic infection might be several factors, such as erythrocyte shortage life span, the suppressed activity of hemopoietic system could also play a major role. Furthermore, Al-Ani et al. and Mohammed et al. [2,33], revealed that anemia in camels infected with blood parasites infection is due to erythro-phagocytosis and the developed anti-erythrocytic auto antibodies alterations in

the bone marrow are an index to the depression of the bone marrow activities.

An increase in Erythrocyte sedimentation rate (ESR) values in diseased camels were in agreement with other investigators [31,34]. Moreover, the significant higher levels of ESR indicated in the current study might reflect the high inflammatory condition response which may trigger Hyper-fibrinogenemia and resulted in erythrocytes clumping with fast sedimentation [35,36].

Increased leucocytes count in the present study which has been seen along with lymphocytosis was also indicated by some authors [2,30], who reported the ability of Hemomycoplasma to maintain the persistent infections and could create super antigens that bind directly to major histocompatibility complex molecules stimulating large numbers of lymphocytes. Moreover, some researchers [37,38], explained that Leucocytosis in blood parasitic infection mostly occurs because of the stimulation of stem cells as well as the lymphoid tissues in the bone marrow. Furthermore, increase leukocytes number could be expected as a result to lymphoid depletion and disorganization with massive lymphocytes, in our results was agreed with Mahran and Mohammed et al. [2,31].

It's expected that the disease might alter the mechanisms of the coagulation system which finally terminated with the development of disseminated intravascular coagulopathy. This could be supported by the haemoconcentration of the blood and a growing of the coagulation activators together with a depression of coagulation inhibitor activities [39-41]. A common predominant coagulation condition in dromedary with Hemomycoplasmosis is a hyper-coagulation state linked with disseminated intravascular coagulation. Thereby, the intensity of this coagulopathy mechanism will depend on the severity of anemia and thrombocytes aggregation state [4,42].

In the present work, the results indicated an obvious change in the indices of clotting factors in diseased camels compared with control camels. A decrease in thrombocytes count and a low level of fibrinogen might reflect the petechial hemorrhages seen on the mucus membranes of diseased animals. Further, this could refer to the liberation of some endogenous mediators

like a platelet-activating factor in inflammatory disorders [36,40].

Results of biochemical changes refer to increase values of AST, ALT, total bilirubin, BUN, icteric index, as well as low levels of total protein, these results were in the same line with previous studies mentioned by some investigators [43,44], who mentioned that the harmful effects and damage to the skeletal or heart muscles, hepatic tissues as well as the erythrocytes might be followed with noticeable increase in the values of Aspartate and Alanine amino transferases, as the abundance of those tissues throughout the body could reflect an ample reservoir of enzymes liable to be released and detected during the pathological situation, Kaneko [45], revealed that hyper-bilirubinemia Hemomycoplasmosis might be the result of excessive erythrocytes destruction and the indirect hepatocellular damage.

The high level of blood urea nitrogen might refer to the indirect harmful effects on renal tissues, Nonetheless, the presence of globins catabolites released from hemoglobin lysis by the reticuloendothelial system due to erythrophagocytosis could be possible also [30], On the other hand, There was a low amount seen in total protein values (Hypoproteinemia) in the current study which was also mentioned by Brakat *et al.* [34], who explain that decreased protein values during infection with blood parasites could attributed to destruction of proteins due to fever impact.

Results indicated an obvious and significant increase of both haptoglobin values and Fibrinogen time. It was shown that the inflammatory response to tissue affection is a reflex by which the host could create protection against any harmful states and starts healing processes [46], As, The immediate and fast reaction response is called acute phase response (APR) and one of the common advantages of APR is alterations in the concentrations of different plasma proteins related to the host reflex, These alterations might be the result of changes in acute-phase protein synthesis in hepatic tissues [47]. Haptoglobin was one of the acute phase proteins, commonly considered a marker of any inflammation in all animals [46].

Moreover, the results of the present work revealed increase fibrinogen amount in diseased camels. It was documented that, Fibrinogen is an

important plasma protein represented as acute-phase response in domestic animals [42], Thus, this type of protein was considered a good marker for inflammatory responses, Therefore, it uses mostly as an indicator for the following inflammatory processes such as peritonitis, endocarditic, nephritis, pneumonia, and enteritis [36].

Results of macroscopic and microscopic pathological features of diseased camels indicated different pathological changes. which were indicated by others [1,30]. The spleen can play a major role in hematopoiesis state and immune-surveillance mechanism, It has been shown that the spleen will increase in its clearing mechanism of antigens and produce new antibodies, and increases the number of reticuloendothelial cells contained within the spleen. These process functions might be terminated with splenic hyperplasia [48]. Moreover, From a histopathological view, show several changes characterized by severe white pulp atrophy, and hemosiderin-laden macrophage beside an infiltration of Langhan's giant cell in the splenic parenchyma, these changes are accordance with other researchers [1,2].

Furthermore, enlarged camel kidneys with different pathological affections could occur due to several causes including hemolytic anemia, medullary hyperemia, degenerative conditions, sub-capsular calcification, cortical and medullar discoloration, hemorrhage in the renal pelvis, focal interstitial nephritis, Such lesions could result in the poor production of the involved animals [6,7,48-50]. Further, on histopathological views diseased liver resulting from Hemomycoplasmosis show dilated central vein containing mononuclear inflammatory cells with pericentral vein infiltration of inflammatory cells which could refer to the area of necrosis in the central hepatic region as well as a degree of diffuse degenerative changes of the hepatocytes in the central hepatic zone, same results were also detected by some investigators [48].

Conclusion

It has been concluded that Hemomycoplasmosis was circulating in this study region, infected camels showed various clinical manifestation, PCR technique is an useful method for detection of *Mycoplasma hemolamae*, Ideal control measures is of need to minimize and eliminate the disease in camels

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Conflict of interest

In the current study there was no conflict in interest

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دراسة دموية ، كيموحيوية وامراضية لخمج الابل وحيدة السنم بالمايكوبلازما الدموية في محافظة البصرة ، العراق

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تم اكتشاف وتشخيص داء الهيمومايكوبلازما الدموية في ابل محافظة البصرة /العراق. أجريت الدراسة لفحص ١٠٠ رأس من الابل المحلية السلالة .ثمانون (٨٠) من الابل تراوحت أعمارهم بين (٨ أشهر - ٥ سنوات) ومن كلا الجنسين اظهرت علامات الخمول وفقر الدم والهزال، وتم استخدام عشرين (٢٠) من الابل السليمة سريريًا كمجموعة سيطرة. أشارت النتائج إلى أن الإبل المريضة اظهرت علامات سريرية مختلفة. وتم تشخيص العامل المسبب الميكوبلازما الدموية *Mycoplasma hemolamae* في مسحات الدم المصبوغة بصبغة الكميذا كما وتم تأكيد التشخيص النهائي باستخدام تقنية تفاعل البلمرة المتسلسل. فضلا عن ذلك أظهر تحليل العلاقة الوراثية لشجرة النسوء والتطور أن عزلات *Mycoplasma hemolamae* المحلية أظهرت جينات مغلقة مرتبطة بعزلة NCBI BLAST *Mycoplasma hemolamae* UK JF٤٩٥١٧١.١ عند التغير الجيني الكلي (٠.٠٣-٠.٠١٪). وأشارت النتائج أيضًا إلى إصابة الابل المريضة بفقر الدم من النوع ذي الكريات كبيرة الحجم قليلة الصباغ مع حدوث زيادة معنوية في معدلات تنقل كريات الدم الحمر ، كما ازدادت معنويًا معدلات العدد الكلي لخلايا الدم البيض والخلايا اللمفية وازدادت ايضا معدلات خميرة الألتنين والاسبارتيت ناقلة الامين والصفراوين الكلي ومؤشر الصفراوين في حين انخفضت معنويًا قيم البروتين الكلي . اشارت النتائج ايضا الى حدوث اختلاف في قيم معدلات استجابة الطور الحاد في الابل المريضة بالمقارنة مع حيوانات السيطرة .تم الكشف عن شحوب الأعضاء الداخلية ، تضخم الطحال ، تضخم الكلى مع تضخم الكبد على جثث الابل أنفاقة كما لوحظ ضمور اللب الأبيض الشديد وكذلك الضامة المحملة بالهيموسيديرين بجانب الأنابيب الكلوية المتدهورة وضمور الكبيبات الكلوية مع توسع الوريد المركزي وتسلل الوريد المحيط بالوسط. ولوحظت الخلايا الالتهابية التي قد تدل على منطقة نخر في منطقة الكبد المركزية في فحوصات التشريح المرضي.