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SAVING THE CAMELS

"Saving the camels" is drawing attention in few countries where either population is on decline or camels die of toxicity or plastic pollution. However, to a lesser extent camels are saved from road accidents also by putting several signboards at camel crossing prone areas and imposing fine if camels are hit by automobiles. The present large camelid population in the world is probably more than 40 million**. The Indian dromedary camel population is still in decline, especially since the 2010s, a reverse trend developed in China. In countries marked by a regular or drastic decline of their camelid population, a tendency to re-increase has been in force since the beginning of the century, except in India**. It needs an urgent population crisis management at government level. While deciding the policies to save the camels in India, it should be pondered upon that how best the population sustainability and a gradual increase in camel population is taking place in other countries including China. The camel population in India is in mortal decline. The economic benefits of rearing a camel have all but disappeared. The road network in Rajasthan has grown by almost 30 times since 1951, slowly but surely eliminating the need for the "ship of the desert". Camels, or camel carts carrying people or goods - so common even a few decades ago - can rarely be seen now. Till the 1960s, Civil Administrative officers in Rajasthan routinely toured their districts on camels. Camel owners in India perhaps lost interest in rearing and breeding camels because of poor economical returns. In fact, the effort made by the Government of Rajasthan – enacting The Rajasthan Camel (Prohibition of Slaughter and Regulation of Temporary Migration or Export) Act, 2015 – has had just the opposite effect. Forced by economic reality, the Raika sold their camels to any buyer, including those whom they suspected of buying it for meat, and even sold in grey market for a meagre price. The ban has benefitted only the meat traders and corrupt officials. Camels in India are unlikely to survive as just milch animals either, despite the many demonstrated benefits of camel milk, for several reasons. Neither production nor demand could possibly sustain an economically successful dairy model*. The dromedary camels in Arabian Peninsula are best thriving as a race animal which is additionally used for meat and milk purposes also. These camels are surplus as feral camels in Australia where their use is not much exploited.

A group of scientists recently published papers on plastic pollution. Camels residing in the UAE are experiencing a regional 1% mortality rate from ingesting plastic pollution***. Polybezoars, the tightly packed collection of indigestible materials, which can include plastics, ropes other litter and salt deposits, that is trapped in the stomach or digestive tract, forming a large stone-like mass, lead to gastrointestinal blockages, sepsis from increased populations of gut bacteria, dehydration and malnutrition.

It is imperative to discuss the pertinent topic "Saving the camels" through this plarform to bring a growing awareness among the cameleers, camel scientists and government authorities for saving this desert creature.

(*Decline in India's camel population is worrying written by Rajiv Mehrishi, former civil servant, Rajasthan cadre, The Indian Express, July 7, 2022; **Faye, B. How many large camelids in the world? A synthetic analysis of the world camel demographic changes. Pastoralism 10, 25 (2020). https://doi.org/10.1186/s13570-020-00176-z, ***(Marcus Eriksen, Amy Lusher, Mia Nixon and Ulrich Wernery. The plight of camels eating plastic waste. Journal of Arid Environments, 2021; Volume 185)

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MERS-COV IN DROMEDARY CAMELS: SEQUENCE-BASED COMPARISON OF ANTIGENICITY AND PATHOGENICITY OF STRUCTURAL AND NON-STRUCTURAL PROTEINS

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ABSTRACT

The goal of this researcher was to map the camel MERS-CoV structural and non-structural proteins and track changes in antigenicity and pathogenicity from 2013 to 2018. This is critical for developing effective diagnostic and control methods. Therefore, the sequences of MERS-CoV structural proteins such as Spike (S), Membrane (M), Nucleocapsid (N) and Envelope (E) and nonstructural proteins, comprising polyprotein-ab (polyab) and Open reading frame-3 (ORF3) were retrieved. The amino acid sequences of each of these proteins were analysed to estimate their antigenic and pathogenic properties from 2013 to 2018. The antigenicity profiles showed variations in antigenicity minimum, maximum, range, and average from 2013 to 2018. MERS-CoV proteins' maximum antigenicity score was declining in the examined time frame. In 2013, the maximum score was 0.86, and by 2018, it had dropped to 0.6. This resulted in a greater range of antigenicity with the onset of MERS-CoV in 2013, with a range of 0.56, which eventually decreased to 0.22 in 2018. The net effect on the mean value of antigenicity score revealed that MERS-CoV antigenicity decreased gradually. Between 2013 and 2018, the mean antigenicity score of structural and nonstructural proteins decreased. Non-structural proteins, on the other hand, had the greatest alterations, with a mean value of 0.52 in 2013 and 0.42 in 2018, representing a loss of 19.2 per cent of their antigenicity score. In contrast, the structural protein showed a mean value of 0.55 in 2013 and 0.53 in 2018, i.e. lost only 3.6% of its antigenicity score. Given that ORF3 was nonantigenic, therefore, all changes in antigenicity changes were attributed to polyab protein. Pathogenicity score has decreased from 0.81 in 2013 to 0.78 in 2018. Further studies are required to map these changes on the virus-host cell interaction level.

Key words: Antigenicity, camels, MERS-CoV, pathogenicity, proteins

MERS-CoV was first identified in Saudi Arabia in 2012 in a patient with severe pneumonia (Zaki *et al*, 2012). Initially the virus was termed as "human coronavirus Erasmus Medical Centre (EMC) or EMC-CoV". This novel coronavirus later was termed as Middle East respiratory syndrome coronavirus (MERS-CoV) according to the announcement of the Coronavirus Study Group of the International Committee on Taxonomy of Viruses (ICTV) (de Groot *et al*, 2013). The MERS-genome CoV is 30 kb (30,119nt) long and encodes four structural proteins (Spike, Envelope, Membrane, and Nucleocapsid) as well as 16 nonstructural proteins (van Boheemen *et al*, 2012).

MERS-CoV infection has a 35.4 per cent fatality rate, and new cases and deaths have continued

till the end of 2018 (WHO, 2018). According to current research, many coronaviruses that are phylogenetically similar to MERS-CoV, such as BatCoV-HKU4, BatCoV-HKU5, and other MERSrelated coronaviruses, are considered to have originated in bats (Woo et al, 2012; van Boheemen et al, 2012; Corman et al, 2014; Anthony et al, 2017). The BatCoV-HKU4 has also been discovered to be capable of activating the MERS-CoV cellular receptor, bolstering the bat origin theory (Wang et al, 2014). There is, however, no direct evidence that MERS-CoV may be isolated from bats (Xu et al, 2019). Because camel isolates are nearly identical to human isolates and many domestic camels are MERS-CoV seropositive, dromedary camels are thought to be the animal reservoir for MERS-CoV (Xu

SEND REPRINT REQUEST TO SABRY MOHAMED EL-BAHR email: selbahar@kfu.edu.sa; sabryelbahr@hotmail.com

et al, 2019). Camels in the Middle East and northern Africa contain antibodies to MERS-CoV or a virus that is quite similar to it, according to serological evidence dating back to the 1980s (Alagaili et al, 2014; Corman et al, 2014; Müller et al, 2014). These findings are not applicable to Bactrian camels or dromedaries from other countries, such as Australia and Kazakhstan (Hemida et al, 2014a). While these findings support the theory that camels can transmit illnesses to humans, initial MERS cases may not have had any interaction with camels. Furthermore, because the MERS-CoV receptor, dipeptidyl peptidase 4, is highly conserved in mammals, other mammalian hosts may be involved (van Doremalen et al, 2017). In this study, the changes in MERS-CoV antigenicity and pathogenicity were be evaluated from 2013 to 2018. The results were further analysed in the light of structural and non-structural protein components, as well as, the specific proteins used in the analysis.

Materials and Methods

Retrieval of input protein data and analytical programs

The sequences of the input proteins of interest (polyab, ORF3, S, M, N, and E) were retrieved from the GenBank at NCBI.

Prediction of the antigenic properties of MERS-CoV proteins

The amino acid sequences of proteins of interest (polyab, ORF3, S, M, N, and E) were utilised for antigenic property analysis, and the VaxiJen v2.0 server (Doytchinova and Flower, 2007) with a threshold of 0.4 was employed (<u>http://www.ddgpharmfac.net/vaxiJen/VaxiJen/VaxiJen.html</u>). A summary of antigenicity statistics for MERS-CoV 2013-2018 is presented in Table 1. The antigenicity score for each of the proteins of interest: polyab, S, M, N, and E was recorded. The algorithm was used to analyse the antigenic property after inserting a threshold value of 0.4.

Prediction of pathogenic and antigenic properties

Using the protein sequences of each chosen MERS-CoV isolate, we used the MP3 program (http://metagenomics.iiserb.ac.in/mp3/application.php) with default settings to estimate pathogenicity scores (Gupta *et al*, 2014). The hybrid findings (SVM+HMM) were taken into account, and the SVM scores were employed in the analysis. The pathogenic score for each of the proteins of interest (polyab, ORF3, S, M, N, and E) was recorded (Table 2). For each isolate, the average scores of all these proteins were also computed.

Statistical analysis

All data handling and presentation were done by MS excel and GraphPad Prism software. The results were presented in Mean±SD or, in some cases, the mean + range is provided. Descriptive statistics were used to express changes in each isolate parameter.

Results and Discussion

MERS-CoV is an emerging infectious virus that is exceedingly dangerous to humans and is zoonotic in nature. Effective vaccination and diagnostic methods for this virus are still mostly unknown. Gaps in our understanding of these pathogens' protective immunity and antigenicity offer obstacles to the development of vaccines and diagnostics. Respiratory sickness caused by the MERS-CoV virus continues to grow for unnoticeable reasons. Since SARS-CoV-2 has emerged, it has become clear that effective therapies against extremely deadly human coronaviruses developed quickly. Despite this fact, the efforts to develop efficient vaccines and diagnostics against MERS-CoV are still in their primary stages. There has been a surge in R&D efforts to produce diagnostic, preventive, and therapeutic solutions for SARS-CoV-2, which has caused millions of affections. In contrast, MERS-CoV with more than 1,700 acetate cases of sickness and 600 deaths in 27 countries has less attention in developing vaccines and diagnostics.

 Table 1. Summary of antigenicity statistics for MERS-CoV 2013-2018.

| Year | 2013 | 2014 | 2015 | 2016 | 2017 | 2018 |
|---------------------|----------|---------|----------|----------|----------|----------|
| Antigenicity scores | 0.5271 ± | 0.503 ± | 0.4891 ± | 0.4911 ± | 0.4941 ± | 0.4911 ± |
| (Mean ± SD) | 0.1305 | 0.1091 | 0.09007 | 0.08907 | 0.08299 | 0.07723 |

 Table 2.
 Summary of pathogenicity statistics for MERS-CoV 2013-2018.

| Year | 2013 | 2014 | 2015 | 2016 | 2017 | 2018 |
|----------------------|----------|----------|----------|----------|----------|---------|
| Pathogenicity scores | 0.8115 ± | 0.7722 ± | 0.7227 ± | 0.7529 ± | 0.7775 ± | 0.776 ± |
| (Mean ± SD) | 0.5868 | 0.6045 | 0.6039 | 0.5104 | 0.5217 | 0.531 |

A summary of MERS-CoV antigenicity and its statistics during 2013-2018 is provided in Fig 1. The number of data entries each year ranged from 12-84 with the highest hits in 2014 followed by 2015. Surprisingly, the antigenicity profiles shoed variations in antigenicity minimum, maximum, range, and average from 2013 to 2018. MERS-CoV proteins' maximum antigenicity score decreased. In 2013, the maximum score was 0.86, and by 2018, it had dropped to 0.6. (Fig 2). This resulted in a greater range of antigenicity with the onset of MERS-CoV in 2013, with a range of 0.56, which eventually decreased to 0.22 in 2018. (Fig 1A, Fig 2). The net effect on the mean value of antigenicity score revealed that MERS-CoV antigenicity decreased gradually. In 2013, the antigenicity score was 0.5271 \pm 0.1305 which decreased to 0.4911 \pm 0.077 in 2018. As the initial data showed declining antigenicity of MERS-CoV, we further investigated the changes in antigenicity in the protein components of MERS-CoV (Fig 3). Both structural and non-structural proteins showed declining mean antigenicity scores from 2013-2018. However, the greater changes were with NS, which showed a mean value of 0.52 in 2013 and 0.42 in 2018, i.e. lost about 19.2% of its antigenicity score. In contrast, the structural protein







showed a mean value of 0.55 in 2013 and 0.53 in 2018, i.e. lost only 3.6% of its antigenicity score. In this study, we used only two NS proteins in all procedures, polyab and ORF3. Given that ORF3 was nonantigenic, therefore, all changes in antigenicity were attributed to polyab. The analysis of MERS-CoV pathogenicity scores from 2013 to 2018 demonstrated a moderate decline. Pathogenicity score has decreased from 0.8115 ± 0.5868 in 2013 to

 0.776 ± 0.531 in 2018. The range of pathogenicity of viral proteins was broad in the early years of MERS-CoV emergence, but it narrowed in subsequent years (Fig 4). The changes in the pathogenicity of MERS-CoV proteins were further analysed according to the protein components, comprising S, N, E, M and Polyab (Fig 5). Among these proteins, polyab and E proteins showed a gradual decrease in pathogenicity.



Fig 3. MERS-CoV nonstructural (NS) and structural (Str) proteins antigenicity scores. (A) Column bar graph showing the NS and Str proteins antigenicity scores during 2013 (B) 2014 (C) 2015 (D) 2016 (E) 2017 (F) 2018.



Fig 4. MERS-CoV pathogenicity scores. Box and whiskers plot showing the range of pathogenicity with cross-line at mean values.

In 2015, molecular diagnostic approaches and their global performances for the sensitive and specific detection of MERS-CoV RNA are wellillustrated in the first external quality evaluation MERS-CoV panel (Pas *et al*, 2015). MERS-CoV could be detected in all laboratories, but with varying degrees of sensitivity. The fact that 8% of labs reported false positives for MERS-CoV in a single assay demonstrates that there is potential for improvement and that confirmatory targets are important. This fact highlights the need for continued assessment of the accuracy of detection methods. In this work, we showed a decreasing antigenicity of MERS-CoV proteins. The impact of these changes on the accuracy of current diagnostics is to be elucidated.

Conflict of interest

The authors declare no conflict of interest.



Fig 5. MERS-CoV proteins pathogenicity scores. (A) E protein (B) M protein (C) E protein (D) S protein (E) Polyab.

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SPATIAL EXPRESSION OF OSTEOPONTIN IN TESTIS, EPIDIDYMIS AND SPERMATOZOA IN DROMEDARY CAMEL

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ABSTRACT

The aim of this study is to clarify the function of osteopontin (OPN) through its expression and localisation in male testis, epididymis and sperm cell of dromedary camel during rutting season. Testis and epididymis parts (caput, corpus and cauda) specimens were obtained from 8 mature male camels and semen was collected from 4 another fertile camels for sperms. OPN mRNA expression and its location was analysed using quantitative real-time polymerase chain reaction (qRT-PCR) and immunohistochemistry (IHC) techniques, respectively. OPN mRNA expression was significantly (P < 0.05) higher in the cauda of epididymis than other epididymal parts and testis. Immunolocalisation revealed high immunoreaction intensity in the elongated spermatids in seminiferous tubules and Leydig cells in interstitial tissue. However, a faint immunostaining was seen in spermatogonia and Sertoli cells. Along the epididymis tract, intense immunoreactivity of OPN was localised in the cytoplasm of the epithelial cells with high concentration in the apical region nearby lumen and the acrosomal part of the cauda epididymal sperms. Immunofluorescence and immunochromogenic staining of OPN was detected on the acrosomal cap and neck of epididymal sperms. These findings suggested that OPN might play an important role in the sperm protection, migration and fertilisation in dromedary camels.

Key words: Dromedary camel, epididymis, expression, osteopontin, spermatozoa, testis

Osteopontin (OPN), also named as Secreted Phosphoprotein1 (SPP1), is an indispensable highly phosphorylated glycoprotein in mammalian reproduction. Firstly, it was isolated from the mineralised matrix of bovine bone (Denhardt and Guo, 1993; Franzen and Heinegård, 1985). Thereafter, it was found in different tissues such as brain (Shin et al, 2005), kidney (Xie et al, 2001) and body secretions like male seminal fluids (Cancel et al, 1999). The function of OPN has been determined according to the expressed cells in the tissues and it thought to play a role in cell adhesion (Wai and Kuo, 2004). Moreover, it was observed in different male reproductive tissues such as testis, epididymis as well as sperm (Lin et al, 2006; RodrÍguez et al, 2000; Siiteri et al, 1995; Wilson et al, 2005; Souza et al, 2009; Kang et al, 2014). Meanwhile, it has been discovered to contribute in several reproductive processes such as spermegg interaction, fertilisation and early embryonic development (Erikson et al, 2007; Souza et al, 2009; Monaco et al, 2009). It has been suggested that the OPN has a potential role in fertilisation (Erikson et al, 2007); spermatogenesis and spermatozoa function (Zhang et al, 2016) and was considered as one of

the decapacitation factors to prevent premature sperm motility activation (Goncalves *et al*, 2007). In addition, OPN has been stated as a sperm surface molecule; where it was found in testes, epididymis and on the surface of epididymal spermatozoa. Therefore, OPN could play a role in maturation during spermatogenesis (Siiteri *et al*, 1995).

In different mammalians, spatial expression of OPN has been thoroughly investigated. The OPN mRNA has been detected in the germ cells of spermatids, epididymis and spermatozoa of the bull (RodrÍguez et al, 2000); Sertoli cells of the mouse (Wilson et al, 2005); both germ and Sertoli cells in the rat testis (Siiteri et al, 1995) and in the testicular interstitium, acrosomes of testicular spermatids and epididymis of the sheep (Zhang et al, 2016). Meanwhile, immunolocalisation of OPN was detected in different locations; in the epididymal sperm, testis and cauda epididymal fluid of bull (Erikson et al, 2007); testes in both rat and mouse (Wilson et al, 2005; Siiteri et al, 1995); spermatogonia, different stages of spermatocytes, acrosomes of spermatids and few sertoli cells of boar; testis, epididymis and cauda epididymal spermatozoa in the sheep (Zhang et al,

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2016) and it has been detected in the seminal plasma of the dromedary camel and its high concentrations was positively correlated with fertility of camels (Waheed *et al*, 2015).

According to previous studies, the expression pattern of OPN has distinct interspecies differences, which indicated that OPN might contribute in several biological processes in various species. Although, there are several studies on detection of OPN in the reproductive system of domestic animal species, but the role of OPN in camel reproductive system has not been reported yet. Therefore, the present study was under taken to clarify the expression and localisation of OPN in dromedary testis, epididymis and epididymal sperm during rutting season to understand its activity in spermatogenesis.

Materials and Methods

Animals and sample collection

Twelve male reproductive tracts of clinically healthy dromedary camels (4-12 years) were obtained from local abattoirs in Saudi Arabia during rutting season (November to April). The testes and caput, corpus and cauda of epididymis were collected from 8 animals. First specimen's part was immediately snap freeze in liquid nitrogen and kept at -80°C for qrt-PCR analyses and the 2nd part was fixed in 10% buffered formalin for immunohistochemistry. In addition, epididymal sperms were collected from the cauda epididymis of the rest 4 males. Sperm samples washed with phosphate-buffered saline (PBS) and suspended sperms were smeared on Superfrost slides, air-dried and then stored at -20°C until use for immunohistochemistry and immunofluorescence.

Gene expression analysis

Briefly, total RNA was extracted using TRIzol Reagent (Invitrogen, Carlsbad, CA, USA) according to the instructions, then RNA pellets were resuspended in UltraPure[™] DEPC-Treated Water (Invitrogen, USA). BioTek Synergy MX reader (BioTek, USA) was used to measure RNA concentration and purity at optical density value 260:280 nm absorbance, which was between 1.8 and 2.0. Reverse transcription reactions were performed using iScriptcDNA Synthesis Kit (BioRad, Hercules, CA, USA). The total of reaction (20 µL) was a mixture of 2 µg RNA templates, 4 µL iScript Reaction Mix, 1 µL iScript Reverse Transcriptase and nuclease-free distilled water. Reaction thermocycle was at 25°C for 5 min, 46°C for 20 min, then at 95°C for 60 seconds to inactivate the reverse transcriptase according to manufacturer's protocol. Gene-specific primers were designed for dromedary camel OPN and glyceraldehyde 3-phosphate dehydrogenase (GAPDH), reference gene, using NCBI primer-blast website (http://www.ncbi.nlm.nih.gov/tools/primer-blast/) and Gen-Bank accession numbers and amplicon length of target genes were presented in table 1. Quantitative real-time PCR (qRT-PCR) carried out using CFX96 Touch Real-time PCR (BioRad, USA). SsoAdvanced SYBR Green Supermix (BioRad, USA) was used to detect the fluorescence emission in a reaction volume of 20 µL. All cDNA templates were run in duplicate and relative quantifications were calculated to the reference gene (GAPDH) directly via CFX ManagerTM software V3.1 (BioRad, Hercules, CA, USA).

| Gene name | Sequences | Accession number | Amplicon Length (bp) | |
|--------------|--------------------------------------|---------------------|----------------------------|--|
| OPN | F: AAGACA CAC AAG ATG GCC GA | VM 01009210E 1 | 107 | |
| Orn | R: TGG CTG TTC CAG TCA GAA GC | AW_010965105.1 | 107 | |
| CADDI | F: CCT GGA GAA ACC TGC CAA ATA | VM 010000967 2 | 207 | |
| GATDII | R: TCG TTG TCG TAC CAG GAA ATG | AWI_010990007.2 | 207 | |

 Table 1. Designed primer sequences, Genbank accession numbers and product sizes used for qRT-PCR.

Tissues immunostaining

Sections of paraffin block samples (5µm thick) were cut and placed on Superfrost slides. After deparaffinised and rehydration, antigen-retrieval buffer was applied at 100°C for 15 min. After cooling, the slides were immersed with 3% hydrogen peroxide following by blocking buffer for 10 min after washing 0.1% (v/v) Tween 20 in Tris-buffered saline (TBST: 3×5min). Sections were then incubated with Rabbit anti-Osteopontin (Abcam, Inc., ab8448, 1:100) over night at 4°C. After washing (TBST: 3×5min), the goat anti-rabbit biotinylated secondary antibody (Abcam, Inc., ab64256) was added to the sections for 1 hour at room temperature then were washed again with TBST. Next, the slides were incubated with streptavidin-HRP conjugate (Abcam, Inc., ab64269) for 20 min then washed 3×5 min TBST. Colour was developed by adding a suitable amount of 3,3'-diaminobenzidine tetrahydrochloridechromogen substrate for 5 min. Slides were counterstained with haematoxylin, dehydrated and cleared, mounted by cover slip and visualised using a Leica DM6000 B

light microscope. Primary antibody was omitted in the negative control sections.

Sperm immunostaining

Sperm-smeared slides were surrounded by Hydrophobic Barrier Pap Pen, then incubated in PBS for 5 min followed by blocking buffer for 15 min at RT. Slides were then incubated with rabbit anti-Osteopontin (Abcam, Inc., ab8448, 1:50) for 1 hour at RT followed by washing (3×5 min PBS). All slides were incubated with goat anti-rabbit fluorescent secondary antibody (FITC) (Abcam, Inc., ab6717, 1;100) for 2 hours in a dark place at RT. After washing (3×5 min PBS), a cover slip was mounted on the slides using aqueous antifade mounting medium. Then slides were visualised immediately using Leica DM6000 B fluorescent microscope. In addition, chromogenic immunostaining of sperm slides were performed similar to that conducted on tissue slides.

Statistical analysis

Data were analysed using SPSS software version 16. Comparisons were made among different tissues with varying expressions as means \pm standard errors *via* a one-way analysis of variance with post hoc analysis. Data were shown as means \pm standard errors.

Results and Discussion

Relative gene expression of OPN in the testis and epididymis

As shown in fig 1, relative gene expression of OPN revealed differences mRNA expression between testis and epididymis parts. Meanwhile, the highest expression of OPN was detected in the cauda of epididymis. The data indicated that OPN mRNA expression in the cauda of epididymis was significantly (P < 0.05) higher compared to the other tissues. However, no significant differences were seen between testis, caput and corpus of epididymis.

Immunolocalisation of OPN in the testis and epididymis

In seminiferous tubules, a highly intense immune-reactivity of OPN was observed in the elongated spermatids. However, spermatogonia and Sertoli cells revealed a faint immune-intensity. In addition, Leydig cells in the interstitial tissue showed strong OPN immune-intensity (Fig 2A). The caput, corpus and cauda of epididymis, revealed intense immune-reactivity of OPN in the cytoplasm of epithelial cells with a highly concentrated intensity in the apical region nearby lumen of epididymis (Figs 2B, C and D). Meanwhile, a strong immune-reactivity was observed in the sperm's acrosome of cauda epididymidis (Fig 2D). No positive immune reaction was observed in all control sections (Figs 2, A1, B1, C1 and D1).

Immunolocalisation of OPN of epididymal sperm

Positive OPN immuno-reactivity was found in the epididymal sperm. Specific immune-localisation of OPN was detected in both acrosomal cap and neck of epididymal sperm in fluorescent (Fig 3A) and chromogenic immunostaining (Fig 3B). However, in other parts of the sperm, no positive immuno-reaction was observed.

OPN is an indispensable highly phosphorylated glycoprotein in mammalian reproduction that was observed in different male reproductive tissues such as testis, epididymis and sperm cells (Lin *et al*, 2006; RodrÍguez *et al*, 2000; Siiteri *et al*, 1995; Wilson *et al*, 2005; Souza *et al*, 2009; Kang *et al*, 2014). Our study examined for the first time the spatial expression of OPN in the male dromedary camel reproductive tract.

In this study, mRNA transcription of OPN was expressed in the testis and all parts of epididymis. Moreover, the highest expression was in the tail (cauda) of the epididymis. OPN expression in different locations along the reproductive tract implies to the need of this vital protein for the supportive and protective function during sperm journey. However, the concentration of this protein at the last trip (storage) is also suggested to have a strong protective role with integrity adhesion



Fig 1. Comparison of OPN expression level in the testis, caput, corpus and cauda epididymis of dromedary camels by qRT-PCR. The gene expressions were normalised to GAPDH and showed as means ± standard errors. The significance was set to P<0.05 and different letters (a, b) indicate significance among examined tissues. The cauda epididymis showed a high expression in comparison with other reproductive tissues.



Fig 2. Immuno-staining of the OPN in the testis and epididymis of male dromedary camels. (A) Testis, showing highly intense immuno-reactivity in both elongated spermatids and interstitial Leydig cells (thin arrows), while less faint immuno-reactivity appeared in spermatogonia and Sertoli cells (thick arrows). (B) Caput epididymis, (C) Corpus epididymis and (D) Cauda epididymis showing highly concentrated intensity in the apical region nearby lumen of epididymis (thin arrows); meanwhile, strong immune-reactivity was observed in the sperm's acrosome of cauda epididymis (thick arrows). (A1-D1) negative control Section. Scale bar, 100 µm.



Fig 3. Fluorescent (A) and chromogenic (B) immunostaining of OPN in epididymal camel sperm. Both acrosomal cap and neck (arrows) of epididymal sperm showing positive immuno-reactivity of OPN. Scale bar, 10 μm.

function that required for sperm maturation, storage and migration. In the same context, similar results were found in other species such as rat and bull by (RodrÍguez *et al*, 2000; Siiteri *et al*, 1995). In previous studies, the OPN immunolocalisation has been detected in the testis and epididymis of different mammalians such as boar, bovine and rat (Lin *et al*, 2006; RodrÍguez *et al*, 2000;

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Siiteri et al, 1995). In the present study, OPN was localised on several regions of the camel testis. The highest signals were localised in the elongating spermatids of seminiferous tubules and testicular interstitium (Leydig cells). However, the low signals were observed in some spermatogonia and Sertoli cell. Presence of OPN in various localised stages of testicular tissue particularly the seminiferous tubules might indicate that it may play a key role in spermatogenesis. Previously, it has been documented that the OPN protein binds to a variety of cell surface integrins (transmembrane receptors) which promote cell-cell and cell-ECM adhesion resulting in cytoskeletal organisation and cellular transduction (Burghardt et al, 2002; Sodek et al, 2000; Johnson et al, 2014). Meanwhile, Sertoli cells to germ cells and germ cells to germ cells adhesion and communication are required to provoke and regulate the spermatogenesis (Jégou and Pineau, 1995). Therefore, OPN seems to share in Sertoli-germ cells, germ-germ cells or both adhesion and communication in the seminiferous tubules.

In similar previous studies, OPN was detected in spermatogonia, different stages of spermatocytes, acrosomes of spermatids, some Sertoli cells and Leydig cells in the boar testis (Kim and Shin, 2007). However, in the sheep testis, it was detected in the acrosomes of spermatids near the lumen of the seminiferous tubule (Zhang *et al*, 2016). In addition, OPN has been presented in both sertoli cells and germ cells in the rat (Siiteri *et al*, 1995; Luedtke *et al*, 2002) and mouse (Wilson *et al*, 2005). Interestingly, these results are closely resembling to that found in our present study. However, in contrast, Cancel *et al* (1999) reported that the OPN was undetected in the testis of bovine.

In the present study, the epididymis of the camel showed clear immunostaining of OPN in the epithelial layer. However, highly concentrated intensity was detected in the apical region nearby lumen of epididymis. Meanwhile, a strong immunereactivity was observed in the sperm's acrosome of cauda epididymidis. Beside cell-cell and cell-ECM adhesion and communication functions, OPN has been reported to promote cell migration, cell death reduction and intracellular calcium alteration (Butler, 1989; Johnson et al, 2014). It is therefore, believed that OPN localisation in the epididymis parts particularly in cauda epididymidis and sperm acrosome promote spermatozoa migration and protect it from death during the long journey and may contribute in ova penetration during fertilisation process. In comparison, similar data have been reported in the rat by Luedtke *et al* (2002). However, in the sheep, it was concentrated on the apical region of the principal cells in the epididymis and on the caudal epididymal spermatozoa (Zhang *et al*, 2016). However, in contrast, OPN was undetected in the epididymis of bovine (Cancel *et al*, 1999).

In the sperm cell, we found OPN in the acrosomal cap and neck of epididymal sperm of camel. Harmonically, Waheed *et al* (2015) reported that the OPN was detected in the seminal plasma of dromedary camel suggesting that OPN has an important role in male's fertility. In another species, OPN was located in the post-acrosomal region and on the midpiece of epididymal sperm of bull (Erikson *et al*, 2007). Furthermore, OPN was observed in the surface of epididymal sperm and epididymal fluid in the rat (Siiteri *et al*, 1995). Therefore, detection of OPN in acrosomal and neck of sperm may provide biofuels to migrate and penetrate during reproductive process.

In conclusion, spatial expression patterns of OPN in testis, epididymis and sperm cell of dromedary camel could play a role in spermatozoal vital functions and spermatogenesis. In addition, the localisation of OPN on the acrosomal cap and neck of camel sperm might carry out a function in the migration, fertilisation and early embryonic development.

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REVERSE DIAGNOSTIC WORKFLOW TO SHORTLIST MERS-COV SPIKE ANTIGENIC EPITOPES IN DROMEDARY CAMELS

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ABSTRACT

In this study, we provide a comprehensive reverse diagnostic workflow, in which, the *in-silico* amino acid composition was employed retrogradely to shortlist the viral spike antigenic epitopes to infer diagnostics efficiency. This study was aimed to explore the analytical estimates of changes in epitope composition among MERS-CoV lineages. This can be used as a predictor of the effectiveness of rapid diagnostic testing. Therefore, MERS-CoV lineagespecific spike protein sequences were extracted, aligned and compared. In addition, the degree of sequence similarity, as well as pairwise comparison, phylogenetic relations and antigenic epitopes analysis, have been conducted. The current findings indicated that no differences were observed in length and range of epitopes for each virus among all studied lineages. Most of epitopes sequences were conserved. However, few sequences showed few single amino acid mutations. About 20% of epitopes were located at the receptor-binding domain (RBD) and 80% of these were located in the other Spike's domains. These mutations were related to lineage 2 and 3 and not for lineage 1, 4 and 5. The number of difference among viruses accession no (ALA49781, ALA49594, ALA49440, ALA50001, ALA49935, ALA49847, ALA49825, ALA49561, ALA49374, ALA49803, ALA49660, ALA49352, ALA49671, ALA49341, AHX00711, AHY22565, AJG44124, AJG44091, ALA49429, ALA49418, ALA49902, AHY22525, AHX71946, AHE78108.1, AHI48672.1, AHI48550) was maximum of 8. No gaps were observed in the epitopes alignment. The identity of spike protein among the lineages ranged from 99.5-100%. The study concluded that any of studied epitopes are suitable for production of rapid tests of MERS CoV in dromedary camels, particularly that produced from lineages 1, 4 and 5.

Key words: MERS CoV, camels, epitopes, viral lineage, rapid test

The Middle East respiratory syndrome coronavirus (MERS-CoV) was initially discovered in a patient with acute respiratory distress syndrome in the Kingdom of Saudi Arabia in October 2012 (Zaki et al, 2012). MERS-CoV is diagnosed primarily by molecular methods, i.e. Real-time reverse transcriptase-polymerase amplification (RT-PCR) (Corman et al, 2012a; 2012b), reverse transcriptionloop-mediated isothermal amplification (RTLAMP) and reverse transcription-recombinase polymerase amplification (RT-RTPA) (Shirato et al, 2014; Abd El Wahed et al, 2013). MERS-CoV or closely related viruses have also been detected in seropositive camels using a variety of serological techniques. Protein microarrays (Reusken et al, 2013a, 2013b; Meyer et al, 2013), a recombinant spike immunofluorescent assay (Buchholz et al, 2013; Annan et al, 2013), an indirect enzyme-linked immunosorbent assay (ELISA) (Alexandersen et al, 2014), microneutralisation, and spike pseudoparticle neutralisation are some of the techniques used (Perera et al, 2013). Molecular tests are relatively expensive and considered problematic for screening large numbers of animals in a short period of time; therefore, a rapid, inexpensive, sensitive, and specific test for the diagnosis of MERS-CoV in camels is required. MERS-CoV antigen was detected in the nasal swabs of dromedary camels using a fast immunochromatographic technique (Song et al, 2015). The identification of MERS-CoV nucleocapsid protein in a short time period utilising highly specific monoclonal antibodies at room temperature is the basis of this assay. The viral spike protein of MERS-CoV, which has both conserved and highly mutable or variable regions in its sequence, is the focus of most contemporary fast diagnostic assays. The accuracy of such testing is then jeopardised by mutations,

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particularly in the virus's antigenic epitopes. This study presents analytical estimates of changes in epitope composition among MERS-CoV lineages.

Materials and Methods

Retrieval of input protein data and analytical programs

The sequences of the input spike protein were retrieved from the previously analysed MERS-CoV lineages (Chu *et al*, 2018; Sabir *et al*, 2016). Table 1 provides an overview of the genomes and proteins utilised in the study. CLC Genomics Workbench 12.0 (QIAGEN, Aarhus, Denmark) and Geneious prime were used to process the sequences (Kearse *et al*, 2012).

Sequence alignment and retrieval of the spike protein

The CLC genomics program's protein sequence capabilities were used to handle the spike protein

sequence. With 10 gaps open and one gap extension cost, a very accurate alignment was achieved using the protein alignment wizard's alignment parameters. To compare the sequences, a pairwise comparison matrix was created. The identity matrix was created after calculating the differences, identity percentage, gaps and mutations.

Phylogenetics

The phylogenetic tree was built using the neighbour-joining (NJ) technique and then evaluated for evolutionary links. Using the default settings, the CLC genomics program was utilised. Distances were calculated using the JTT substitution model. The neighbour-joining method was tested to 100 Bootstrap resampling repeats. (Romesburg, 2004).

Spike's antigenic epitopes

The potential antigenic epitopes in studied MERS-CoV lineages were searched at EMBOSS

Table 1. The accession numbers (no.) and description of the genomes and proteins used in this study.

| Lineage | Accession no. of full genome | Accession no. of Spike | Description |
|---------|------------------------------|---------------------------|---|
| 5 | Camel/Jeddah/Jd87/2015 | ALA49781 | Spike protein [Middle East respiratory syndrome-related coronavirus]. |
| 5 | Camel/Jeddah/N62(b)/2014 | ALA49594 | Spike protein [Middle East respiratory syndrome-related coronavirus]. |
| 5 | Camel/Jeddah/D38/2014 | ALA49440 | Spike protein [Middle East respiratory syndrome-related coronavirus]. |
| 5 | Camel/Taif/T68/2015 | ALA50001 | Spike protein [Middle East respiratory syndrome-related coronavirus]. |
| 5 | Camel/Riyadh/Ry79/2015 | ALA49935 | Spike protein [Middle East respiratory syndrome-related coronavirus]. |
| 5 | Camel/Riyadh/Ry159/2015 | ALA49847 | Spike protein [Middle East respiratory syndrome-related coronavirus]. |
| 5 | Camel/Riyadh/Ry136/2015 | ALA49825 | Spike protein [Middle East respiratory syndrome-related coronavirus]. |
| 3 | Camel/Jeddah/D90/2014 | ALA49561 | Spike protein [Middle East respiratory syndrome-related coronavirus]. |
| 3 | Camel/Jeddah/401/2014 | ALA49374 | Spike protein [Middle East respiratory syndrome-related coronavirus]. |
| 3 | Camel/Jeddah/Jd175/2015 | ALA49803 | Spike protein [Middle East respiratory syndrome-related coronavirus]. |
| 3 | Camel/Jeddah/S100/2014 | ALA49660 | Spike protein [Middle East respiratory syndrome-related coronavirus]. |
| 3 | Camel/Riyadh/Ry23N/2014 | ALA49352 | Spike protein [Middle East respiratory syndrome-related coronavirus]. |
| 3 | Camel/Jeddah/S73/2014 | ALA49671 | Spike protein [Middle East respiratory syndrome-related coronavirus]. |
| 3 | Camel/Jeddah/F13A/2014 | ALA49341 | Spike protein [Middle East respiratory syndrome-related coronavirus]. |
| 2 | KFU-HKU/13/2013 | AHX00711 | Spike protein [Middle East respiratory syndrome-related coronavirus]. |
| 2 | Camel/KSA/376/2013 | AHY22565 | Spike protein [Middle East respiratory syndrome-related coronavirus]. |
| 2 | Camel/UAE/D1209/2014 | AJG44124 | S [Middle East respiratory syndrome-related coronavirus]. |
| 2 | Camel/UAE/D1164.14/2014 | AJG44091 | S [Middle East respiratory syndrome-related coronavirus]. |
| 4 | Camel/Jeddah/D36/2014 | ALA49429 | Spike protein [Middle East respiratory syndrome-related coronavirus]. |
| 4 | Camel/Jeddah/D35/2014 | ALA49418 | Spike protein [Middle East respiratory syndrome-related coronavirus]. |
| 4 | Camel/Riyadh/Ry179/2015 | ALA49902 | Spike protein [Middle East respiratory syndrome-related coronavirus]. |
| 4 | Camel/KSA/505/2014 | AHY22525 | Spike protein [Middle East respiratory syndrome-related coronavirus]. |
| 4 | Camel/Qatar/2/2014 | AHX71946 | Spike protein [Middle East respiratory syndrome-related coronavirus]. |
| 1 | Camel/Jeddah-Camel-1/2013 | AHE78108.1 | S [Middle East respiratory syndrome-related coronavirus] |
| 1 | Taif/1/2013 | AHI48672.1 | S protein [Middle East respiratory syndrome-related coronavirus] |
| 1 | Wadi-Ad-Dawasir_1/2013 | AHI48550 | S protein [Middle East respiratory syndrome-related coronavirus] |

antigenic prediction tool (Kolaskar and Tongaonkar, 1990). The antigenic determination is based on a semi-empirical approach based on physicochemical properties of amino acid residues and their frequencies of occurrence in experimentally known segmental epitopes. The minimal length of antigenic region was set to six. The output format was set to EMBOSS motif.

Results

Antigenic epitopes

Antigenic epitope analysis requests were sent to the EMBOSS antigenic prediction tool. Based on the output epitopes, the 15 epitopes with the highest epitope score were extracted and compared among MERS-CoV lineages. Table 2 summarises the

Table 2. The antigenic epitopes predicted by EMBOSS antigenic detection in MERS-CoV lineages. The epitopes are in descending order according to the predicted score. Top 15 epitopes for each virus were selected.

| Virus | # | In RBD (YES/ No) | Sequence | length | range | Conserved/ mutations no. | score |
|--|----|------------------------|--|--------|------------|--|-------|
| AHE78108.1 | 1 | No | YIWLGFIAGLVALALCVFFILCCTGCGTN | 29 | 1298->1326 | Conserved | 1.258 |
| AHI48550.1 AHX71946 1 | 2 | No | NYYCLRACVSVPVSVIYD | 18 | 647->664 | Conserved | 1.243 |
| AHY22525 | 3 | No | SGFCGQGTHIVSFVVNAP | 18 | 1114->1131 | Conserved | 1.216 |
| AHY22565.1 AJG44124.1 | 4 | Yes | YSPCVSIVPST | 11 | 523->533 | Conserved | 1.210 |
| ALA49341.1 | 5 | No | ARDLICAQYVAGYKVLPPLM | 20 | 920->939 | Conserved | 1.205 |
| ALA49552.1 ALA49418.1 ALA49429.1 | 6 | No | YGPLQTPVGCVLGLVNSSLFVEDCKLPL GQSLCALPDTP | 39 | 704->742 | Conserved | 1.204 |
| ALA49440.1 | 7 | Yes | NPTCLILATVPHNLT | 15 | 475->489 | Conserved | 1.203 |
| ALA49561.1 ALA49594.1 | 8 | No | TTLLDLTYEMLSLQQVVKALNESYIDLK | 28 | 1257->1284 | Conserved | 1.187 |
| ALA49660.1 ALA49671.1 | 9 | Yes | NYNLTKLLSLFSVNDFTCSQISPAAIASN CYSSLILDYFSYPLS | 44 | 408->451 | T424I (ALA49341.1) L411F (ALA49374.1) | 1.178 |
| ALA49803.1 | 10 | No | SVFLLMFLLTPTESYVDVGPDSVKSACIEVDIQQT | 35 | 4->38 | Conserved | 1.178 |
| ALA49825.1 ALA49847.1 | 11 | No | ASQLGNCVEYSLYGVSGRG | 19 | 597->615 | Conserved | 1.176 |
| ALA49902.1 | 12 | No | NHTLVLLPDGCGTLLRAFYCILEP | 24 | 166->189 | Conserved | 1.173 |
| ALA49935.1 ALA50001.1 | 13 | No | TLNAFVAQQLVRSESAALSAQLAKD | 25 | 1077->1101 | Conserved | 1.172 |
| | 14 | No | SFGVTQEYIQTTIQKVTVDCKQYVCNGF | 28 | 787->814 | V810I (AJG44091.1) V810I (AHX00711.1) | 1.168 |
| | 15 | No | GLYFMHVGYYPSNHIEVVSAYGLCDAA | 27 | 1133->1159 | A1159S (AHY22565.1) | 1.165 |
| AHX00711.1 | 1 | No | YIWLGFIAGLVALALCVFFILCCTGCGTN | 29 | 1298->1326 | Conserved | 1.258 |
| AJG44091.1 | 2 | No | NYYCLRACVSVPVSVIYD | 18 | 647->664 | Conserved | 1.243 |
| | 3 | No | SGFCGQGTHIVSFVVNAP | 18 | 1114->1131 | Conserved | 1.216 |
| | 4 | Yes | YSPCVSIVPST | 11 | 523->533 | Conserved | 1.210 |
| | 5 | No | ARDLICAQYVAGYKVLPPLM | 20 | 920->939 | Conserved | 1.205 |
| | 6 | No | YGPLQTPVGCVLGLVNSSLFVEDCKLPLGQSLCAL PDTP | 39 | 704->742 | Conserved | 1.204 |
| | 7 | Yes | NPTCLILATVPHNLT | 15 | 475->489 | Conserved | 1.203 |
| | 8 | No | TTLLDLTYEMLSLQQVVKALNESYIDLK | 28 | 1257->1284 | Conserved | 1.187 |
| | 9 | Yes | NYNLTKLLSLFSVNDFTCSQISPAAIASN CYSSLILDYFSYPLS | 44 | 408->451 | T424I (ALA49341.1) L411F (ALA49374.1) | 1.178 |
| | 10 | No | SVFLLMFLLTPTESYVDVGPDSVKSACIEVDIQQT | 35 | 4->38 | Conserved | 1.178 |
| | 11 | No | ASQLGNCVEYSLYGVSGRG | 19 | 597->615 | Conserved | 1.176 |
| | 12 | No | NHTLVLLPDGCGTLLRAFYCILEP | 24 | 166->189 | Conserved | 1.173 |
| | 13 | No | TLNAFVAQQLVRSESAALSAQLAKD | 25 | 1077->1101 | Conserved | 1.172 |
| | 14 | No | GLYFMHVGYYPSNHIEVVSAYGLCDAA | 27 | 1133->1159 | A1159S (AHY22565.1) | 1.165 |
| | 15 | No | HATLFGSVACEHI | 13 | 670->682 | Conserved | 1.155 |

Table 2 continued

| ALA49374.1 | 1 | No | YIWLGFIAGLVALALCVFFILCCTGCGTN | 29 | 1298->1326 | Conserved | 1.258 |
|------------|----|-----|---|----|------------|--|-------|
| | 2 | No | NYYCLRACVSVPVSVIYD | 18 | 647->664 | Conserved | 1.243 |
| | 3 | No | SGFCGQGTHIVSFVVNAP | 18 | 1114->1131 | Conserved | 1.216 |
| | 4 | Yes | YSPCVSIVPST | 11 | 523->533 | Conserved | 1.210 |
| | 5 | No | ARDLICAQYVAGYKVLPPLM | 20 | 920->939 | Conserved | 1.205 |
| | 6 | No | YGPLQTPVGCVLGLVNSSLFVEDCKLPLGQSLCA LPDTP | 39 | 704->742 | Conserved | 1.204 |
| | 7 | Yes | NPTCLILATVPHNLT | 15 | 475->489 | Conserved | 1.203 |
| | 8 | No | TTLLDLTYEMLSLQQVVKALNESYIDLK | 28 | 1257->1284 | Conserved | 1.187 |
| | 9 | Yes | TKLLSLFSVNDFTCSQISPAAIASNCYSSLILDYFSYPLS | 40 | 412->451 | T424I (ALA49341.1) | 1.178 |
| | 10 | No | SVFLLMFLLTPTESYVDVGPDSVKSACIEVDIQQT | 35 | 4->38 | Conserved | 1.178 |
| | 11 | No | ASQLGNCVEYSLYGVSGRG | 19 | 597->615 | Conserved | 1.176 |
| | 12 | No | NHTLVLLPDGCGTLLRAFYCILEP | 24 | 166->189 | Conserved | 1.173 |
| | 13 | No | TLNAFVAQQLVRSESAALSAQLAKD | 25 | 1077->1101 | Conserved | 1.172 |
| | 14 | No | SFGVTQEYIQTTIQKVTVDCKQYVCNGF | 28 | 787->814 | V810I (AJG44091.1) V810I (AHX00711.1) | 1.168 |
| | 15 | No | GLYFMHVGYYPSNHIEVVSAYGLCDAA | 27 | 1133->1159 | A1159S (AHY22565.1) | 1.165 |

epitopes sequences, their respective location on either RBD or other S protein domains, the range of amino acid, conservation among lineages and the predicted mutations. The epitopes were arranged in descending order, according to their antigenic scores.

Spike alignment

The spike protein sequences of various MERS-CoV lineages were aligned (Fig 1). The alignment showed a mostly conserved amino acid sequence with few mutations, which are summarised in table 3. These mutations were related to lineage 2 and 3. However, these mutations were few and involved only single amino acid. The current findings indicated that there were no differences observed in length and range of epitopes for each virus among all studied lineages (Table 2). Most of epitopes sequences were conserved. However, few sequences underwent little mutation involving single amino acids (Table 2). Except for AHX00711.1 and AJG44091.1, single amino acid mutations were observed at epitope no. 9, 14 and 15 (Table 2). At epitope 9, these mutations were T424I (ALA49341.1) and L411F (ALA49374.1) (Table 2). At epitope 14, these mutations were V810I (AJG44091.1) and V810I (AHX00711.1) (Table 2). At epitope 15, this mutation was A1159S (AHY22565.1) (Table 2). For AHX00711.1 and AJG44091.1, the single amino acid mutations were at epitopes no. 9 and 14 (Table 2). At epitope 9, these mutations were T424I (ALA49341.1) and L411F (ALA49374.1). At epitope 14, this mutation was A1159S (AHY22565.1) (Table 2). Data summarised in table 3 indicated that 20% of epitopes sequences are located at the receptor-binding domain (RBD) and 80% of these sequences are located away from the RBD.

This finding suggests the reliability of using a rapid test based on spike protein epitopes in dromedary camels by targeting multiple domains epitopes on the surface of MERS-CoV spike.

 Table 3. List of observed mutations in virus spike in the studied lineages.

| Mutation | Present in all lineages (Yes/No) | lineage | Accession number of mutants |
|----------|--|---------|-----------------------------------|
| T424I | No | 3 | ALA49341.1 |
| L411F | Yes | 3 | ALA49374.1 |
| V810I | Yes | 2 | AJG44091.1 |
| V810I | Yes | 2 | AHX00711.1 |
| A1159S | Yes | 2 | AHY22565.1 |

Pairwise comparison matrix

Pairwise comparison matrix revealed the absence of gaps in the alignment that indicates the lack of amino acid insertions or deletions in the spike protein among the lineages (Fig 2). In addition, the number of differences among viruses was a maximum of 8. The highest difference was 8 and it was among virus no 25 when matched with virus no 23 and 22 (Fig 2). Fortunately, most of these mutations are not involved in the antigenic epitopes. Pairwise comparison matrix revealed a higher identity of the spike protein among the lineages which ranged from 99.5 -100% (Fig 3).

Phylogenetic analysis

The spike protein of MERS-CoV was clustered in 3 main lineages (Fig 4). This indicates that the virus diversity is less common in virus spike, compared with the full genome.



Fig 1. Sequence alignment of spike protein from different MERS-CoV lineages.

| | | 1 | 2 | 3 | - 4 | 5 | 6 | 7 | 8 | 9 | 10 | 15 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 |
|------------|------|-----|-----|----|-----|-----|-----|---|-----|---|----|-----|----|-----|-----|-----|----|-----|----|----|----|-----|-----------|----|----|----|
| AHE78108.1 | T., | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| AH148550.1 | 2 | 1 | | 0 | 0 | .0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| ALA49561.1 | t | 2 | 3 | | Ó | 0 | Ó | 0 | â | 0 | Ó | 0 | 0 | Ó | 0 | 0 | 0 | Ó | Ô | Ó | 0 | 0 | 0 | 0 | Ó | 0 |
| ALA49374.1 | 4 | 3 | 4 | | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | Ó | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| ALA49352.1 | 5 | | 3 | 2 | 3 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| AHY22525.1 | 6 | 1 | 2 | 1 | 2 | 1 | | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| ALA49440.1 | 7 | 1 | 2 | -1 | 2 | 1 | 0 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| ALA50001.1 | 8 | 1 1 | 2 | | 2 | 1 | 0 | 0 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| ALA49935.1 | 9 | 1 | - 2 | 1 | 2 | 1 | 0 | 0 | 0 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| ALA49847.1 | 10 | 1 | 2 | 1 | 2 | | Ó | 0 | 0 | 0 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | .0 |
| ALA49825.1 | - 11 | 1 | 2 | 1 | 2 | 1 | 0.0 | 9 | | 0 | 0 | | 0 | 0 | .0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| AHX71946.1 | 12 | 2 | - 3 | 2 | 3 | 2 | | | 5 | 1 | 1 | 1 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| ALA49429.1 | 13 | 3 | 4 | 1 | 2 | 3 | 2 | 2 | 2 | 2 | 2 | 2 | 3 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| ALA49418.1 | - 34 | 3 | 4 | 1 | 2 | 3 | 2 | 2 | 2 | 2 | 2 | 2 | 3 | 9 | | 0 | 0 | 0 | 0 | 0 | 0 | . 0 | 0 | 0 | 0 | 0 |
| ALA49902.1 | 15 | 3 | 3 | 2 | 3 | 2 | 1 | 1 | 1 | 1 | 1 | 1 | 2 | 1 | - 1 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| ALA49660.1 | 16 | . 4 | 5 | 2 | 3 | - 4 | 3 | 3 | 3 | 3 | 3 | 3 | | 3 | 3 | 4 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| ALA49671.1 | 17 | | 5 | 2 | 3 | 4 | 3 | 3 | 3 | 3 | 3 | 3 | 4 | 3 | 3 | | 2 | | 0 | 0 | 0 | . 0 | 0 | 0 | 0 | 0 |
| AJG44124.1 | 18 | 3 | 4 | 3 | .4 | 3 | 2 | 2 | 2 | 2 | 2 | 2 | 3 | 4 | - 4 | 3 | 5 | 5 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| ALA49781.1 | 19 | 2 | 3 | 2 | 3 | 2 | 1 | 1 | 1 | 1 | 3 | 1 | 2 | 3 | 3 | 2 | 4 | - 4 | 3 | | 0 | 0 | 0 | 0 | 0 | 0 |
| ALA49594.1 | 20 | 2 | 3 | 2 | 3 | 2 | | 1 | 1 | 1 | 1 | 1 | 2 | 3 | 3 | 2 | 4 | - 4 | 3 | 0 | | 0 | 0 | 0 | 0 | 0 |
| AJG44091.1 | 21 | 4 | 5 | 4 | 5 | 4 | 3 | 3 | 3 | 3 | 3 | 3 | 4 | 5 | 5 | 4 | 6 | 6 | 3 | 4 | 4 | | 0 | 0 | 0 | 0 |
| AHX00711.1 | 22 | 5 | 6 | 5 | 0 | 5 | 4 | | - 4 | 4 | 4 | - 4 | 5 | 0 | 6 | 5 | 7. | 7 | 4 | 5 | 5 | 3 | · · · · · | 0 | 0 | 0 |
| AHY22565.1 | 23 | 5 | 6 | 5 | 6 | 6 | 4 | 4 | 4 | 4 | 4 | 4 | 5 | 6 | .6 | - 5 | 7 | 7 | 4 | 5 | 5 | 5 | 0 | | 0 | 0 |
| ALA49341.1 | 24 | 3 | 4 | 3 | 4 | 3 | 2 | 2 | 2 | 2 | 2 | 2 | 3 | 4 | 4 | 3 | 5 | 5 | 4 | 3 | 3 | 5 | 6 | e | - | 0 |
| ALA49803.1 | 25 | 5 | 6 | 3 | 4 | 5 | 4 | 4 | 4 | 4 | 4 | 4 | 5 | . 4 | 4 | 5 | 5 | 5 | 6 | 5 | 5 | 7 | 8 | | 6 | |

Fig 2. Comparative pairwise matrix for sequences of spike protein from different MERS-CoV lineages. The upper diagonal panel is the number of amino acid differences.

| | | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 |
|--------------|----|---------|-----------|---------|-----------|---------|-----------|----------------|----------------|----------------|----------------|----------------|-----------|-----------|----------------|-----------|---------|---------|---------|-----------|----------------|---------|---------|---------|--------|--------|
| AHE78108.1 | 1 | | 7.3939E-4 | 0.0015 | 0.0022 | 0.0015 | 7.3939E-4 | 7.3939E-4 | 7.3939E-4 | 7.3939E-4 | 7.3939E-4 | 7.3939E-4 | 0.0015 | 0.0022 | 0.0022 | 0.0015 | 0.0030 | 0.0030 | 0.0022 | 0.0015 | 0.0015 | 0.0030 | 0.0037 | 0.0037 | 0.0022 | 0.0037 |
| AHI48550.1 | 2 | 99.9261 | | 0.0022 | 0.0030 | 0.0022 | 0.0015 | 0.0015 | 0.0015 | 0.0015 | 0.0015 | 0.0015 | 0.0022 | 0.0030 | 0.0030 | 0.0022 | 0.0037 | 0.0037 | 0.0030 | 0.0022 | 0.0022 | 0.0037 | 0.0044 | 0.0044 | 0.0030 | 0.0044 |
| ALA49561.1 | 3 | 99.8522 | 99.7783 | | 7.3939E-4 | 0.0015 | 7.3939E-4 | 7.3939E-4 | 7.3939E-4 | 7.3939E-4 | 7.3939E-4 | 7.3939E-4 | 0.0015 | 7.3939E-4 | 7.3939E-4 | 0.0015 | 0.0015 | 0.0015 | 0.0022 | 0.0015 | 0.0015 | 0.0030 | 0.0037 | 0.0037 | 0.0022 | 0.0022 |
| ALA49374.1 | 4 | 99.7783 | 99.7044 | 99.9261 | | 0.0022 | 0.0015 | 0.0015 | 0.0015 | 0.0015 | 0.0015 | 0.0015 | 0.0022 | 0.0015 | 0.0015 | 0.0022 | 0.0022 | 0.0022 | 0.0030 | 0.0022 | 0.0022 | 0.0037 | 0.0044 | 0.0044 | 0.0030 | 0.0030 |
| ALA49352.1 | 5 | 99.8522 | 99.7783 | 99.8522 | 99.7783 | | 7.3939E-4 | 7.3939E-4 | 7.3939E-4 | 7.3939E-4 | 7.3939E-4 | 7.3939E-4 | 0.0015 | 0.0022 | 0.0022 | 0.0015 | 0.0030 | 0.0030 | 0.0022 | 0.0015 | 0.0015 | 0.0030 | 0.0037 | 0.0037 | 0.0022 | 0.0037 |
| AHY22525.1 | 6 | 99.9261 | 99.8522 | 99.9261 | 99.8522 | 99.9261 | | 1.0547E- 16 | 1.0547E- 16 | 1.0547E- 16 | 1.0547E- 16 | 1.0547E- 16 | 7.3939E-4 | 0.0015 | 0.0015 | 7.3939E-4 | 0.0022 | 0.0022 | 0.0015 | 7.3939E-4 | 7.3939E-4 | 0.0022 | 0.0030 | 0.0030 | 0.0015 | 0.0030 |
| ALA49440.1 | 7 | 99.9261 | 99.8522 | 99.9261 | 99.8522 | 99.9261 | 100.0000 | | 1.0547E- 16 | 1.0547E- 16 | 1.0547E- 16 | 1.0547E- 16 | 7.3939E-4 | 0.0015 | 0.0015 | 7.3939E-4 | 0.0022 | 0.0022 | 0.0015 | 7.3939E-4 | 7.3939E-4 | 0.0022 | 0.0030 | 0.0030 | 0.0015 | 0.0030 |
| ALA50001.1 | 8 | 99.9261 | 99.8522 | 99.9261 | 99.8522 | 99.9261 | 100.0000 | 100.0000 | | 1.0547E- 16 | 1.0547E- 16 | 1.0547E- 16 | 7.3939E-4 | 0.0015 | 0.0015 | 7.3939E-4 | 0.0022 | 0.0022 | 0.0015 | 7.3939E-4 | 7.3939E-4 | 0.0022 | 0.0030 | 0.0030 | 0.0015 | 0.0030 |
| ALA49935.1 | 9 | 99.9261 | 99.8522 | 99.9261 | 99.8522 | 99.9261 | 100.0000 | 100.0000 | 100.0000 | | 1.0547E- 16 | 1.0547E- 16 | 7.3939E-4 | 0.0015 | 0.0015 | 7.3939E-4 | 0.0022 | 0.0022 | 0.0015 | 7.3939E-4 | 7.3939E-4 | 0.0022 | 0.0030 | 0.0030 | 0.0015 | 0.0030 |
| ALA49847.1 | 10 | 99.9261 | 99.8522 | 99.9261 | 99.8522 | 99.9261 | 100.0000 | 100.0000 | 100.0000 | 100.0000 | | 1.0547E- 16 | 7.3939E-4 | 0.0015 | 0.0015 | 7.3939E-4 | 0.0022 | 0.0022 | 0.0015 | 7.3939E-4 | 7.3939E-4 | 0.0022 | 0.0030 | 0.0030 | 0.0015 | 0.0030 |
| ALA49825.1 | 11 | 99.9261 | 99.8522 | 99.9261 | 99.8522 | 99.9261 | 100.0000 | 100.0000 | 100.0000 | 100.0000 | 100.0000 | | 7.3939E-4 | 0.0015 | 0.0015 | 7.3939E-4 | 0.0022 | 0.0022 | 0.0015 | 7.3939E-4 | 7.3939E-4 | 0.0022 | 0.0030 | 0.0030 | 0.0015 | 0.0030 |
| AHX71946.1 | 12 | 99.8522 | 99.7783 | 99.8522 | 99.7783 | 99.8522 | 99.9261 | 99.9261 | 99.9261 | 99.9261 | 99.9261 | 99.9261 | | 0.0022 | 0.0022 | 0.0015 | 0.0030 | 0.0030 | 0.0022 | 0.0015 | 0.0015 | 0.0030 | 0.0037 | 0.0037 | 0.0022 | 0.0037 |
| ALA49429.1 | 13 | 99.7783 | 99.7044 | 99.9261 | 99.8522 | 99.7783 | 99.8522 | 99.8522 | 99.8522 | 99.8522 | 99.8522 | 99.8522 | 99.7783 | | 1.0547E- 16 | 7.3939E-4 | 0.0022 | 0.0022 | 0.0030 | 0.0022 | 0.0022 | 0.0037 | 0.0044 | 0.0044 | 0.0030 | 0.0030 |
| ALA49418.1 | 14 | 99.7783 | 99.7044 | 99.9261 | 99.8522 | 99.7783 | 99.8522 | 99.8522 | 99.8522 | 99.8522 | 99.8522 | 99.8522 | 99.7783 | 100.0000 | | 7.3939E-4 | 0.0022 | 0.0022 | 0.0030 | 0.0022 | 0.0022 | 0.0037 | 0.0044 | 0.0044 | 0.0030 | 0.0030 |
| ALA49902.1 | 15 | 99.8522 | 99.7783 | 99.8522 | 99.7783 | 99.8522 | 99.9261 | 99.9261 | 99.9261 | 99.9261 | 99.9261 | 99.9261 | 99.8522 | 99.9261 | 99.9261 | | 0.0030 | 0.0030 | 0.0022 | 0.0015 | 0.0015 | 0.0030 | 0.0037 | 0.0037 | 0.0022 | 0.0037 |
| ALA49660.1 | 16 | 99.7044 | 99.6305 | 99.8522 | 99.7783 | 99.7044 | 99.7783 | 99.7783 | 99.7783 | 99.7783 | 99.7783 | 99.7783 | 99.7044 | 99.7783 | 99.7783 | 99.7044 | | 0.0015 | 0.0037 | 0.0030 | 0.0030 | 0.0044 | 0.0052 | 0.0052 | 0.0037 | 0.0037 |
| ALA49571.1 | 17 | 99.7044 | 99.6305 | 99.8522 | 99.7783 | 99.7044 | 99.7783 | 99.7783 | 99.7783 | 99.7783 | 99.7783 | 99.7783 | 99.7044 | 99.7783 | 99.7783 | 99.7044 | 99.8522 | | 0.0037 | 0.0030 | 0.0030 | 0.0044 | 0.0052 | 0.0052 | 0.0037 | 0.0037 |
| AJG44124.1 | 18 | 99.7783 | 99.7044 | 99.7783 | 99.7044 | 99.7783 | 99.8522 | 99.8522 | 99.8522 | 99.8522 | 99.8522 | 99.8522 | 99.7783 | 99.7044 | 99.7044 | 99.7783 | 99.6305 | 99.6305 | | 0.0022 | 0.0022 | 0.0022 | 0.0030 | 0.0030 | 0.0030 | 0.0044 |
| ALA49781.1 | 19 | 99.8522 | 99.7783 | 99.8522 | 99.7783 | 99.8522 | 99.9261 | 99.9261 | 99.9261 | 99.9261 | 99.9261 | 99.9261 | 99.8522 | 99.7783 | 99.7783 | 99.8522 | 99.7044 | 99.7044 | 99.7783 | | 1.0547E- 16 | 0.0030 | 0.0037 | 0.0037 | 0.0022 | 0.0037 |
| ALA49594.1 | 20 | 99.8522 | 99.7783 | 99.8522 | 99.7783 | 99.8522 | 99.9261 | 99.9261 | 99.9261 | 99.9261 | 99.9261 | 99.9261 | 99.8522 | 99.7783 | 99.7783 | 99.8522 | 99.7044 | 99.7044 | 99.7783 | 100.0000 | | 0.0030 | 0.0037 | 0.0037 | 0.0022 | 0.0037 |
| AJG44091.1 | 21 | 99.7044 | 99.6305 | 99.7044 | 99.6305 | 99.7044 | 99.7783 | 99.7783 | 99.7783 | 99.7783 | 99.7783 | 99.7783 | 99.7044 | 99.6305 | 99.6305 | 99.7044 | 99.5565 | 99.5565 | 99.7783 | 99.7044 | 99.7044 | | 0.0022 | 0.0037 | 0.0037 | 0.0052 |
| AHX00711.1 | 22 | 99.6305 | 99.5565 | 99.6305 | 99.5565 | 99.6305 | 99.7044 | 99.7044 | 99.7044 | 99.7044 | 99.7044 | 99.7044 | 99.6305 | 99.5565 | 99.5565 | 99.6305 | 99.4826 | 99.4826 | 99.7044 | 99.6305 | 99.6305 | 99.7783 | | 0.0044 | 0.0044 | 0.0059 |
| AHY22565.1 | 23 | 99.6305 | 99.5565 | 99.6305 | 99.5565 | 99.6305 | 99.7044 | 99.7044 | 99.7044 | 99.7044 | 99.7044 | 99.7044 | 99.6305 | 99.5565 | 99.5565 | 99.6305 | 99.4826 | 99.4826 | 99.7044 | 99.6305 | 99.6305 | 99.6305 | 99.5565 | | 0.0044 | 0.0059 |
| ALA49341.1 | 24 | 99.7783 | 99.7044 | 99.7783 | 99.7044 | 99.7783 | 99.8522 | 99.8522 | 99.8522 | 99.8522 | 99.8522 | 99.8522 | 99.7783 | 99.7044 | 99.7044 | 99.7783 | 99.6305 | 99.6305 | 99.7044 | 99.7783 | 99.7783 | 99.6305 | 99.5565 | 99.5585 | | 0.0044 |
| AL & 40803 1 | 25 | 99 6305 | 99.5565 | 99 7783 | 99 7044 | 99 6305 | 997044 | 99 7044 | 99 7044 | 99 7044 | 99,7044 | 997044 | 99 6305 | 99 7044 | 99 7044 | 99.6305 | 99 6305 | 99.6305 | 99 5565 | 99.6305 | 99.6305 | 99.4826 | 99.4087 | 99 4087 | 995565 | |

Fig 3. Comparative pairwise matrix for sequences of spike protein from different MERS-CoV lineages. The upper diagonal panel is the distance. The lower diagonal panel is the identity per cent.



Fig 4. Cladogram of spike protein from different MERS-CoV lineages.

Discussion

MERS-CoVs have been sequenced and classified in both humans and camels since the first human MERS-CoV was discovered (Cotten *et al*, 2014; Lau *et al*, 2016; Sabir *et al*, 2016). Sabir *et al* (2016) sequenced and analysed typical MERS-CoV genomes from Saudi Arabia, including 67 from camels and discovered different clade B MERS-CoV lineages. Co-

infections with MERS-CoV and other coronaviruses were prevalent, as were additional non-MERS-CoVs. Another study sequenced 10 different camel MERS-CoVs from Abu Dhabi and discovered viruses in many clade B lineages, including a 6th lineage and a camel MERS-CoV within clade A. The clade A MERS-CoVs are assumed to be older and not circulating today, therefore, this study provides valuable insight into camel MERS-CoV variety in nature (Lau et al, 2016). Additional efforts to sequence MERS-CoV from camels have focused on nucleocapsid and spike genes as possible locations for finding genetic diversity (van Doremalen et al, 2017). Several human coronaviruses are known to have originated from zoonotic sources (Millet et al, 2016; Muhairi et al, 2016). At a live animal market in the Emirate of Abu Dhabi's eastern region, 376 camels were checked for MERS-Cov (Yusof et al, 2017). From 139 samples, 126 whole genomes and 3 nearly complete genomes were recovered. Five of the remaining 10 samples yielded spike gene sequences. Within clade B, the genomes of camel MERS-CoV represented 3 recognised and 2 potentially novel lineages. Camel and human MERS-CoV sequences are jumbled together within lineages. In the camel samples, the researchers discovered 10 recombination events. The junctions between ORF1b and S were the most common recombination breakpoints. MERS-CoV infection in humans may have resulted from the continual transfer of various MERS-CoV lineages from camels, according to evidence. The camel MERS-CoV genomes sequenced in this investigation support this idea (Yusof et al, 2017).

The current findings indicated that there were no differences observed in length and range of epitopes for each virus among all studied lineages. Most of epitopes sequences were conserved. However, few sequences underwent little mutation involving single amino acids. The top 15 epitopes in dromedary camels have a conserved sequence, indicating that a quick test based on spike protein epitopes is reliable. According to the present data, 20% of epitope sequences are found near the RBD, whereas the remaining 80% are found distant from the RBD. In dromedary camels, this research proved the reliability of the previously mentioned rapid test based on spike protein epitopes. In the current study, the alignment of spike protein sequences from several MERS-CoV lineages indicated a small number of alterations. Lineages 2 and 3 were affected by these changes. Using rapid testing for MERS-CoV detection based on epitopes from lineages 1, 4, and 5 seems to be effective, based on the current findings.

Furthermore, given the changes in lineages 2 and 3 were rare and involved just a single amino acid, these quick tests may be successful when employing any epitope from these lineages.

The current findings revealed the absence of gaps in the alignment that indicates the lack of amino acid insertions or deletions in the spike protein among the lineages. This finding confirmed the effectiveness of any of studied epitopes for rapid test designing in dromedary camels. The current finding indicated that, the number of difference among viruses accession number was a maximum of 8, most of them were not involved in the antigenic epitopes. This finding confirmed the suitability of any of the studied epitopes for production of rapid tests of MERS CoV in dromedary camels. The current findings indicated a higher identity of the spike protein among the lineages which ranged from 99.5 -100%. This finding provides new evidence of the effectiveness of any of the studied epitopes for the production of rapid tests of MERS CoV in dromedary camels as illustrated above.

Because identifying antigens and epitopes using an experimental method may be difficult, expensive, and time-consuming, using an in-silico strategy to uncover novel epitopes has become the preferred alternative. This approach is recognised as one of the most effective in identifying antigens because it screens the whole microbial proteome using a variety of prediction algorithms. In conclusion, our comprehensive technique encompasses antigenic epitope screening both horizontally (through the whole coding areas of the Spike) and vertically (across various MERS-CoV lineages). Mutations in the targeted epitopes might have an influence on the diagnostics' population coverage and efficiency. After examining current MERS-CoV mutants across lineages, we evaluated for immunogenicity conservation in the chosen epitopes to provide more diagnostic options. The efficiency of diagnostics based on the provided configurations is expected to be high due to the observed low mutagenicity rate of MERS-CoV. Combining the present findings with experimental confirmation is a pre requisite for successful diagnostics.

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VIRULENCE GENES AND ANTIMICROBIAL RESISTANCE PROFILE OF *Escherichia coli* ISOLATES FROM DIARRHOEIC NEONATAL DROMEDARY CAMELS

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ABSTRACT

In the present study, *Escherichia coli* were isolated from rectal swabs of total 48 (20.68%) diarrhoeic neonatal dromedary camels during the five years study period in an organised farm. The PCR for amplification of virulence genes revealed that 31 (64.58%) isolates harboured at least one virulence gene. The detection rates of *stx1*, *stx2*, *eae*, *F41*, *K99* and *sta* virulence genes were 4.16%, 2.08%, 35.41%, 14.58%, 18.75% and 16.66%, respectively. Based on occurrence of these virulence genes the isolates were pathotyped into shigatoxigenic *E. coli* (STEC) (6.25%), enteropathogenic *E. coli* (EPEC) (20.83%) and enterotoxigenic *E. coli* (ETEC) (29.16%). Atypical combinations of EPEC+ETEC (8.33%) were also detected. The *E. coli* isolates from all three neonatal camels having acute haemorrhagic enteritis and mortality were found to be of STEC type. In antibiotic sensitivity test, most prevalent resistance was observed against amoxicillin, cloxacillin, erythromycin and lincomycin whereas lowest resistance was observed against gentamicin and amikacin. Findings of this study indicate that neonatal camels are the probable reservoir of multidrug resistant and zoonotic STEC. Young age (below 7 days), housing system with loose sandy ground and winter season were identified as important risk factors for high incidence of neonatal camel calf diarrhoea in the present study.

Key words: Antimicrobial resistance, camel, Escherichia coli, neonatal diarrhoea, PCR, virulence genes

The occurrence of neonatal diarrhoea or colibacillosis caused by Escherichia coli in neonatal camels is one of the important infectious diseases as it incurs significant economic losses due to high morbidity and mortality rate resulting from severe diarrhoea and septicemia (Mohammed et al, 2003). It was believed that strains of *E. coli* colonise the host's intestine with different virulence factors and induce diarrhoea by escaping the immune system (Cho and Yoon, 2014; Desvaux et al, 2020). E. coli causing neonatal calf diarrhoea were mainly pathotyped on the basis of presence of virulence factors as enteropathogenic E. coli (EPEC), enterotoxigenic E. coli (ETEC) and shigatoxigenic E. coli (STEC) which include subgroup enterohaemorrhagic (EHEC), enteroinvasive (EIEC), enteroaggregative (EAEC) and enteroadherent E. coli (EAdEC) (Andrade et al, 2012). These pathotypes have mostly been related to mild to severe diarrhoea causing high rates of morbidity and mortality particularly during the early neonatal period in calves (Andrade et al, 2012). Each diarrhoeagenic E. coli pathotype represents a collection of strains that possess similar

virulence factors and cause similar diseases with similar pathology (Robins-Browne et al, 2016). The STEC is considered as zoonotic pathogen causing haemorrhagic colitis and haemorrhagic uraemic syndrome in human beings (Nataro and Kaper, 1998). The pathogenicity of STEC is mediated mainly through Shiga toxins 1 and 2 encoded by stx1 and stx2 genes, respectively (Paton and Paton, 1998). The pathogenicity of ETEC is attributed to the expression of fimbrial antigens F41, F5 and F17, and the elaboration of one or more enterotoxins like heatstable enterotoxins (sta) and heat-labile enterotoxins (LT) (Ryu et al, 2020). The EPEC pathotype involved in young calf diarrhoea and dysentery induce attaching and effacing (AE) lesions on intestinal cells due to the production of the protein intimin (eae) (Mainil and Fairbrother, 2014).

During the past decade, drug resistance in enterobacteriaceae has increased worldwide which is considered as potential threat for public health (Prestinaci *et al*, 2015). Since *E. coli* is present as gut commensal in humans and animals, it has become one of the microorganisms that are commonly resistant to

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antimicrobials due to the selective pressure imposed by the antimicrobial drugs used in the treatment of food animals and humans (Zhao *et al*, 2012). In present study, characterisation of *E. coli* pathotypes isolated from diarrhoeic neonatal dromedary camels and their antimicrobial resistance pattern was investigated.

Materials and Methods

Animals, sample collection and pathological studies

This study was conducted during the period from 2016 to 2020 in an organised dromedary camel farm situated at Bikaner, India which is an arid region within Thar desert. The neonatal camels of the farm were kept along with their dam in a corral having loose sandy soil with free access to colostrum since birth. The faecal swabs were directly collected from the rectum of the diarrhoeic neonatal camels using sterile cotton swabs for bacterial culture. These calves were not given any antimicrobials before sampling. The faecal samples were also collected in sterile containers (sterile clinicol™, Himedia, India) and investigated for presence of oocysts of coccidia and cryptosporidia and eggs of helminths using direct wet mount examination method. The necropsy was performed on 3 diarrhoeic neonatal camels having mortality and tissue samples from internal organs were collected in 10% formal saline for histopathology. The formalin fixed tissue samples were embedded in paraffin, cut into 4-5 micron sections using a semi automatic microtome (Wewox®, India) and stained with haematoxylin and eosin (HE) stain.

Bacterial culture and antimicrobial susceptibility testing

The rectal swab samples collected from diarrhoeic neonatal camels were inoculated on MacConkey and Eosin Methylene Blue (EMB) agar media and incubated at 37 °C for 18-24 hours. These *E. coli* colonies were further cultured on Mueller Hinton agar for determination of antimicrobial susceptibility using the agar disc diffusion method (Humphries *et al*, 2018). The antibiotic discs were chosen keeping in mind their common use in livestock farming in India. The antibiotic discs (HiMedia, India) included in the present study were: amoxicillin (AMX) (10µg), cloxacillin (COX) (5µg), cefotaxime (CTX) (30µg), tetracycline (TE) (30µg), doxycycline hydrochloride (DO) (30µg), erythromycin (E) (15µg), lincomycin (10µg), gentamicin (GEN)

(10µg), amikacin (AK) (30µg), streptomycin (S) (10µg), amoxicillin/ sulbactum (AMS) (30/15µg), trimethoprim (TR) (5µg), ciprofloxacin (CIP) (5µg), enrofloxacin (EX) (10µg), ceftriaxone (CTR) (30µg) and chloramphenicol (C) (30µg). The diameter of the zones of inhibition was measured by antibiotic zone scaleTM (HiMedia, India) and the zones were graded as sensitive and resistant to the drugs tested by referring to Zone Size Interpretative Chart (HiMedia, India) in accordance to Performance Standards for Antimicrobial Disk Susceptibility Tests, Clinical and Laboratory Standards Institute (CLSI) (Humphries *et al*, 2018). Multiple-antibiotic resistance was defined as resistance to 2 or more antibiotic classes.

DNA extraction and PCR for detection of virulence genes

Pure and characteristic lactose fermenting pink coloured colonies from MacConkey agar were selected for DNA extraction using MericonTM DNA bacteria kit (Qiagen, Germany). The PCR for molecular identification of *E. coli* isolates was carried out using the primer sequence targeting uidA gene encoding β - glucuronidase of *E. coli* to amplify a 486bp fragment (Heininger *et al*, 1999). For detection of different virulence genes (*stx1, stx2, eae, K99, F41* and *sta*), multiple PCR was performed using different primer sets (Table 1) and PCR cycling conditions described previously (Franck *et al*, 1998).

Results

Incidence, clinical and pathological findings

In the present study, E. coli was isolated from rectal swab samples of 48 (20.68%) diarrhoeic neonatal camels over the period of 4 years with case fatality rate of 6.25%. No significant difference was found in occurrence of diarrhoea in male and female neonatal camels. No evidence of any parasitic infection was found in any of the faecal samples collected from these diarrhoeic neonatal camels. An association between age of neonatal camels and occurrence of diarrhoea was observed. The incidence of diarrhoea was appreciably more in camels of age group below 7 days (n=41) compared to camels of age group 7 days and above (n=7) (Table 2). The important clinical signs in diarrhoeic neonatal camels were profuse, foulsmelling, yellow to pale yellow or greenish, watery to pasty diarrhoea soiling the tail and hindquarters. In 3 neonatal camels having mortality, the severity of the symptoms were more pronounced and characterised by anorexia, weakness and mucous and blood mixed faeces.

The necropsy of these neonatal camels showed gross lesions of dark red diffusely congested small and large intestinal mucosa with presence of moderate amount of mucous and blood mixed contents in the lumen (Fig 1). The abomasum also showed dark red congested mucosa with blood mixed contents. The liver was enlarged and showed multifocal pale areas throughout its surface. Kidneys were enlarged with moderate to severe congestion. The other organs were not showing any significant gross changes. Histopathology of small intestine revealed areas of desquamation with presence of free



Fig 1. Moderate to severely congested small intestinal loops.

epithelial cells in lumen, mucosal epithelial necrosis, hyperemia of the villi, villus stunting and fusion, and mild to moderate infiltration of eosinophils in the lamina propria and crypt region (Fig 2). The submucosa showed mild to moderate thickening, oedema and dilatation and congestion of submucosal capillaries. Histopathology of liver showed prominent vacuolar degenerative changes in hepatocytes with congestion of central vein and sinusoidal capillaries. Histopathology of kidney showed congestion of glomerular capillaries and occasionally atrophied and distorted glomeruli.



Fig 2. Histopathology of small intestine showing desquamation of villous epithelium and atrophied villi with hyperemic blood vessels (arrow). HE X 100.

| Pathotype | Target virulence gene | Oligonucleotide sequences (5'-3') | Product size (bp) | References | |
|-----------|-----------------------|-----------------------------------|-------------------|-----------------------------|--|
| | atr 1 | F: TTCGCTCTGCAATAGGTA | 555 | Poton et al 1005 | |
| STEC | SIXI | R: TTCCCCAGTTCAATGTAAGAT | 555 | raton <i>et al</i> , 1995 | |
| SIEC | atr 2 | F: GTGCCTGTTACTGGGTTTTTCTTC | 110 | Paton <i>et al,</i> 1993 | |
| | 5122 | R: AGGGGTCGATATCTCTGTCC | 110 | | |
| EPEC | 222 | F: ATATCCGTTTTAATGGCTATCT | 425 | Vu and Kanar 1002 | |
| | eue | R: AATCTTCTGCGTACTGTGTTCA | 423 | Tu ana Raper, 1992 | |
| | Γ/1 | F: GCATCAGCGGCAGTATCT | 280 | Fidock <i>et al,</i> 1989 | |
| | Γ41 | R: GTCCCTAGCTCAGTATTATCACCT | 560 | | |
| ETEC | V00 | F: TATTATCTTAGGTGGTATGG | 214 | Roosendaal et al, | |
| EIEC | K99 | R: GGTATCCTTTAGCAGCAGTATTTC | 514 | 1984 | |
| | ata | GCTAATGTTGGCAATTTTTATTTCTGTA | 100 | Sekizaki <i>et al,</i> 1985 | |
| | stu | AGGATTACAACAAAGTTCACAGCAGTAA | 190 | | |

Table 1. Details of primers used for amplification of different virulence genes.

 Table 2.
 Summary of age, sex and result of virulence gene PCR in diarrhoeic neonatal camels.

| Total | S | ex | Age (| days) | Result of virulence gene PCR | | | | | | |
|--------|------|--------|---------|---------|------------------------------|--------------|----------------|---------------|---------------|---------------|--|
| camels | Male | Female | <7 days | ≥7 days | stx1 | stx 2 | eae | F41 | K99 | sta | |
| 48 | 21 | 27 | 41 | 7 | 2 (4.16%) | 1 (2.08%) | 17 (35.41%) | 7 (14.58%) | 9 (18.75%) | 8 (16.66%) | |

| Pathotype | Virulence genes | No. of isolates (%) | Total No. of isolates (%) | | |
|---------------------|-----------------|---------------------|---------------------------|--|--|
| CTTC | stx1+eae | 2 (4.16%) | 2 ((25%) | | |
| SIEC | stx2+eae | 1 (2.08%) | 5 (6.25%) | | |
| EPEC | еае | 10 (20.83%) | 10 (20.83%) | | |
| | F41 | 5 (10.41%) | | | |
| | K99 | 1 (2.08%) | 14 (20 1 (0/) | | |
| EIEC | K99+ sta | 6 (12.5%) | 14 (29.16%) | | |
| | sta | 2 (4.16%) | 1 | | |
| Mined (EDEC ETEC) | eae+ F41 | 2 (4.16%) | 4 (9.229/) | | |
| MIXED (EPEC+ETEC) | eae+ K99 | 2 (4.76%) | 4 (0.33%) | | |
| None | None | 17 (35.41%) | 17 (35.41%) | | |

Table 3. Summary of virulence gene profile and pathotypes of E. coli isolates from diarrhoeic neonatal camels.

Distribution of virulence genes and pathotypes

The screening for presence of virulence genes in *E. coli* isolates from diarrhoeic neonatal camels revealed 31 (64.58%) isolates possess one or more virulence genes, whereas in 17 (35.41%) of the isolates no virulence genes could be detected and considered non-pathogenic (Table 3). The individual incidence of virulence genes *viz.*, stx1, stx2, eae, F41, K99 and sta in *E. coli* isolates were 2 (4.16%), 1 (2.08%), 17 (35.41%), 7 (14.58%), 9 (18.75%) and 8 (16.66%), respectively (Table 2). Based on the distribution of virulence genes, the *E. coli* isolates were pathotyped as STEC (6.25%), EPEC (20.83%), ETEC (29.16%) and mixed type (8.33%) (Table 3). The *E. coli* isolates from all the 3 neonatal camels having acute haemorrhagic enteritis and mortality were found to be of STEC type.

Antimicrobial resistance

The antimicrobial resistance profiles of all *E. coli* isolates against the tested antibiotics are summarised in Table 4.

Discussion

In this study, a high incidence of neonatal camel calf diarrhoea was observed which was mainly attributed to unhygienic living conditions, overcrowding and damp floors which support and shelter infectious agents (Cho and Yoon, 2014). Since camels are seasonal breeders, maximum calving in India usually took place in winter season particularly in the months of January and February. Moreover, the calving shed of the present study had loose sandy soil in which wet conditions prevailed for longer time due to winter months. Highest prevalence rate of *E. coli* infection during winter season was also recorded in cattle and buffalo calves in earlier studies (Awad *et al*, 2020). The neonatal calves below 7 days showed maximum incidence of calf diarrhoea

which was mainly attributed to the non appearance of humoural immunity and pessimistic response to cell mediated immunity in calves (Mohan *et al*, 1990). The clinical signs of yellowish or greenish diarrhoea with occasional presence of mucous and blood in *E. coli* infected camels of the present study were in agreement with camel calf diarrhoea cases reported earlier (Yeshiwas and Fentahun, 2017). Similarly, the pathological lesions of acute enteritis with desquamation of mucosal epithelium and atrophy of villi were frequently reported in intestine of diarrhoeic calves due to *E. coli* infection (Awad *et al*, 2020).

Table 4. Summary of antimicrobial resistance profile of *E. coli* isolates.

| Antimicrobial group | Antimicrobial agents | No. of resistant E. coli isolates (%) | | | |
|---------------------------|---------------------------|--|--|--|--|
| | Amoxicillin | 48 (100%) | | | |
| 6 lactores | Cloxacillin | 48 (100%) | | | |
| p- lactains | Cefotaxime | 6 (12.5%) | | | |
| | Cephoxitin | 12 (25%) | | | |
| Totragualinas | Tetracycline | 27 (56.25%) | | | |
| Tetracyclines | Doxycycline | 24 (50%) | | | |
| Magralidas | Erythromycin | 48 (100%) | | | |
| Macrondes | Lincomycin | 48 (100%) | | | |
| | Gentamicin | 5 (10.41%) | | | |
| Aminoglycosides | Amikacin | 5 (10.41%) | | | |
| | Streptomycin | 22 (45.83%) | | | |
| β- lactamase inhibitor | Amoxicillin/ sulbactum | 21 (43.75%) | | | |
| Folate inhibitor | Trimethoprim | 40 (83.33%) | | | |
| Quinalanas | Ciprofloxacin | 20 (41.66%) | | | |
| Quinoiones | Enrofloxacin | 21 (43.75%) | | | |
| Cephalosporins | Ceftriaxone | 11 (22.91%) | | | |
| Chloramphenicol | Chloramphenicol | 33 (70.83%) | | | |

The antimicrobials used for susceptibility testing in the present study were routinely used in veterinary practice as therapeutics or as growth promoters in India. The antibiotic resistance pattern observed in E. coli isolates of the present study was comparable with those observed in E. coli isolates from camel and cattle calves from Tunisia and India (Bessalah et al, 2016; Sharma et al, 2017). The high prevalence of antimicrobial resistance against commonly used drugs in human medicine in E. coli isolates of the present study pointed to the judicious use of antimicrobials in livestock farms. Although, there was difference in occurrence of virulence factors in E. coli isolates, however, the antimicrobial susceptibility pattern was more or less similar among them. This may be due to the fact that all diarrhoeic neonatal camels of the present study were from a farm where continuous use of these antibiotics for various types of ailments was practicsed since long time.

Characterisation and identification of genes encoding virulence factors and subdivision of diarrhoeic *E. coli* into pathotypes were necessary for understanding the disease epidemiology and pathogenesis (Garcia et al, 2020). The majority of diarrhoeic neonatal camels of the present study were found infected with ETEC infection during first 6 days after birth was in agreement with earlier studies (Guler et al, 2008; Foster and Smith, 2009). The 2nd most prevalent pathotype in diarrhoeic neonatal camels was EPEC with detection rate of 20.83% which was comparable with previous studies in diarrhoeic cattle and buffalo calves (Guler et al, 2008; Awad et al, 2020). However, Foster and Smith (2009) claimed that the significance of EPEC as a calf pathogen was questionable as it can be isolated from both healthy and diarrhoeic calves. The STEC pathotypes were detected in 6.25% of E. coli isolates which was lower than those reported in previous studies in diarrhoeic cattle and buffalo calves (Awad et al, 2020). In the present study, the E. coli isolated from neonatal camels having acute haemorrhagic enteritis and mortality were found to be of STEC type. Globally, STEC was an important cause of life threatening diarrhoeal disease in both animals and humans and association of STEC pathotype in causing haemorrhagic dysentery in young calves had been frequently reported (Robins-Browne et al, 2016). The shiga toxins destroyed intestinal microvilli resulting into haemorrhagic diarrhoea in calves (Nataro and Kaper, 1998). Mixed pathotypes with combinations of EPEC with ETEC were frequently reported in earlier studies (Awad et al, 2020; Ryu et al, 2020). It

was speculated that these atypical combinations may result in the emergence of new pathotypes which may be more pathogenic and cause severe diarrhoea in calves (Awad *et al*, 2020).

Among diarrhoeic neonatal camels of the present study, ETEC were the most common pathotype, whereas STEC were found responsible for acute haemorrhagic enteritis and mortality. Young age (less than 7 days), calving pen with loose sandy ground and peak winter season were found associated with high incidence of neonatal camel calf diarrhoea in the present study. The studies on virulence genes and antimicrobial resistance pattern in *E. coli* isolates from diarrhoeic neonatal camels can be crucial for camel farmers and veterinarians in selection of antimicrobials for effective management and prevention of the disease and to minimise the emergence of multidrug resistant *E. coli* which may pose health risks to both animals and humans.

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ANTIBACTERIAL PROPERTIES OF Ocimum sanctum, Moringa oleifera AND Murraya koenigii LEAF EXTRACTS AGAINST Corynebacterium pseudotuberculosis ISOLATED FROM CAMEL (Camelus dromedarius)

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ABSTRACT

In the present study, antibacterial properties of methanolic and chloroform extracts of *Ocimum sanctum*, *Moringa oleifera* and *Murraya koenigii* leaves against *Corynebacterium pseudotuberculosis* (CPs) isolated from abscess in dromedary camel were screened using agar well diffusion assay and minimum bactericidal concentration (MBC) were determined using broth microdilution technique. MBC of selected plant extracts varied from 3.125 to 12.5 mg/ ml. Chloroform extracts of *Ocimum sanctum* and *Murraya koenigii* had highest antibacterial properties; while it was lowest in methanolic extract of *Moringa oleifera* and *Murraya koenigii* leaves.

Key words: Antimicrobial, Camel, Corynebacterium, Moringa, Murraya, Ocimum

Corynebacterium pseudotuberculosis (CPs) is an important pathogen of domestic animals including sheep, goat, horses, cattle and camel (Dorella et al, 2006). In camel, it causes enlargement and suppuration of peripheral and visceral lymph nodes (Tejedor-Junco et al, 2004; Wernery and Kinne, 2016; Ranjan et al, 2018) and plays an important role in superficial septic wounds (Zidan et al, 2013). In vitro sensitivity tests suggest that CPs isolated from different animal species are sensitive for most of the common antibiotics (Judson and Songer, 1991). However, after growing CPs as biofilm, in an attempt to mimic the environment of natural infection, the bacterium was found highly resistant to all the tested antimicrobials (Olson et al, 2002). Research reports published in the recent past also suggest emergence of drug resistance problem in CPs (Abdel-Wahab and Shigidi, 2013; Algammal, 2016).

There are many medicinal plants containing useful phytochemical constituents which have antibacterial properties and their therapeutic values help in treating many bacterial infections (Abuga *et al*, 2021). Masese *et al* (2016) found Moringa oleifera, Murraya koingii and Ocimum sanctumare as an effective reducing agent for the synthesis of AgNPs which were highly stable and had significant activity against Escherichia coli and Staphylococcus aureus. Moodley et al (2018) found that the biosynthesised nanoparticle preparations from M. oleifera leaf extracts exhibit potential for application as broad-spectrum antimicrobial agents. The extract of leaves of Ocimum sanctum has demonstrated effective antimicrobial property against A. actinomycetemcomitans, suggesting its possible use as an effective and affordable "adjunct" in the management of periodontal conditions in humans (Mallikarjun et al, 2016). Murraya koenigii extracts have demonstrated antibacterial effects particularly on E. coli and Staphylococcus as compared to antibiotics such as Gentamycin and Amikacin (Irfan et al, 2016). Fouad (2019) found antibacterial efficacy of Moringa oleifera leaf extract against pyogenic bacteria isolated from a dromedary camel (Camelus dromedarius) abscess. Zubair (2020) evaluated the inhibitory effect and antibiofilm activity of Moringa oleifera and Citrus sinensis extracts against those of pathogenic Pseudomonas

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aeruginosa and Staphylococcus aureus and found that extracts have effectively blocked MRSA and ESBL development in the biofilm matrix. However, studies on antibacterial properties of medicinal plant extracts in camels is meager. The present investigation is, therefore, undertaken to study the antibacterial properties of Ocimum sanctum, Moringa oleifera and Murraya koenigii leaf extracts against Corynebacterium pseudotuberculosis isolated from an abscess of a camel (Camelus dromedarius).

Materials and Methods

Bacterial culture and characterisation

The pure colonies of CPs were isolated from pus sample from enlarged, suppurated, cervical lymph node of a dromedary camel housed at ICAR-National Research Centre on Camel, Bikaner, India. The organism was identified on the basis of culture characteristics, morphological features after Grams staining, result of various biochemical tests (Nabi, 2021) and quadruplex PCR test (Almeida *et al*, 2017).

Collection of plants, identification and extract preparation

Fresh leaves of Ocimum sanctum, Moringa oleifera and Murraya koenigii were collected from different localities of Bikaner, Rajasthan and were authenticated by scientists from ICAR-Central Institute for Arid Horticulture, Bikaner. Collected leaves were rinsed with distilled water, dried in shed at room temperature for 15 days and ground to obtain a coarse powder. Methanolic and chloroform extracts of each plant leaves were prepared. Fifty gram dried leaf powder was soaked overnight in 200 ml methanol/ chloroform and the mixture was shaken vigorously several times in between. Next day, the mixture was filtered with Whatman filter paper number one. The filtrate was evaporated to dryness in vaccuo at 50°C using rotary film evaporator, and stored at -20°C till further use. Extractability or yield (%) of each extract was calculated using a formula: Extractability or yield (%) = (weight of extract obtained in gram/ weight of leaf powder taken in gram) *100 (Mazhangara et al, 2020).

The extract obtained was dissolved in 10% dimethylsulfoxide (DMSO; HiMedia Laboratories Private Limited, Mumbai, India) to a desired concentration and sterilised by passing through a 22 μ m (pore size) filter (HiMedia Laboratories Pvt Ltd., Mumbai, India) before use.

Evaluation of anti-microbial properties of plant extracts

The antimicrobial activities of plant-extracts were screened using agar well diffusion test (Kavitha, 2017) with slight modifications. Briefly, 0.2 ml of diluted inoculum ($1X10^5$ CFU/ml) of the CPs was swabbed on the Brain Heart Infusion (BHI) Agar supplemented with 5% defibrinated sheep blood. Thereafter, using a sterilised cork borer, wells of 5 mm diameter were punched. Using a micropipette, 100 µl of the plant extract solution (100 mg/ml) were added to the wells. The plates were incubated aerobically at 37 ± 2 °C for 24 to 48 h and the zone of inhibition (in mm) was measured with the help of a Vernier caliper. The test was performed in triplicates with controls.

The minimum bactericidal concentrations (MBC) of the methanolic and chloroform extracts were determined using broth micro-dilution technique as per the standard CLSI methods (Wayne, 2008) with slight modifications (Jahan *et al*, 2011).

Standardisation of inoculum size

To ensure an exact number of bacteria present in the inoculum, one or two isolated colonies were inoculated into 5 ml of BHI broth (supplemented with 0.1% Tween 20 to prevent clumping of colonies) and inoculated at 37°C for 24-48 hours. Thereafter, the inoculum was centrifuged at 4,000 rpm for 5 minutes with appropriate aseptic precautions. The supernatant was discarded and the pellet was re-suspended in sterile Phosphate Buffer Saline (PBS) pH 7.4 and centrifuged again at 4000 rpm for 5 min. The process was repeated until the supernatant was clear. The pellet, thereafter was suspended in 5 ml sterile PBS and optical density was recorded at 500 nm. Serial dilutions (two-fold) were done in PBS under aseptic conditions until the optical density was in a range of 0.8 to 1.0. The actual number of colony forming units was estimated after inoculating 100 µl of the bacterial suspension over BHI Agar with 5% defibrinated sheep blood and incubating at 37°C for 24-48 hours. The required dilution factor was calculated and the dilution was carried out to obtain a final concentration of 5 X 10⁶ cfu/ ml (Norman *et al*, 2014).

Preparation of the microplate

In a sterile 96 micro well plate, different test herbal solutions (200 μ l each) were pipetted into the first row under aseptic conditions. To all other wells, 100 μ l of BHI broth was added. Serial dilutions were performed by transferring 100 μ l from the corresponding wells in the first row to the next row so that at the end, 100 μ l of the test herbal extract was present in each well in a serially descending concentration (50, 25, 12.5, 6.25, 3.125, 1.562, 0.781, 0.391, 0.195 and 0.098 mg/ml). Now, 60 µl of 3.3 X strength BHI broth, 20 µl sterile PBS and 20 µl of bacterial suspension (5 X 10⁶ cfu/ ml) was poured into each well to obtain a concentration of 5 X 10^5 cfu/ ml and a final volume 200 µl in each well. In addition, one media control (herbal extract and bacterial culture), one bacterial control (herbal extract and BHI broth) and one extract control (BHI broth plus bacterial culture) were also run simultaneously. The micro well plate was covered with lid and sealed with tape and incubated at 37°C for 48 hours. The MBC value was determined by sub-culturing each test dilutions (by transferring 100 µl) on BHI agar with 5% defibrinated sheep blood plates at 37°C for 24-48 hours. The highest dilution (or lowest extract concentration) showing no bacterial growth was taken as MBC (Norman et al, 2014).

Statistical analysis

The values obtained were analysed by one-way ANOVA using computer software Statistical Package of Social Sciences (SPSS-20).

Results and Discussion

Plant extracts

The colour, consistency and extractability percentage of different plant extracts are given in table 1. The methanolic extract of *Ocimum sanctum*

appeared as blackish, semi-solid paste like with extractability 5.58%. The chloroform extract was brown-black coloured flakes with extraction per cent 2.80. In corroboration with the present findings Agarwal *et al* (2010) reported extractability of ethanolic *O. sanctum* leaf extract to be 6%. Likewise, Shafi *et al* (2018) reported the extraction percentage for hydro-alcoholic extract (1:1 water and ethanol) to be 9.6%.

Methanolic *M. oleifera* leaf extract obtained was brown-blackish, semi solid mass with 7.32 % yield. The chloroform extract was dark green in colour with extractability 2.32%. Nikkon *et al* (2003) reported extraction percentage of *M. oleifera* root barks to be 3.33 % using ethanol as extraction media.

Methanolic leaf extract of *Murraya koenigii* was brown-black solid mass with 0.81 % extractability. The chloroform extract was also similar in colour and consistency with extractability was 1.70%. Vats *et al* (2011) reported extraction percentage of *M. koenigii* roots as 4.03, 1.31, 0.59 and 9.4% for petroleum ether, chloroform, ethyl acetate and ethanol extracts, respectively. Kavitha (2017) reported that organic extracts obtained were viscous in nature and brownish in colour, but yield percentage recorded was 7.0, 6.5 and 9.2 % (v/w) for hexane, chloroform and ethanol, respectively.

Evaluation of antibacterial property

Results of agar well diffusion test and estimation of Minimum Bactericidal Concentration

Table 1. Colour, consistency and extractability percentage of different plant extracts used with methanol and chloroform as solvents.

| S. No. | Plant | Solvent used | Colour | Consistency | Extractability % |
|--------|------------------|--------------|-------------|----------------------------------|------------------|
| 1. | Ocimum sanctm | Methanol | Blackish | Blackish Semi-solid (Paste like) | |
| | | Chloroform | Brown-black | Powder (Flakes) | 2.80 |
| 2. | Moringa oleifera | Methanol | Brown-black | Semi-solid | 7.32 |
| | | Chloroform | Dark green | Semi-solid | 2.32 |
| 3. | Murraya koenigii | Methanol | Brown-black | Semi-solid | 0.81 |
| | | Chloroform | Brown-black | Semi-solid | 1.70 |

Table 2. Zone of inhibition and MBC of different plant extracts against C. pseudotuberculosis.

| S.No | Plant | Solvent used | Zone of inhibition(mm)* | MBC (mg/ml) |
|------|------------------|--------------|-----------------------------|-------------|
| 1 | Ocimum sanctum | Methanol | 12.667±0.667 ^a | 6.25 |
| | | Chloroform | 14.000 ± 1.000^{ab} | 3.125 |
| 2 | Moringa oleifera | Methanol | 14.667±0.667 ^{abc} | 12.5 |
| | | Chloroform | 16.00±1.555 ^{bc} | 6.25 |
| 3 | Murraya koenigii | Methanol | 14.667±0.667 ^{abc} | 12.5 |
| | | Chloroform | 17.000±0.577 ^c | 3.125 |

*Data are presented as mean \pm S.E. as measurement of inhibition zone (mm). Means and standard errors determined from 3 biological replications. The values with different superscript differ significantly (P< 0.05) within a column.

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(MBC) are given in table 2. In the wake of emerging problem of multidrug resistant bacteria there is a continuing need for new preparations particularly low cost natural products as they are readily accepted by patients (Martin and Ernst, 2013). Nevertheless, antibacterial properties of a plant extract in *in vitro* tests is reported to vary with several factors like type and strain of bacteria, inoculum size, type of media, type of solvent and extraction procedure, part of the plant used and time of collection and total amount of herbal extract used (Mandal *et al*, 2012).

Osmium sanctum

The zone of inhibition for methanolic and chloroform extracts of O. sanctum varied from 12 to 15 mm in diameter. In corroboration of the present findings, Aqil et al (2005) reported that inhibition zone for ethanolic extract of O. sanctum leaves against methicillin resistant Staph. aureus (MRSA) varied from 11 to 18 mm in diameter when 100 µl of plant extract with concentration 100 mg/ml was used. An inhibition zone of 10 mm diameter was reported when aqueous or ethanolic extracts of O. sanctum were used in concentration 10 mg/ml against Aeromonas hydrophila (Harikrishan and Balasundaram, 2008). Agarwal et al (2010) reported that inhibition zone of ethanolic extract (at concentration 10 mg/ml) of O. sanctum varies from 12 to 19 mm in diameter against Strepto. mutans. Jahan et al (2011) also recorded zone of inhibition of ethanolic extract of O. sanctum against Staph. aureus to vary between 10.66 to 15.66 mm.

MBC for methanolic and chloroform extract of O. sanctum were found to be 6.25 and 3.125 mg/ ml, respectively. MIC of ethanolic extract against different strains of MRSA turned to vary from 1.3 to 8.2 mg/ml (Aqil et al, 2005). Likewise, initial MIC of ethanolic extract of O. sanctum leaves ranged from 2.4- 9.4 mg/ml and 4.7- 18.8 mg/ ml for resistant and sensitive Staph. aureus strains, respectively (Jahan et al, 2011). Goyal and Kaushik (2011) reported that MIC of ethanolic and methanolic extracts of O. sanctum leaves varied from 1024 to > 4096 μ g/ml. In the present study, chloroform extract of O. sanctum had more potent antibacterial activity than methanolic extract. In concurrence with this observation, Shokeen et al (2005) also recorded that chloroform extract of leaves of O. sanctum have highest percentage of inhibition of Neisseria gonorrhoeae among hexane, benzene, chloroform, ethyl acetate, acetone and 70% ethanol extracts. However, perusal of available reports suggests large

variation in MIC and MBC values of *O. sanctum* leaf extracts against different bacteria. MIC as low as 0.25 mg/ml was reported by Adiguzel *et al* (2005) and 0.02 mg/ml by Akinvemi *et al* (2005). On the other hand, Shafi *et al* (2018) reported MIC to vary from 62.5 to 125 mg/ml for hydro-alcoholic extract of *O. sanctum* leaves against common mastitis pathogens like *Staph. aureus, Strepto.* spp, *E. coli, Coryne.* spp, *Pseudomonas* spp and *Klebsiella* spp. They further reported that MIC for *Coryne.* spp was 62.5 mg/ml.

O. sanctum, a plant from family Labiatae, known as *Tulsi* in hindi, have several pharmacological activities, like hypoglycemic, antipyretic, analgesic, anti-inflammatory, antistress, immune-modulatory, radio-protective, anti-tumour and anti-bacterial (Bhargava and Singh, 1981; Godhwani *et al*, 1987).

Moringa oleifera

Mean diameter of inhibition zone for methanolic and chloroform extract of M. oleifera recorded was 14.68 and 16.00 mm, respectively. Rahman et al (2009) studied antibacterial activity M. oleifera leaves against 4 gram negative and 6 gram positive bacteria and found that zone of inhibition for fresh leaf juice varied between 15.23 to 25.2 mm, for powder from fresh leaf juice was 29.25 to 42.3 mm and ethanol extract of fresh leaves was 16.25 to 21.5 mm. Peixoto et al (2011) also reported that mean diameter of zone of inhibition for aqueous and ethanolic extract of M. oleifera leaves varied from 14.4 to 30.0 mm depending upon the type and concentration of extract used and genus of the test bacteria. Among ethanol, chloroform and hexane extracts of M. oleifera leaves, methanolic extract was found most effective against E. Coli, S. dysenteriae, Salmonella spp., Enterobacter spp., K. pneumoniae and S. marcescens (Rahman et al, 2010). Large variation in MIC has been reported (from 0.041 to 50 mg/ml) for crude seed extracts (ethanolic or chloroform extracts) against gram negative organisms (Chandrasekhar et al, 2020).

MBC of methanolic and chloroform extract of *M. oleifera* was found to be 12.5 and 6.25 mg/ml, respectively. Likewise, Fouad *et al* (2019) reported that MIC values of cold water extract and ethanolic extract of *M. oleifera* leaves were 25 mg/ml and 390 μ g/ml, respectively against CPs isolated from pus in camel. However, lower MIC values were reported in several other studies. For example, the MIC values of methanolic, ethyl acetate and hexane extracts of *M. oleifera* leaves against some Gram negative bacteria were reported to vary from 62.5 to 1000 μ g/mL (Rahman *et al*, 2010). Recently, GarciaBeltran et al (2020) reported significant antibacterial activity of ethanolic and aqueous extracts against pathogenic Vibrio anguillarum and Photobacterium damselae strains at a concentration ranging from 0.25 to 1.00 mg/ml. They further opined that antibacterial activity of M. oleifera extracts could be attributed to certain active components that might act in a synergistic way to inhibit the bacterial growth and viability. Deoxy-niazimicine extracted from M. oleifera leaves is reported to be effective against several pathogenic bacteria (Nikkon et al, 2003). Flavonoids and glucomoringin present in M. oleifera also attribute antibacterial potential against certain bacteria (Onsare and Arora, 2015; Galuppo et al, 2013). Low levels of the isothiocyanate derivative compounds are some additional constituents that inhibit some Gramnegative and Gram-positive bacteria.

Moringa or Drumstick tree (Moringa oleifera) is widely cultivated in tropical to subtropical regions across the world (García-Beltran et al, 2020). The dry leaves of the plant contain high concentration of macro and micronutrients, tannins, sterols, saponins, trepenoids, phenolics, alkaloids and flavanoids (Gopalkrishnan et al, 2016). Antibacterial activity of M. oleifera leaf extract could be attributed to phenolic compounds, flavonoids, saponin, tannin and cyanogenic glycosides (Rauha et al, 2000; Doughari et al, 2007; Verma et al, 2009; Garcia-Beltran et al, 2020). However, marked variation in phytochemical composition and thereby antioxidant and antimicrobial activities of 13 different cultivars of Moringa oleifera obtained from different locations across the globe has been reported (Ndhlala et al, 2014) that may result into variation in antibacterial potential of different extracts.

Murraya koenigii

Zone of inhibition for methanolic and chloroform extracts of *M. koenigii* leaves varied from 14 to 21 mm in diameter. Likewise, in a study zone of activity (inhibition zone) ranged from 6 to 20 mm in diameter depending upon the organic solvent used and species of bacteria (Naz *et al*, 2015). In this study methanolic leaf extract showed most promising antibacterial agent among n-hexane, acetone and methanolic extract. Nagappan *et al* (2011) also reported that the diameter of inhibition zone for carbazole alkaloids and essential oil of *Murraya koenigii* varies from 8.0 mm to 18.0 mm and highest susceptibility with inhibition zone of 18.5 \pm 0.5 mm, 18.5 \pm 0.5 mm and 18.0 \pm 0.5 mm was recorded against *S. aureus, P. aeruginosa* and *S. pneumoniae*, respectively.

The MBC of *M. koenigii* leaf extracts was recorded as 3.125 and 12.5 mg/ml for chloroform and methanolic extracts, respectively. Present study indicated that chloroform extract of M. koenigii leaves has higher antimicrobial activity than methanolic extract. MIC of chloroform extract of M. koenigii leaves was 125µg/ ml against Kleb. pneumoniae, while methanolic extract had no antimicrobial activity against tested bacteria and fungi (Panghal et al, 2011). On the contrary, Kavitha (2017) reported that ethyl alcohol extract displayed highest antibacterial activity when compared to hexane and chloroform extracts of M. koenigii leaves. They recorded MIC and MBC of ethyl alcohol extract of M. koenigii leaves against different bacteria which varied from 12.05 to 25 mg/ml and 25 to 50 mg/ml, respectively. Likewise, Rath and Padhy (2014) observed that MIC and MBC of methanolic extract of M. koenigii leaves against different multidrug resistant gram positive and gram negative bacteria causing urinary tract infections in humans varied from 1.41 to 21.67 mg/ ml.

Murraya koenigii (Linn) *Spreng.*, commonly known as "*Curry patta*" in Hindi, is a member of the family Rutaceae. The antimicrobial activity of *M. koenigii* leaves is largely attributed to several carbazole alkaloids present in it (Naz *et al*, 2015; Nalli *et al*, 2016). Seven pyranocarbazoles with antibacterial activities were extracted from methanolic extract of *Murraya koenigii* (L.) through bioassay guided fractionation (Joshi *et al*, 2017).

In the present study, highest antibacterial activity is recorded in chloroform extract of *Ocimum sanctum* and *Murraya koenigii* and lowest in methanolic extract of *Moringa oleifera* and *Murraya koenigii* leaves. Variations in the phytochemical levels of the different cultivars may be an important factor behind variation recorded in antibacterial activity. The antibacterial compounds from these plants may be used as a constituent of topical antiseptic preparations.

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The Satellite Meeting took place from 1 (Friday) to 3 (Sunday) July 2022 following the ICAR 2020 conference at the University of Bologna, Italy. The official language of the meeting was English and no translation was provided. The scientific program includes original and review presentations on all aspects of reproduction, genetics, production and welfare in New and Old World Camelids. The major topics covered were male and female reproductive physiology and endocrinology, gynecology, theriogenology and reproductive efficiency; andrology and artificial insemination; superovulation and embryo transfer; cryo-preservation of gametes and other assisted reproductive methods; gestation, parturition and neonatology; mammary gland and milk production; camelid breeding and genetics; interaction between genotype and phenotype and camel behaviour and welfare. The papers were presented in 8 sessions, i.e. embryology, female reproduction, male reproduction (two sessions), nutrition, milking, welfare, cell culture and genetics. A field trip to Ferrara and visit of Azienda Caretti dairy and Parmigiano cheese factory also took place.

INTERNATIONAL CONFERENCE ON THE SAFETY OF CAMELS

The First International Conference on the Safety of Camels will be organised jointly by Camel Club and International Camel Organisation on 27th July 2022 at Riyadh. The opening session will be on the concept of tampering in camels followed by first session on the effect of plastic surgery on camels and session two on the effect of drugs and hormones on behaviors and appearance. The invited speakers are from USA, Saudi Arabia, Egypt, Sudan and Bahrain.

CAMEL DAIRY MARKET 2022-2027

The global camel dairy market size reached a value of US\$ 6.9 Billion in 2021. Looking forward, IMARC Group expects the market to reach US\$ 8.6 Billion by 2027, exhibiting a CAGR of 3.1% during 2022-2027. On a regional level, the market has been classified into Middle East, Africa, Asia, Oceania, and Rest of the world, where Africa currently dominates the global market. Some of the major players in the global camel dairy market include Camelicious, Al Ain Dairy, Desert Farms, Vital Camel Milk, Tiviski Dairy, Camilk Dairy, Camel Dairy Farm Smits, Camel Milk Co Australia and Camel Milk South Africa.

ANTIGENIC COMPONENTS OF Echinococcus granulosus HYDATID CYST FLUID FROM DROMEDARY CAMELS (Camelus dromedarius)

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ABSTRACT

This study is designed to investigate the components of hydatid cyst fluid (HCF), the larval stage of *Echinococcus granulosus*, that acted as antigens during infection in dromedary camels and to identify the antigenic fractions specific to this metacestode. Hydatid cysts were obtained from an infected slaughtered camel in Al-Ahsa central abattoir, Kingdom of Saudi Arabia. Crude antigen extract was prepared from hydatid cyst fluid (HCF). SDS-PAGE fractionation of HCF on 7-20% acrylamide gel revealed 11 protein fractions when stained by Commassie blue stain. The molecular weight of these fractions ranged from ~180 to 22KDa. Western immunoblotting against serum from the camel infected with hydatid cyst identified 4 antigenic components of molecular weight of ~180, 55, 48 and 22KDa. Reaction with sera collected from camels with parasitic infections other than *E. granulosus* and from healthy camels free from parasitic infections failed to identify any antigenic component of HCF apart from one component of 58kDa with serum from camels suffering from mixed infection of *Nematodirus* and strongyle worms. The rest of antigenic components identified by HCF infection serum seems to be specific to this larval stage.

Key words: Dromedary camels, electrophoresis, Echinococcus granulosus, hydatidosis, immunoblots

Hydatidosis is a disease caused by infection of intermediate hosts with the larval stage (hydatid cyst) of the dog tapeworm Echinococcus granulosus. The disease is present in many African and Middle East countries (Kamhawi, 1995; Shambesh et al, 1997; Battelli et al, 2002; Sadjjadi, 2006). It is endemic in the Kingdom of Saudi Arabia affecting both humans and their domestic animals (Abu-Eshy, 1998; Al Mofleh et al, 2000; Adewunmi and Basilingappa, 2004; Fahim and Al Salamah, 2007; Ibrahim, 2010; Rashed et al, 2004). Diagnosis of the disease, particularly human cases were improved lately by the use of imaging techniques including ultrasonography, computed tomography (CT scanning) and magnetic resonance imaging (MRI) and immunological assays (WHO, 2003; Zhang et al, 2003). Immunological assays depends on hydatid cyst fluid (HCF) antigens as a source of antigenic material (Burgu et al, 2000; Kanwar et al, 1994; Musiani et al, 1978; Oriol et al, 1971; Piantelli et al, 1977; Pozzuoli et al, 1974). These immunoassays are used to detect antibodies to HCF antigens but they lack sensitivity and specificity (Babba et al, 1994). In addition, they do not discriminate between current and previous

infection. Nevertheless, western blotting has been used extensively for the study of parasite systems. Enzyme-linked immunoelectrotransfer blot (EITB) was reported to be the most sensitive serological assay for confirmation of hydatidosis (Verastegui *et al*, 1992). It also showed high specificity due to the high resolution of HCF antigenic components (Kharebov *et al*, 1997).

The detection of circulating parasite antigens in host's blood, would be an ideal approach for diagnosis of the disease and is more superior than antibody detection assay as it can provide specific parasitic diagnosis (Chaya and Parija, 2013). It is also considered a useful approach for assessment of treatment efficacy and has a high degree of specificity compared to antibody detection assays (Sadjjadi *et al*, 2009). Soluble antigens of other parasites circulating in body fluids have been detected using antigendetection immunoassays (Janardhan *et al* 2011; Cai *et al* 2014) serving as a confirmatory guide for current infection.

In the present study, the HCF components that acted as antigens during the course of infection

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were investigated. The antigenic fractions specific to HCF that will react potently, in western blotting, with serum from naturally infected camels and could identify possible candidates for diagnosis of infection.

Materials and Methods

Parasitological methods

One hundred faecal samples were obtained from slaughtered camels in Al-Ahsa central abattoir and these were examined for parasitic infections other than *E. granulosus* hydatid cyst using faecal flotation technique (Dryden *et al*, 2005) utilising magnesium sulfate as a flotation solution as well as sedimentation method.

Crude hydatid cyst fluid (HCF) extract

Hydatid cysts fluid was obtained from an infected camel slaughtered in Al-Ahsa central abattoir, Kingdom of Saudi Arabia. Crude antigen extract was prepared from hydatid cyst fluid (HCF) according to Al-Olayan and Helmy (2012). The HCF was aspirated aseptically and 25x protease inhibitor cocktail in 100 mM phosphate buffer, pH 7.0 immediately added. HCF was then centrifuged at 3000g for 30 min at 4°C and the supernatant was collected and dialysed, using cellulose membrane with molecular weight cut-off of 3.5kDa, against 3 changes of deionised water per 24 h. The dialysate then centrifuged again at 3000g for 30 min at 4°C and the supernatant was collected. Protein contents were estimated and antigen extracts were aliquoted and stored at -70°C until needed.

Serum samples

Serum samples were collected from eight camels infected with hydatid cyst at the slaughterhouse. These had mixed infection of *Nematodirus*/strongyle, while one camel had *Trichuris* infection and 2 camels had *Eimeria* spp. infection. Serum from a healthy camel calf free from parasitic infections was also collected. Samples from camels with the mixed infections and those with *Eimeria* spp. infection were pooled together. Serum samples were aliquoted and stored at -20°C until needed.

SDS-PAGE fractionation of hydatid cyst fluid (HCF)

The HCF crude extract was subjected to SDS-PAGE gradient gel electrophoresis (Laemmli, 1970) on 7 – 20% gradient gel. Coomassie Blue stain was used for visualisation of the gel protein banding pattern. A calibration curve based on the molecular weight markers was constructed and used to calibrate the molecular weight of individual HCF proteins. For permanent records, the gel was rinsed in distilled water and photographed.

Electrophoretic transfer of HCF proteins on NC membrane

An unstained gel containing HCF proteins separated by SDS-PAGE was soaked in transfer buffer (Electrode buffer, methanol and D.W) and laid on two pieces of filter paper (6µm pore size, Whatman) pre-soaked in transfer buffer and laid on top of the anode plate of a Sartoblot II-S semidry electroblotter (Sartorius Ltd., Germany). A nitrocellulose membrane (0.45µm pore size, Sartorius Ltd., Germany) previously cut to the size of the gel and soaked in transfer buffer then laid on top of the gel and again covered by two soaked filter papers at the cathode side. Electrophoretic transfer to nitrocellulose membrane was conducted for 90 minutes at room temperature with a constant current of 0.8 mA per cm² of gel.

Detection of antigenic components of HCF

Following the transfer of HCF proteins onto nitrocellulose membrane, the membrane was transferred into a sandwich box and the excess protein binding sites were blocked in 5% dried milk in blocking buffer, pH 7.4 overnight with gentle shaking. The blocked membrane then was rinsed with PBS. The reactivity of the separated proteins was examined by incubation of strips of the membrane overnight at room temperature with 1/50 dilution in blocking buffer of serum collected. The negative control serum from the healthy camel calf was also included in the run. The unbound antibodies were then removed by washing the membranes with seven changes of PBS over a period of 2 hours, before a peroxidase labelled goat anti-camel IgG (Alpha Diagnostic INTL, INC, USA) diluted to 1/2500 in blocking buffer was added and incubated for 2 hours. After washing, the membrane in PBS as above to remove excess conjugate, the labelled antigen/antibody complexes was visualised by incubation in 4-chlro-1-α-naphthol substrate solution, pH 7.5. Colour development was allowed to occur over 20 - 30 minutes, and the reaction then stopped by washing in distilled water and permanent records were made by photography.

Results

Parasitological finding

Faecal examination of slaughter camels revealed the presence of a mixed infection with *Nematodirus* and strongyle eggs in 8 camels (Fig 1a), *Trichuris* sp. eggs in a single camel (Fig 1b) and *Eimeria* oocyst in 2 of the surveyed camels (Fig c).

Hydatid cyst fluid (HCF) protein profile

Crude HCF extract showed 11 individual protein bands with molecular weight ranging from 180 - 22k.Da in 7 – 20% gradient polyacrylamide gel stained with Coomassie blue stain (Fig 2, lane 2). Three of the detected components were in the high molecular weight part of the gel (180 – 130kDa). The 48, 42 and 22 components showed the highest staining intensity.

Antigenic components of hydatid cyst fluid (HCF)

Infection serum from the camel naturally infected with hydatid cyst reacted with 4 antigenic components of HCF with molecular weight of ~180, 55, 48 and 22kDa (Fig 3, lane 2). Serum from camels with mixed infection of *Nematodirus* and strongyle worms reacted with one antigenic component of HCF with molecular weight of ~58kDa (Fig 3, lane 3). Serum collected from healthy camels and camels infected with *Trichuris* and/or *Eimeria* spp. failed to recognise any of the HCF components (Fig 3, lanes 1, 4 and 5).

Discussion

Hydatidosis in farm animals is generally asymptomatic (Urquhart et al, 2006) and a definitive diagnosis can only be made by necropsy. The identification of antigenic components of this larval stage of Echinococcus granulosus is important for diagnosis of the disease in these intermediate hosts. In the present study, the components of the hydatid cyst fluid obtained from naturally infected dromedary camels have been characterised using SDS-PAGE on gradient 7-20% polyacrylamide gels. Coomassie blue staining of fractionated HCF components revealed the presence of 11 protein bands ranging from 180 to 22kDa. Similarly, Hassanain et al (2021) using 10% homogenous gel, detected 10 protein bands ranging from 200 to 14kDa in HCF from naturally infected camels. The slight difference in the number and molecular range of these components probably attributed to difference in gels used. Doganay et al (2013) using 15% homogenous gels stained with silver stain detected 11 and 10 protein bands ranging from 200 to about 6.5kDa in HCF originated from sheep and donkey, respectively; however, Kordafshari et al (2010) using 5% homogenous gels detected 9 bands in HCF from sheep.

In order to determine the components of the cyst fluid that acted as antigens during infection and

to allocate those specific to this larval stage, sera from camels naturally infected with hydatid cyst, camels infected with Nematodirus/strongyle, Trichuris and Eimeria spp. and also negative control serum from healthy camels free from parasitic infections were analysed by western immuoblotting. Results showed that four of the cyst fluid components with molecular weight ranging from ~180 to ~22kDa are antigenic during infection as indicated by their reaction to infection serum and confirming the usefulness of this technique in diagnosis of infection in intermediate hosts. Two of these antigens, namely 48 and 22kDa reacted potently with this serum. Hassanain et al (2021) also detected 4 antigenic components with molecular weight ranging from 200 to 22kDa by sera from infected camels and 6 bands ranging from 200 to 14kDa using serum from confirmed human cases. Al-Olayan and Helmy (2012) using sera from confirmed that human cases were able to detect 11 bands in HCF originated from camels with molecular weight ranging from 110 to 16.8kDa. Sera from confirmed human cases when probed with hydatid cyst fluids from sheep and donkey identified 3 components with molecular weight ranging from 56 to 24kDa and only one component with molecular weight of 24kDa, respectively (Doganay et al, 2013).

Serum from dromedary camels having mixed infection with Nematodirus/strongyle worms in the present study was able to react with a single component with molecular weight of 58kDa of HCF indicating a possible shared epitope between the antigenic components of these parasites. This 58kDa antigen was not present in the Coomassie blue stained gel, yet was detected by western immunoblotting, possibly due to the fact that this technique is more sensitive than Coomassie blue. Coomassie blue has a detection limit of 1µg protein (Greenfield, 2014), while as little as 100pg of protein can be detected by immunoblotting (Towbin et al, 1979). Sera from animals with other parasitic infection such as Haemonchus contortus, Spirocerca lupi and Oesophagostomum radiatum have been reported to be detected antigenic components of HCF obtained from cattle (Kagiko, 1985). Similarly, sera from animals infected with other larval cestodes were able to react with HCF antigens (Kordafshari et al, 2010).

Negative control sera from dromedary camels infected with *Trichuris* or *Eimeria* sp. in the present study failed to react with any of the HCF antigenic components. This is probably due to lack of HCF components in these parasites. Antiserum raised against HCF antigens was unable to react with any



Fig 1. Parasitological findings. (a) Mixed Nematodirus and strongyle worms eggs (b) Trichuris spp., Egg (c) Eimeria spp. oocyst.



Fig 2. Protein profile of hydatid cyst fluid (HCF) on 7-20% polyacrylamide gel stained by Coomassie blue. Lane 1- Molecular weight markers. Lane 2- HCF extract.

antigenic components of *Trichuris vulpis*, *Bonostomum* phlebotomum and Ascaris suum (Kagiko, 1985).

The 4 antigenic components detected by sera from dromedary camels naturally infected with hydatid cyst seems to be unique to this parasite at least under the condition used in the present study.

In conclusion, the present study confirms the usefulness of western immunoblotting in serodiagnosis of hydatidosis in intermediate hosts and identifies the antigenic components of this larval stage of *E. granulosus* in dromedary camels. The study also allocated antigenic components specific to this parasite under the circumstances used in the present experiment, of which the 48 and 22kDa fractions that reacted potently with this serum may represent



Fig 3. Hydatid cyst fluid (HCF) antigenic components identified by: Lane 1- Negative control serum. MM- Molecular weight markers. Lane 2- Infection serum from camels naturally infected with hydatid cyst. Lane 3- Serum from camels with mixed infection of *Nematodirus* and strongyle worms. Lane 4- Serum from camels infected with *Trichuris* spp. Lane 5- Serum from camels infected with *Eimeria* spp.

possible candidates for specific diagnosis of this infection.

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COMPARATIVE ANALYSIS OF SELECTED IMMUNE PARAMETERS IN BLOOD OF THE MAJAHEEM AND MAGATEER DROMEDARY CAMEL BREEDS

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ABSTRACT

The present study investigated the composition of blood leukocytes in the Magateer and Majaheem camel breeds using immune cell labeling and flow cytometry. In addition, the phagocytosis activity of blood neutrophils and monocytes were compared between the two breeds. Although the total number of leukocytes did not differ significantly between the two camel breeds, a significantly higher fraction and absolute number of neutrophils was observed in blood of the Majaheem breed compared to the Magateer breed. In contrast to this, the fraction of eosinophils was significantly lower in blood of the Majaheem than the Magateer breed. The comparison of lymphocyte composition between the two breeds revealed significantly more B cells (relative and absolute count) in blood of the Magateer breed camel than the Majaheem camels. The two breeds showed comparable phagocytosis activity for their neutrophils and monocytes. Collectively, the present study compared selected cellular immune parameters between the two main breeds of the dromedary camel and identified similarities and differences.

Key words: Breed, dromedary camel, immune parameters, flow cytometry, leukocytes, Magateer, Majaheem

The impact of animal breed on innate and adaptive immunity has been investigated for several species (Schilling *et al*, 2019; Khatab *et al*, 2021; Lin *et al*, 2022; Ordonez *et al*, 2022; Ortega *et al*, 2022). In the dromedary camel, several components of the immune system have been recently characterised (Hussen and Schuberth, 2020). The phenotype and function of leukocytes are influenced by several physiologic (Gaashan *et al*, 2020) and pathologic factors (Hussen *et al*, 2018 and Hussen, 2019). Animal breed is one of the most important factors with key effect on the immune competence.

In the dromedary camel, several immunogenomic studies have described the genomic diversity of immunity-related genes in domesticated and wild camels, including genes encoding for B cell receptors, T cell receptors and MHC molecules (Antonacci *et al*, 2011; Vaccarelli *et al*, 2012; Ciccarese *et al*, 2014; Plasil *et al*, 2016; Futas *et al*, 2019; Plasil *et al*, 2019; Lado *et al*, 2020; Ming *et al*, 2020). Animal breeding programmes have traditionally focused on animal selection based on animal production capacity. However, intensive research is currently undertaken on selecting animal breeds with higher immune competence and disease resistance (Gavora and Spencer, 1983; Nino-Soto *et al*, 2008; Begley *et al*, 2009; Cartwright *et al*, 2011). For the dromedary camel, several breeds have been characterised based on animal size, coat colour and linear measurements (Kohler-Rollefson, 1993; Al-Atiyat *et al*, 2016; Meghelli *et al*, 2020).

Studies on the impact of dromedary camels breed on the cellular immune system are scarce. Therefore, the aim of the present study was to comparatively analyse the cellular composition of leukocytes in blood samples collected from the Magateer and the Majaheem dromedary camel breeds. In addition, the phagocytosis activity of blood phagocytes, including neutrophils and monocytes was compared between the two breeds.

Materials and Methods

Animals and blood sampling

Blood samples from jugular vein were collected into vacutainer tubes containing EDTA from 33 apparently healthy dromedary camels (n=33) including 15 animals of the Magateer breed (n=15) (mean age 9.3 \pm 2.4 years) and Majaheem breed (n=18) (mean age 9.6 \pm 2.1 yeras) from three camel farms in Al-Ahsa region in eastern Saudi Arabia. Cell separation from the collected blood samples was performed within one hour from the sampling.

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Cell separation

Leukocytes were separated from blood samples after hypotonic lysis of red blood cells. The lysis was performed by incubating 1 mL blood in 5 mL distilled water for 20 sec followed by the addition of 5ml double concentrated PBS to restore tonicity. This haemolysis procedure was repeated until complete lysis of red blood cells. The cells were washed two times in PBS ($500 \times g$, $250 \times g$, 10 min, 10° C). Separated leukocytes were finally suspended in staining puffer (PBS containing 5 g/L BSA, 100 mg /L NaN₃) at 5 x 10^{6} cells/mL.

Flow cytometry

Cell labeling was performed in round-bottomed 96-well microtitre plate using 5×10^5 leukocytes per well as previously described (Hussen, 2021). All incubation and centrifugation steps were performed at 4°C. Separated leukocytes were incubated with unlabeled primary monoclonal antibodies (mAbs) specific for the cell surface molecules, CD4, WC-1, MHCII and CD14 (Hussen and Schuberth, 2020) for 15 min in the dark. After two washings in staining buffer, the cells were incubated with fluorochromelabeled anti mouse IgM, IgG1 and IgG2a secondary antibodies (Invitrogen) for 15 min in the dark. After two washings, labeled cells were analysed on an Accurie C6 flow cytometer (BD Biosciences) by acquisition of at least 100 000 total leukocytes. Collected flow cytometric data was analysed using the CFlow Software (V 1.0.264.21; BD Biosciences). Leukocyte count was estimated and under microscope using the Neubauer counting chamber after staining of blood sample with Türk Solution.

Flow cytometric analysis of bacterial phagocytosis

For monocyte identification, separated leukocytes were firstly labeled with APC-conjugated mouse IgG2a against CD14. Labeled leukocytes were then incubated in 96 well plates $(1 \times 10^5/\text{well})$ with FITC-labeled S. aureus (50 bacteria/cell) for 45 minutes at 37°C and 5% CO₂. After incubation (15 min; 4°C), the percentage of monocytes and neutrophils with elevated green fluorescence among total cells was calculated after flow cytometric analysis.

Statistical Analyses

The statistical software program GraphPad Prism was used for statistical analysis. Differences between means were tested with the unpaired student's t test with significant differences if the p value was less than 0.05.

Based on animal size, coat colour and linear measurements, several breeds have been characterised within the dromedary camel species (Kohler-Rollefson, 1993; Al-Atiyat *et al*, 2016; Meghelli *et al*, 2020). However, the most common classification of the Arabian camel differentiates between the Majaheem breed (black camel) and the Magateer breed (white camel). In the dromedary camel, several myeloid and lymphoid immune cell populations and subpopulations were characterised during the recent years using flow cytometric analysis (Hussen, 2019; Hussen and Schuberth, 2020; Hussen *et al*, 2020; Hussen, 2021).

The comparison between the two camel breeds regarding their relative composition of leukocytes (Fig 1A) revealed significantly higher fraction of neutrophils in blood of the Majaheem (72.0 \pm 1.2% of leukocytes) than the Magateer (67.8 \pm 1.4% of leukocytes) breed (p < 0.05). In contrast to this, the fraction of eosinophils was significantly lower in blood of the Majaheem $(5.5 \pm 0.5\%)$ of leukocytes) than the Magateer (7.9 \pm 1.3% of leukocytes) breed (p < 0.05). However, the fraction of monocytes and lymphocytes did not show any significant differences between the two breeds (Fig 1B). With exception of the absolute number of neutrophils, the absolute counting of total leukocytes and their populations did not show any significant difference between the two breeds (p >0.05). The Majaheem camels (8565.9 \pm 456 cell / μ l blood) had significantly (p < 0.05) more numbers of neutrophils in their blood than the Magateer breed $(7658.5 \pm 748 \text{ cell} / \mu \text{l blood})$ camels (Fig 1C). The numbers of eosinophils, lymphocytes and monocytes were comparable between the two breeds (p > 0.05).

Although the percentage of lymphocytes and their absolute numbers did not differ between the two breeds, the Magateer breed camel showed more B cells in their blood than the Majaheem camels. This difference was significant for both the relative fraction of B cells (18.8 ± 1.4 versus $15.2 \pm 1.1\%$ of lymphoctres for the Majaheem breed) and their absolute numbers (271.9 ± 42 versus 201.0 ± 38 cell / µL blood for the Majaheem breed) (Fig 2).

Given the role of B cells in the humoral immune response through the production of antigen-specific antibodies (Cyster and Allen, 2019; Dhenni and Phan, 2020), the reduced numbers of B cells in blood of the Majaheem breed may have an impact on their response to B cell stimulating antigens. To test this hypothesis, further studies are needed to comparatively analyse B cell functional responsiveness (proliferation, antibody production) toward monoclonal and polyclonal stimulation in different camel breeds.

To investigate the breed-related effect on the immune cell function in camels, we analysed the

phagocytosis activity of neutrophils and monocytes in blood from the Magateer and Majaheem camels *in vitro*. The incubation of camel leukocytes with FITCconjugated *Staphylococcus aureus* (*S. aureus*) bacteria (Fig 3A) resulted in similar phagocytosis activity for







Fig 2. A) Separated camel leukocytes were labeled with monoclonal antibodies to the lymphocyte markers CD4, WC1 and MHCII.
B) The relative fractions of CD4-positive helper T cells, gamma delta T cells and B cells were estimated by flow cytometry based on the cell-staining with CD4, WC1 and MHCII, respectively. C) The absolute cell numbers of lymphocyte subsets were calculated by multiplication of the estimated cell percentage within total lymphocytes with the total lymphocyte count. Data for the two camel breeds were presented as mean and standard error of the mean. Differences between the means were calculated using the t-test and were considered significant (*) if p< 0.05.

the two breeds. The proportions of neutrophils and monocytes that have ingested the bacteria did not differ significantly between the two camel breeds (Fig 3B).

The identification and selection of camel breeds with the superior capacity to mount effective immune responses would significantly contribute to reduced disease occurrence and improved camel production and reproduction. Studies on bovine breeds indicated that dairy cows could be classified based on their genetic background as high, moderate, or low immune responders (Mallard *et al*, 2015). The more balanced and robust immune responses in high responder animals could be linked to lower disease occurrence. An effective immune response was regulated by the balanced response of both



Neutrophils Monocytes



innate and adaptive immune arms of the immune system. Cytokines and chemokines are key players in the regulation of immune responses and the communication between immune cells (Kimber *et al*, 2000; Gatla *et al*, 2019). Although the present

study identified some differences in selected immune parameters between the two main camel breeds, the characterisation of camel breeds with higher immune responsiveness and disease resistance requires the analysis of a wide range of humoral and cellular components of the camel immune system. Especially the characterisation of cytokines responsible for polarisation of the camel innate and adaptive immune responses toward type 1, type 2, or type 17 immune responses which would improve our understanding of immune competence in camel.

Collectively, the present study compared selected cellular immune parameters between the two main breeds of the dromedary camel and identified similarities and differences. The Magateer dromedary camels had more neutrophils but less B cells in their blood than the Majaheem camels. The two breeds showed comparable phagocytosis activity for their neutrophils and monocytes. The clinical relevance of these differences on the camel immune response to pathogens should be evaluated using *in vivo* and *ex vivo* future studies.

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NEUTROPHILS EXTRACELLULAR TRAPS FORMATION AND REACTIVE OXYGEN SPECIES (ROS) PRODUCTION BY MILK IMMUNE CELLS FROM CAMELS WITH SUBCLINICAL MASTITIS

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ABSTRACT

Subclinical mammary gland infections are within the most important infectious diseases in dromedary camels with high impact on milk production and animal health. Using flow cytometry, the present study analysed the capacity of milk phagocytes to form neutrophil extracellular traps (NETs) and to produce reactive oxygen species (ROS) *in vitro*. Based on the California mastitis test, clinically healthy camels were divided into animals with subclinical mastitis (n = 5) and camels with healthy mammary gland (n = 5). The *ex vivo* ROS production and the NETs formation activity of milk phagocytes were compared between healthy and affected animals. A basic fraction of phagocytes ($10.0 \pm 1.7\%$ of total cells) with positive staining with the NETs-sensitive dye SYTOXTM Green was detected in milk samples from healthy camels. The NETs-positive fraction was significantly lower in milk from camels with subclinical mastitis ($4.8 \pm 1.5\%$ of total cells) compared to milk samples from healthy camels. Stimulation of milk cells with the gram-negative bacteria *E. coli* resulted in enhanced ROS production in milk phagocytes from both healthy and affected camels. The two groups, however, did not differ in the ROS level in their unstimulated or stimulated phagocytes. In conclusion, the present study identified basic levels of NETs formation by milk phagocytes separated from healthy camels. The reduced NETs formation by cells from infected camels may play a role in the pathogenesis of subclinical mammary gland infections in camels.

Key words: Camel, flow cytometry, immune cells, milk, Neutrophils NETosis, ROS

Neutrophil extracellular traps (NETs) are structures composed of DNA, histones, and antimicrobial proteins that are released extracellularly by neutrophils and other immune cells as a means for trapping and killing invading pathogens. Pisanu et al (2015) reported the formation of NETs in mammary alveoli of sheep suffering bacterial mastitis, providing detailed information for understanding pathogenic mechanisms enacted by bacteria to survive the action of the innate immune system in the mammary gland. Xie et al (2022) carried out research on the neutrophil extracellular traps (NETs) and reactive oxygen species (ROS) formation capacity of polymorphonuclear cells (PMN) during different lactational stages to Holstein cows and found it an excellent model to mimic inflammation and study fundamental aspects of the production of NETs and ROS in vitro.

Camels may be affected by all types of mastitis similar to other dairy animals (Al-Ashqar *et al*, 2015; Alebie *et al*, 2021; Geresu *et al*, 2021; Ranjan *et al*, 2021). Bovine milk somatic cells are typically represented by epithelial cells, neutrophils, macrophages, and lymphocytes as the major cell types (Riollet *et al*, 2000). Kaskous *et al* (2021) suggested that 150×10^3 cells/ml in milk is a limit value for healthy camel milk. If the somatic cell count (SCC) exceeds this limit, subclinical or clinical mastitis of the udder may occur and the milk may be contaminated with microbes. Aljumaah *et al* (2020) found that the objective SCC test possesses considerable diagnostic merit for early detection of subclinical mastitis in camels. Subclinical mastitis is associated with huge economic losses due to the reduced milk yield and quality and high treatment costs. In addition, it is a public health concern for camel milk consumers (Osman *et al*, 2014).

Milk phagocytes, including macrophages and neutrophils, are the primary effector cells of the mammary gland innate immune system with a key role during mammary gland infections (Alhussien *et al*, 2021). They contribute to the early elimination of bacterial pathogens by several antimicrobial functions, including phagocytosis, production of

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reactive oxygen and nitrogen species, and formation of cellular traps (Lippolis *et al*, 2006; Aulik *et al*, 2010; Swain *et al*, 2014). The aim of the present study was to investigate NETs formation and ROS production capacity by milk phagocytes from healthy camels and camels with subclinical mastitis.

Materials and Methods

Animals

Ten clinically healthy Majaheem dromedary she camels reared on a private camel farm at the Al-Ahsa camel market in eastern Saudi Arabia were included in the study. After discarding the first few milk jets, teat ends were cleaned and disinfected and 10 ml milk sample was collected for the California Mastitis Test (CMT) into sterile glass tubes. Another 50 ml of freshly milked sample was taken into sterile plastic tubes for cell separation and flow cytometry. Milk of all studied animals underwent CMT (Schalm and Noorlander, 1957; Seligsohn et al, 2020). For this, 3 ml of each quarter milk were added to an equal amount of CMT fluid and the mixture was rotated by circular movement. The reactions were graded according to the Scandinavian scoring system (Seligsohn et al, 2020). Animals with milk samples of a test score equal to or more than score 3 in the absence of clinical signs of mastitis were classified as subclinical mastitis animals. For healthy she-camels (n = 5 animals) with a test score of less than 3 and without clinical signs of mastitis, pooled composite milk samples representing all 4 quarters were prepared for flow cytometry. In the affected group (n = 5 animals), milk samples collected from affected quarters were further processed for flow cytometry.

Cell separation for flow cytometry

Milk samples were diluted with cold PBS (20 ml milk and 20 ml PBS) in conical 50 ml polypropylene tubes and the tubes were centrifuged at 1000×g and 4 °C for 20 min without brake. After removing the fat layer using a spatula, the supernatant was discarded. The cell pellet was resuspended with 30 ml cold PBS and washed twice at 600×g and 4°C for 10 min. Milk cell pellets were suspended in 1 ml cell culture medium (RPMI 1640) at a concentration of 5×10^6 cells/ml.

Analysis of the formation of neutrophil extracellular traps (NETs) by flow cytometry

Cell labeling was performed in a roundbottomed 96-well microtitre plate. For this, 100 μ l of the cell suspension (5 x 10⁵ cells per well) of each sample were pipetted into the well of a microtitre plate. To each well of the microtitre plate, one drop of the DNA-sensitive dye SytoxGreen (Invitrogen, Germany) and 10 μ l of the cell viability dye propidium iodide (PI; 2 μ g/ml, BD Biosciences, Germany) were added. After 15 min incubation at room temperature, the labeled cells were analysed on a FACS Calibur (BD Biosciences) by the acquisition of at least 50000 total cells. Collected flow cytometric data were analysed using the FCS Expres Software (V3; BD Biosciences).

Flow cytometric analysis of reactive oxygen species (ROS)

ROS generation was measured in 96-well round-bottom microtitre plates (Corning, NY, USA) as previously described (Hussen, 2021). Separated milk cells (5×10^5 /well in RPMI medium) were incubated for 30 min (37° C, 5% CO₂) with heat-killed *E. coli* (50 bacteria/cell). After 15 min of incubation the ROSsensitive dye dihydrorhodamine (DHR)-123 (1µg/mL final, Mobitec, Goettingen, Germany) was added to the wells. After incubation, labeled cells were washed with PBS and the relative amount of generated ROS was determined by flow cytometry.

Statistical Analyses

Data were processed with the Microsoft office Excel® program (version 2016 Microsoft) and statistical analysis was performed using the software program Prism (GraphPad software version 5, GraphPad Software, San Diego, USA). The unpaired student's t-test was used to compare the mean of the two groups. The results for each analysed parameter were presented graphically as means \pm standard error of the mean (SEM). Results were considered statistically significant if the p-value was less than 0.05.

Results and Discussion

The mammary gland immune response to mastitic pathogens has been investigated for several animal species (Guiguen *et al*, 1996; Winnicka *et al*, 1999; Leitner *et al*, 2012; Blagitz *et al*, 2013; De and Mukherjee, 2013; Zecconi *et al*, 2020). Studies on the functional capacities of immune cells in the camel mammary gland are limited. The present study compared some antibacterial functions of milk leukocytes between healthy camels and camels with subclinical mastitis. Based on the results of California Mastitis Test (CMT), camels with a CMT test score of \geq 3 in the absence of signs of clinical mastitis were considered as subclinical mastitis animals (Seligsohn *et al*, 2020).

Macrophages and neutrophils are key effector innate immune cells of the mammary gland with an essential role during mammary gland infections (Swain et al, 2014; Alhussien et al, 2021). In present study, antimicrobial function of milk phagocytes (granulocytes and macrophages) was analysed by evaluation of ROS production. The basal and stimulation-induced ROS production by milk phagocytes were analysed using dehydrohodamin-123 (Fig 1A). Basal ROS values of phagocytes were comparable (p > 0.05)between SCM and healthy milk samples. In addition, stimulation with E. coli induced similar response (p > 0.05) in phagocytes from SCM and healthy milk samples (Fig 1B).

The formation of neutrophil extracellular traps (NETs or NETosis) is a key antibacterial effector function of cells of myeloid lineage including neutrophils and macrophages (Ciliberti et al, 2021). Using NETosis, the pathogens are killed after trapping it into an extracellular network of processed chromatin or DNA decorated with histones in addition to cytoplasmic proteins from neutrophilic granules (Lippolis et al, 2006; Aulik et al, 2010; Remijsen et al, 2011).

Neutrophil extracellular traps (NETs) also function as critical cytotoxins at infection site to promote "neutrophil apoptosis" through process of "NETosis" to achieve extracellular entrapment of pathogens (Bryzek et al, 2019).

In present study, NET-formation was analysed by flow cytometry using green fluorescence dye SYTOX[™] Green (Invitrogen, Germany). NET formation by milk phagocytes (neutrophils and macrophages) was compared between healthy camels and camels with subclinical mastitis. The

E. coli



A) Flow cytometry analysed of ROS-production







Fig 1. A) Stimulated or unstimulated cells were stained with the ROS-sensitive dye dehydroeorhodamin-123 and analysed by flow cytometry. After gating on milk phagocytes, the ROSproduction capacity was analysed by measuring the mean fluorescence intensity (MFI) of DHR in the green fluorescence detector FL1. B) Comparative presentation of ROS-amount in stimulated and unstimulated phagocytes from healthy and mastitic camels. * indicates significant differences (T test p < 0.05).

A) Flow cytometric analysis of netosis in milk phagocytes



B) Net formation in phagocytes from healthy and mastitic camels





Fig 2. A) Flow cytometric analysis of NET-formation. Milk cells separated from healthy camels and camels with subclinical mastitis were stained with the DNA-sensitive dye SYTOXTM Green and analysed by flow cytometry. After gating on milk phagocytes, NET-formation was estimated as the percentage of SYTOXTM Green-positive cells with enhanced green fluorescence. B) Comparative presentation of net formation in phagocytes from healthy and mastitic camels. * indicates significant differences (T test p < 0.05).

percentage of milk phagocytes that formed NETs was significantly lower in milk from camels with subclinical mastitis (4.8 ± 1.5 % of total phagocytes) compared to healthy camels (10.0 ± 1.7) (Fig 2).

In conclusion, the present study identified basic levels of NETs formation by milk phagocytes separated from healthy camels. The reduced NETs formation by cells from infected camels may play a role in pathogenesis of subclinical mammary gland infections in camels.

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New research and experience always broaden our knowledge, and help us adopting new diagnostic methods and treatments. Camel Publishing House has taken a step forward to compile this knowledge in form of a book and this Herculian task was accomplished with the help of dedicated editors. viz. Drs. T.K. Gahlot and M.B. Chhabra. Selected Research on Camelid Parasitology is most comprehensive guide to Camelid Parasitology. The classic reference book serves as a one stop resource for scientific information on major aspects of Camelid Parasitology. Featuring abundant photographs, illustrations, and data, the text covers camelid protozoa, helminths, and arthropods of dromedary and New World camelids. This hard bound book of 304 pages contains seroepidemiological studies, immunological and other diagnostic procedures, and new treatments of parasitic diseases. There are at least 17 countries involved in camelid parasitology research, viz. Ethiopia, France, India, Iran, Jordan, Kenya, Libya, Mauritania, Nigeria, Sultanate of Oman, Pakistan, Saudi Arabia, Sudan, Sweden, United Arab Emirates, Uganda and U.S.A. As per published papers in Journal of Camel Practice and Research (JCPR), 173 authors have contributed 72 manuscripts which are appropriately placed in 5 sections. The text of each manuscript published previously in JCPR remains the same except the pattern of numbering the references in the body of text. This book indicates a swing of camelid research during period 1994-2008 and will help identifying the missing links of research in this subject.

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PARASITOLOGICAL AND MOLECULAR INCIDENCE OF Trypanosoma evansi IN DROMEDARY CAMELS OF GUJARAT, INDIA

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ABSTRACT

The present study was aimed to assess the incidence of *T. evansi* infections in camel in Saurashtra region of Gujarat, India, through microscopy and polymerase chain reaction (PCR) methods. Blood samples were collected from 192 camels, randomly. The diagnostic sensitivity and specificity of Field's stain, Giemsa stain and RoTat1.2 polymerase chain reaction (PCR) assays for detection of *T. evansi* in blood samples was evaluated. *T. evansi* infection recorded in camels based on Field's stain, Giemsa stain and RoTat1.2 PCR assays was 3.23%, 8.85% and 22.39%, respectively. Sensitivity of Field's stain was 35.29% while PCR test had 100% sensitivity in comparison to Giemsa stain for the detection of *T. evansi* in blood samples. The analytical sensitivity of newly developed RoTat1.2 PCR assay was determined as 1.07 pg of purified whole blood genomic DNA. Epidemiologically, *T. evansi* was an important pathogen in camels of all age groups but more prevalent in adult animals and in monsoon season.

Key words: Camels, Field's Stain, Giemsa stain, Polymerase chain reaction (PCR), RoTat1.2 VSG gene, Trypanosomosis

T. evansi infection is widely prevalent in different parts of India and is of significant economic importance in livestock production (Mahran, 2004; Juyal et al, 2007). The disease has been reported from almost all states of India viz., Haryana, Punjab, Uttar Pradesh and Jammu and Kashmir in northern India; Rajasthan, Gujarat and Maharashtra towards west andra Pradesh, Karnataka, Tamil Nadu towards south and Bihar and West Bengal in eastern India (Juyal et al, 2007; Ravindran et al, 2008; Kumar et al, 2015; Maharana et al, 2016). Though, the disease has been studied for the past many decades, the definite diagnosis still suffers from low sensitivity and specificity and as a result, the epidemiology of the disease is far from completely understood. The parasitological examinations frequently fail to detect patent infections because parasitemia is scanty in peripheral blood in chronic forms (Killick- Kendrick, 1968; Abdel-Rady, 2008). Antibody detection based serological diagnosis has limitations of differentiation between current and past infections, persistent titres and the occurrence of false-positive results (Bhutto et al, 2010). Accordinly, very high rate of prevalence of T. evansi in camels was recorded through various serological tests such as CATT/T. evansi, formol gel

test, ELISA/VSG RoTat1.2, immune trypanolysis compared to PCR and standard trypanosome detection methods (STDM) (Tehseen *et al*, 2015; Hassan-Kadle *et al*, 2019).

Alternatively, polymerase chain reaction (PCR) has been developed for detection of trypanosomes (Masiga et al, 1992; Claes et al, 2004; Aradaib and Magid, 2006; Konnai et al, 2009; Ghorui et al, 2012; Elhaig et al, 2013). PCR assays have been designed to target different genome sequences and there exists a consensus regarding the difference of sensitivity and specificity between the different PCR methods (Taylor et al, 2008; Pruvot et al, 2010; Sengupta et al, 2010; Tehseen et al, 2015). However, the sensitivity of the specificity of different available primers is varying (Pruvot et al, 2010; Padmaja, 2012). Based upon Rode Trypanozoon antigen type (RoTat) 1.2., a variable surface glycoprotein (VSG) gene, the T. evansi is classified as Type A (presence of RoTat1.2 gene) and Type B (absence of RoTat1.2 gene). T. evansi Type A is commonly found while Type B is rare and only reported from some part of Africa (Li et al, 2020). Based on the specificity of the targeted gene (Urakawa et al, 2001) and wide spread nature of T. evansi type A, the present study was aimed to identify T. evansi

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infection in camels and to compare the parasitological techniques with RoTat1.2 PCR assay.

Materials and Methods

Study area and sample collection

A total of 192 blood samples were collected from camels at Veterinary Clinical Complex, Veterinary College, Junagadh and animal health camps organised by the institute during year 2017-20. The common clinical signs were loss of appetite, a decrease in productivity and weight loss of animals. A detailed clinical history and animal parameters like age, sex and breed were recorded. Blood samples were collected from the jugular vein into blood collection vials containing an anticoagulant (EDTA) for laboratory examination. Trypanosoma parasites were identified through microscopic examination and further confirmation was done by polymerase chain reaction (PCR) assay. To study the seasonal influence on infection rate, three distinct seasons were recognised in a year like rainy/monsoon season between July and October while the other two dry seasons prevail from November to February (winter) and from March to June (summer). For epidemiological study, animals were also grouped age wise, i.e. less the 5 years, 5-10 years and more than 10 years.

Parasitological examination of samples

Thin blood smears were subjected to Giemsa and Field's stains for parasitological examination. The parasites were identified according to the characters described by Soulsby (1982). Each slide was labeled on the smear indicating the animal breed, animal age, sex and date of collection. The remaining blood samples were preserved at -20°C for isolation of whole blood genomic DNA to test *T. evansi* infection through the PCR technique.

DNA extraction and RoTat1.2 PCR

Whole blood genomic DNA was isolated from 200 μ l whole blood samples of camels using commercial GeneJET Whole Blood Genomic DNA Purification Mini Kit (Thermo Scientific, Lithuania). The manufacturer's protocol was followed for the DNA purification and DNA was eluted in 200 μ l elution buffer. The DNA was stored at -20°C immediate after isolation until further use.

For molecular confirmation of *T. evansi* infection in camel, a set of primers specific to *T. evansi* RoTat 1.2 VSG gene were designed based on sequence available in NCBI (Accession No. AF317914) using online Primer3 web tools (http://primer3.ut.ee/). The primers were picked as LtF3: Forward primer 5'-CCA GGA GAC AGC TAC CTA GA-3' and LtB3: Reverse primer 5'-TGG CTG GTC GTC AAC TTT G-3' which amplify 219 bp fragment of RoTat1.2 gene of T. evansi. The designed primers were checked in-silicon for its specificity using the Primer-BLAST programme of NCBI (https://www.ncbi.nlm.nih.gov/tools/ primer blast/index.cgi? LINK_LOC= BlastHome). The amplification of the targeted DNA sequence was done in a thermal cycler (Applied Biosystem, USA) in a 200 µL tubes holding a volume of 25 µL reaction mixture. The master mix consisted of 2.5 µL of DreamTaq Green buffer (Thermo Scientific, Lithuania), 0.5 µL of 10 mM dNTP mix (Thermo Scientific, Lithuania), 1 μL each (10 pmol) of the primers, 0.2 μL of DreamTaq DNA Polymerase (Thermo Scientific, Lithuania) and 4 µL of template DNA isolated from camel blood found microscopically positive for T. evansi. The nuclease-free water was used in place of DNA as a negative control. The volume was made up to 25 µL with nuclease-free water. The PCR reaction was done at laboratory optimised condition viz., initial denaturation at 95°C for 3 min followed by 35 cycles of denaturing at 96°C for 15 s, primer annealing at 60°C for 20 s and primer extension at 72°C for 25 s. This was followed by the last cycle of extension at 72°C for 5 min and hold at 4°C for an indefinite time. The amplified products were resolved in 1.2% agarose containing $0.5 \,\mu$ g/ml ethidium bromide and visualised by UV transillumination and photographs were taken.

Amplified products from a positive sample were purified using Gene JET Gel Extraction Kit (Thermo Scientific, Lithuania) following the manufacturer's protocol and 10 μ l was submitted alogwith forward and reverse primes for Sanger sequencing to commercial service provider (Eurofins Genomics India Pvt. Ltd., Bengaluru, India). Obtained sequences were aligned and checked using BioEdit programme and BLASTn (NCBI, USA). Finally, sequence was submitted to GenBank (NCBI, USA).

All 192 samples tested through microscopic test were also tested using currently optimised RoTat1.2 PCR assay as discussed above.

Specificity and sensitivity of the PCR primers

To assess the specificity of the RoTat1.2 PCR assay, the total genomic DNA extracted from whole blood of different animals infected with other common haemoparasites viz., *Babesia bigemina*, *Theileria annulata*, *T. orientalis*, *B. canis vogeli*, *B. gibsoni*, *B. equi*, *B. cabali*, *Ehrlichia canis*, *Anaplasma marginale*

and Hepatozoon canis present in the laboratory were included in PCR assay and reactions were noted after resolving the PCR products on 1.2% agarose gel.

The analytical sensitivity of the PCR assay was assessed by the use of different concentrations of DNA diluted in nuclease-free water (NFW). The concentration of whole blood genomic DNA isolated from a microscopically positive blood sample was determined through Qubit®dsDNA BR assay kit in Qubit™ 4 Fluorometer (Thermo Scientific, Singapore) as per the manufacturer's instructions. To assess the threshold limit of PCR assay, DNA was diluted in five fold serial dilutions with NFW and the reaction was performed with each dilution as a template (1 µl) at optimised conditions. The amplification of the DNA sequence was confirmed by agarose gel (1.2%) electrophoresis containing ethidium bromide.

Statistical analysis

Chi square (χ^2) test was used for comparing the diagnostic methods and different epidemiological parameters and p<0.05 was considered as a significant difference between the tests. Using Giemsa stain as gold standard, the sensitivity and specificity of RoTat1.2 PCR and Field's stain microscopy were determined using Fischer's extract test at a 95% confidence interval (CI).

Results and Discussion

The microscopic examinations of thin blood smears revealed 3.23% and 8.85% infections of Trypanosoma evansi with Field's and Giemsa stains, respectively in camels. The difference between the two staining methods was statistically significant (p<0.05). When Giemsa stain was taken as gold standard, the sensitivity of Field's stain was found 35.29% with a range of 14.21 to 61.67%, specificity was 100% with a range of 97.91 to 100.00% Positive Predictive Value (PPV) was 100.00% and Negative Predictive Value (NPV) was 94.09% with a range of 91.80% to 95.76 at 95% confidence interval (CI). The present finding was in aggrement with results of Mendiratta et al (2006) where 34.57% sensitivity, 100% specificity and PPV and 87.23% NPV of Field's stain was observed in comparison to Leishman's stain for the detection of Plasmodium falciparum in human blood smear. However, higher sensitivity (97.72%) of Field's stain was recorded by Gaikwad and Chaya (2016). Though, Field's staining was low cost and rapid method but due to its lower sensitivity, Giemsa stain was preferred over it (Monzón et al, 1990).

Selection of most suitable target genes/nucleic acid fragments and designing of oligo-primers were the prerequisite for development of specific PCR assay. In present study, we targeted 219 bp fragments of very specific RoTat1.2 VSG genes of T. evansi. It was successfully amplified and optimised without any non-specific reactions (Fig 1A). To confirm the amplified product of targeted gene, sequence was generated from purified PCR product and submitted to GenBank (NCBI, USA) and accession was obtained (MZ032003). Upon BLASTn analysis (NCBI, USA), the newly generated sequence was aligned with 22 sequences of VSG gene of T. evansi available in GenBank. They showed 100% identities with maximum sequences (n=17; 10 sequences were having 100% query coverage) and 99.02% identities with 4 sequences (only 46% query coverage). Only one sequence (MT501210) which was having 100% query coverage shows 98.63% identities. This confirmed that the amplified product was from targeted organism. Moreover, the assay was found highly specific to detect the targeted organism as the primers pair did not react to the DNA of other commonly available haemoprotozoans in this region like Babesia bigemina, Theileria annulata, T. orientalis, B. canis vogeli, B. gibsoni, B. equi, B. cabali, Ehrlichia canis, Anaplasma marginale and Hepatozoon canis or host DNA at the optimised PCR conditions (Fig 1B).

RoTat1.2 VSG gene was targeted by many researchers for the specific diagnosis of T. evansi in animals including camels. Recently, Kumar et al (2021) targeted 200 bp fragment of RoTat1.2 gene to develop loop-mediated isothermal amplification (LAMP) assay for detection of T. evansi in domestic animals. Similarly, Li et al (2020) targeted RoTat1.2 gene fragment to develop recombinase polymerase amplification (RPA) lateral flow assay for detection of active T. evansi infection. Boushaki et al (2019) targeted 488 bp fragment of RoTat1.2 VSG and reported 11.2% prevelance of T. evansi in camels in Algeria compared to only 2.4% prevelance of T. evansi through Giemsa stained thin blood smear examination. However, Tehseen et al (2015) has compared the RoTat1.2 PCR with TBR1/2 PCR for the diagnosis of *T. evansi* in camels and they found almost comparable results. Though, T. evansi without RoTat1.2 VSG (called T. evansi Type B) was also recorded in certain part of Africa and Saudi Arabia (Ngaira et al, 2005; Salim et al, 2011; Alanazi et al, 2018) but in India it was not recorded till now.

Another important feature to be studied for a good primer was its higher analytical sensitivities.

Here, the analytical sensitivity of the assay was found upto1.07 pg of DNA (Fig 1A) which was comparable to the other PCR assay for diagnosis of *T. evansi* (Omanwar *et al*, 1999; Fernández *et al*, 2008; Sengupta *et al*, 2010; Pruvot *et al*, 2010).

In the present study, 22.39% samples were found positive for *T. evansi* using PCR assay (Fig 2) which is significantly (p<0.05) higher as compared to microscopy (Table 1). While considering the Giemsa staining technique as a gold standard, the sensitivity



Fig 1. Analytical sensitivity and specificity of RoTat1.2 PCR for identification of *T. evansi* in camels. A. Determination of sentisivity on *T. evansi* positive samples [S- PCR on undiluted DNA, 1st to 8th - PCR on serial five-fold diluted DNA, N- no template control (negative); M- DNA ladder (100 bp DNA ladder, ready-to-use, Thermo scientific, Lithuania)]. B. Assessment of specificity of RoTat1.2 PCR [1. Babesia bigemina, 2. Theileria annulata, 3. T. orientalis, 4. B. canis vogeli, 5. B. gibsoni, 6. B. equi, 7. B. cabali, 8. Ehrlichia canis, 9. Anaplasma marginale, 10. Hepatozoon canis, N- Negative control (host DNA), P- positive control].

of PCR test was found 100% with a range of 80.49% to 100.00%, specificity was 85.14% with a range of 78.99 - 90.06%, PPV 39.53% (31.44% to 48.25%) and NPV 100% at 95% CI. PPV indicate the probability that the disease was present when the test was positive and NPV indicated about the probability that the disease was not present when the test was negative. Having 100% sensitivity and NPV for a test are good indicatiors for its utility in epidemiological studies as well as diagnosis of infected animals without any false negative results. Lower specificity and PPV of PCR was just because of inherent low sensitivity of microscopy. Similarly, Ereqat et al (2020) recorded 14.3% more positivity to T. evansi in animals in Palestine through 18S rRNA PCR (17%) compared to wet mount microscopy (2.7%). They recorded highest prevalence of T. evansi in camel (about onethird) compared to other domestic animals. Likewise, Ravindran et al (2008) also recorded significantly higher positivity of T. evansi infection through PCR (19.84%) comapared to Giemsa stained thin blood smear examination (1.5%). Among the different animals studied by him, the higest incidence of T. evansi was recorded in camels (~ 81% of total positive case) followed by donkeys and least in dogs. The low sensitivity of microscopy using thin blood smear may be related to low parasitaemia which might be due to early and/or chronic infection, visual mistakes made during the examination of slides, destruction of red blood cells due to hemolysis, the thickness, dirtiness or unsuitable blood smear staining compared to PCR (El-Naga and Barghash, 2016). Blood smear examination proved to be of limited value in diagnosis of subacute or chronic cases (Herbert and Lumsden, 1976; Desquesnes, 2004). In contrast, a high sensitivity of PCR with purified whole blood DNA was confirmed and was successful in diagnosis of infectious diseases as compared to



Fig 2. Identification of *T. evansi* infection in camels using RoTat1.2 PCR [1- negative control, 2- positive control, 3 to 14- field samples and M- 100 bp DNA ladder (100 bp DNA ladder, ready-to-use, Thermo Scientific, Lithuania)]. Here, samples 7, 11 and 14 showing positive reaction for *T. evansi* infection while, only sample no. 14 found positive through microscopy (Giemsa stain).

parasitological method (Gonzales *et al*, 2003; Abdel-Rady, 2006; Baticados *et al*, 2011).

Considering the PCR assay as an epidemiological tools to identify the *T. evansi* infection in camels, the highest incidence of infection was recorded in monsoon followed by summer and lowest in winter (Table 2). This might be due to the good environmental conditions for the fly to breed thus led to higher occurrence of disease (Rayulu *et al*, 2007; Maharana *et al*, 2016; Barghash, 2016).

Age wise incidence of *T. evansi* infection in camels was determined where significantly lower incidence of infection was noted in less than 5 years age groups compared to more than 5 years aged animals (Table 2). Similarly, Giro and Kula Jilo (2020) reported higher incidence of T. evansi infection in >4 years (18.12%) aged followed by 3-4 years (6.98%) and lowest in <3 years old camels (4.67%). Contrarily, some other scientists reported higher incidence of the disease in young camel of less than 5 years of age (Njiru et al, 2004; Singh et al, 2004). The incidence of infection varied with geographic area which may be correlated with the presence of vectors population. However, stress, inadequate nutrition, inadequate exercise, close confinement, transportation and managemental negligence might have played a vital role for predisposing the disease in young and adult group (Gutierrez et al, 2000; Njiru et al, 2002; Njiru et

| | Giemsa stain | Field's stain | PCR assay |
|---------------------|--------------|---------------|-----------|
| Positive | 17 | 6 | 43 |
| Negative | 175 | 186 | 149 |
| Percentage positive | 8.85% | 3.23% | 22.39% |

Table 1. Detection of *T. evansi* infections in camels (n=192) through microscopy and RoTat1.2 PCR assay.

| Table 2. | Sex wise, age wise and seasonal incidence of T. evansi |
|----------|--|
| | in camels through RoTat1.2 PCR assay. |

| Parameters | Total samples | Incidence (%) | | |
|--------------------|---------------|---------------|--|--|
| Sex wise incidence | | | | |
| Male | 88 | 16 (18.18%) | | |
| Female | 104 | 27 (25.96%) | | |
| Age wise incidence | | | | |
| < 5 years | 77 | 11 (14.28%) | | |
| 5-10 year | 90 | 26 (28.88%) | | |
| >10 years | 25 | 06 (24.00%) | | |
| Seasonal incidence | | | | |
| Summer | 74 | 16 (21.62%) | | |
| Monsoon | 91 | 23 (25.27%) | | |
| Winter | 27 | 04 (14.81) | | |

al, 2004; Moghaddar and Diantpor, 2009; Tadesse *et al,* 2012).

Trypanosomosis, which is a vector-borne disease, has little difference between the sex, however, in animals of present study a higher incidence of *T. evansi* was recorded in females (25.96%) compared to males (18.18%) (Table 2). This could be due to successive pregnancies and stress of lactations in females. Similarly, Rayulu *et al* (2007) and Padmaja (2012) reported higher incidence in females whereas it was lower in geldings. This might be due to prevailing managemental practices and population ratio of male to female (Njiru *et al*, 2002; Singh *et al*, 2004; Barghash *et al*, 2014; El-Naga and Barghash, 2016).

In conclusion, the *T. evansi* was more prevalent in adult animals during monsoon season in Saurashtra region of India. Though, microscopy was still considered as gold standards, the molecular test like PCR based on RoTat1.2 gene may be the method of choice for epidemiological studies of *T. evansi* with significantly higher sensitivity along with 100% NPV.

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BABESIOSIS AND ANAPLASMOSIS IN CAMELS (Camelus dromedarius) OF SAUDI ARABIA

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ABSTRACT

An epidemiological study was conducted on the occurrence of babesiosis and anaplasmosis infection in camels (*Camelus dromedarius*) in the Taif region of Saudi Arabia. A total of 102 blood samples were collected from apparently healthy camels, of varying ages and sex, from three different areas of the Taif region. The blood samples were investigated using Giemsa-stained blood smears and species-specific Polymerase chain reaction (PCR) (targeting 18S rRNA and the major surface protein–1 β encoding genes for *Babesia* and *A. marginale*, respectively). The overall prevalence was 64.70% with a higher infection rate of *Anaplasma* (46.10%) than *Babesia* sp. (18.62%). In addition, there is a co-infection of both pathogens with prevalence rate 19.70%. According to age: the infection rate was highly significant in the younger animals (\leq 5 years) (33.33% and 58.97%) than older animals (>5 years) (9.52% and 38.09%) for *Babesia* and *Anaplasma*, respectively at p> 0.05. On the other hand, according to gender, the infection rate in males (29.73% and 72.97%) was higher than in females (12.31% and 30.77%) for *Babesia* and *Anaplasma* sp., respectively at p> 0.05. In conclusion, the present study adds insight into the epidemiology of babesiosis and anaplasmosis in the Taif region, Makkah Province of Saudi Arabia that needs control strategies to focus on the livestock.

Key words: Anaplasma; Babesia; Camelus dromedarius; prevalence; Saudi Arabia

Babesia and Anaplasma species are the most important tick-borne haemoparasites that may cause a serious threat to livestock, pets, and wildlife throughout the world (Guglielmone et al, 2015). Babesiosis and anaplasmosis are two separate diseases that often present in the same animal together (Kocan et al, 2010). Babesia species are transmitted by ixodid ticks to the vertebrate host, where they replicate in the red blood cells (Homer et al, 2000). Anaplasmosis is caused by A. marginale, which is worldwide spread and endemic in various regions in Africa and Asia (Kocan et al, 2003; 2010). Anaplasmosis is transmitted by at least 20 tick species (Stiller and Marchette, 1982) and disease causes serious health problems leading to reductions in animal productivity and substantial economic losses (El-Ashker et al, 2015).

Tick and tick-borne diseases remain a major threat to animals, causing serious economic losses in tropical and subtropical countries, including Saudi Arabia (Al-Nabati *et al*, 2022). These infections are regarded as a serious health problem, as they affect animal health, productivity, and performance including *Babesia* and *Anaplasma* infections (Megersa, 2010). Recently, it was reported a low prevalence of *Anaplasma platys* (5.3%) in local camels, however all samples (170 camels) tested negative for *Babesia* spp. and *Theileria* spp. in Riyadh Province of Saudi Arabia (Alanazi *et al*, 2020). In Asir Province, another study carried out in camels found that the overall prevalence was 2% with *Anaplasma* sp., while all the blood samples were free from *Babesia* sp. (Alshahrani *et al*, 2020). According to Al-Nabati *et al* (2022) the estimated overall prevalence of *Anaplasma* infection in camels was 44.99% in Riyadh and Eastern Region of Saudi Arabia. While *Babesia* sp. infection was not observed in any blood samples in the same study.

However, the prevalence of *Babesia* and *Anaplasma* species in Saudi Arabian camels, especially in the western region is least studied. Therefore, this study contributes to understanding the epidemiology of Babesiosis and Anaplasmosis infections in local camels in the Taif region of Makkah Province of Saudi Arabia.

Materials and Methods

Study area and blood sample collection

A total of 102 blood samples of apparently healthy camels (females (n=65), aged 3-12 years;

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males (n=37), aged 1-7 years) were collected from three different areas of the Taif region (21°5668571N 40°7019237E, 21°25732N 40°50762E, and 21°2606711N 40°510672E). Data about camels such as age, gender was also recorded for each camel. About 2ml of blood samples (from ear veins) of camels were collected in EDTA coated tubes and obtained through veterinarians as per their periodic examination from the period December 2020 to February 2021.

Microscopic examination

Smears were made for all samples and stained with 10% buffered Giemsa, and examined under a light microscope for *Babesia* sp. and *Anaplasma* sp. diagnoses (Schalm, 1971).

DNA extraction

DNA was extracted manually by using low TKM1 (100mM Tris-HC1, pH 7.4, 250mM sucrose, 10mM EDTA) and high TKM2 (Tris HCl 10 mM pH 7.6, 10 mM KCl, 10 mM MgCl₂, 0.4 M NaCl, and 2mM EDTA) salt buffer according to Ahmad *et al* (2007). DNA was finally dissolved in 100 µl autoclaved Milli-Q water for further evaluation.

PCR amplification

Two different polymerase chain reactions were performed on the extracted DNA for *Babesia* sp. and *A. marginale* detection. Forward Bab-sp-F and reverse Bab-sp-R primers were used to amplify a 428 bp of small 18S rRNA gene fragment targeting *Babesia* sp. While MAR1bB2F and MAR1bB2R primers were used to amplify a 265 bp of the major surface protein–1 β encoding gene (MAR1bB2) targeting *A. marginale* (Table 1).

PCR amplification was done in a total reaction volume of 20 µl: 7 µl H₂O, 1 µl (20 pmole) of each forward and reverse primers, 1 µl extracted DNA, and finally 10µl of 2× master mix. For both reactions: PCR amplification was done in a total reaction volume of 20 µl: 7 µl H₂O, 1 µl (20 pmole) of each forward and reverse primers, 1 µl extracted DNA, and finally 10µl of 2× master mix. The PCR reaction was set up with initial denaturation at 94°C (5 mins), 40 cycles of denaturation at 94°C (30 s), annealing at 61°C or 57 °C (30 s), and then extension at 72°C (45 s) for *Babesia* sp. and *A. marginale*, respectively. The final extension at 72°C (10 mins) was necessarily done for complete amplification. PCR products were separated on 1.5 % agarose gel (at 100V, 60 min), visualised, and then photographed by a gel documentation system. A low molecular weight DNA marker (50-1500 bp) was used in the agarose gel to confirm the amplified amplicon sizes.

Sequencing and phylogenetic evaluation

PCR products of *Babesia* sp. and *A. marginale* was subjected to sequencing using an ABI Prism 3730 Genetic Analyser automated sequencer. Sequences were aligned with others in the Genbank using online NCBI BLAST, phylogenetically estimated, and finally viewed as rectangular cladogram in the phylogenetic Tree View (Kuznetsov and Bollin, 2021).

Statistical analysis

The significant differences regarding the prevalence of *Babesia* and *Anaplasma* and their risk factors, such as age, gender, and source of the camels were calculated by c2 tests using a program in Statistical Package for the Social Sciences (SPSS), version 20.0, at P< 0.05.

Results

Babesia and *Anaplasma* sp. were detected microscopically from Giemsa's-stained blood films as shown in Fig 1. The overall infection of haemoparasites in camels was 64.70%, where 66 animals out of 102 were infected. There was a significant higher infection rate for *Anaplasma* sp. (46.10%) in comparison to *Babesia* sp. (18.62%) in camels at p < 0.05 (Table 2). There was a co-infection of *Babesia* and *Anaplasma* in 13 out of 102 (19.70%) camels of the total samples. PCR evaluation detected more positive samples than the parasitological assay as shown in Table 2.

According to the age the maximum infection rate was found in the younger animals (≤5 years) for

Table 1. Oligonucleotide sequences of primers used for PCR and sequencing in the present study.

| Targeted Parasite | Targeted gene | Primers' name | Primers' sequences | PCR product (bp) | Reference |
|----------------------|-----------------------------|------------------|--------------------------------|---------------------|--------------------------------------|
| Babesia sp. | Babesia sp. 18S rRNA | | 5'-GTTTCTGCCCCATCAGCTTGAC-3' | 428 | Hilpertshauser <i>et al,</i> 2006 |
| 1 | | Bab-R | 5'-CAAGACAAAAGTCTGCTTGAAAC -3' | | |
| | major surface | MAR1bB2F | 5'-GCTCTAGCAGGTTATGCGTC-3' | 2/5 | El-Naga and |
| A. marginale | protein-1β encoding gene | MAR1bB2R | 5'-CTGCTTGGGAGAATGCACCT-3' | 265 | Barghash, 2016. |

Babesia (33.33%) and *Anaplasma* (58.97%) (Table 3). On the other hand, this rate was significantly decreased in older animals (>5 years) for *Babesia* (9.52%) and *Anaplasma* (38.09%) at p < 0.05. The prevalence in camels concerning gender was significantly different at p < 0.05. The infection rate in males (29.73% and 72.97%) was higher than in females (12.31% and 30.77%) for *Babesia* sp. and *Anaplasma* sp., respectively. According to source the imported camels (80%) are highly infected than the local ones (44.33%) for *Anaplasma* sp., but this was contrary to *Babesia* sp. prevalence in local (16.49%) and imported (15.80%) animals as shown in Table 3.

Extracted DNA was used to amplify two separate genes' loci, 18S rRNA and major surface protein–1 β encoding gene, for both *Babesia* sp. and *A*.

marginale, to yield amplicons of 428 bp, and 265 bp, respectively. The present results report the success of PCR amplification for both selected portions as shown in Fig 2. However, the presence of other lower or higher bands, than the expected size of amplicons is non-specific.

Randomly selected PCR products from both loci were sequenced by using their forward/ reverse primers and were blasted with other related sequences in different countries. Phylogenetic trees were constructed from those sequences according to higher percentage identity and query coverage range (Fig 3).

The BLAST analysis showed that the present sequence of the major surface protein- 1β encoding gene related to *A. marginale* was found in

| | Prevalence in total 102 samples | | | |
|-----------------|---------------------------------|-------------------------------|---------------|--|
| Parasite | PCR = <i>n</i> (%) | Blood smear and PCR =n (%) | Total = n (%) | |
| Babesia (+ve) | 11 (10.78%) | 8 (7.84%) | 19 (18.62%) | |
| Anaplasma (+ve) | 13 (12.74%) | 34 (33.33%) | 47 (46.10%) | |
| Total | 24 (23.53%) | 42 (41.18%) | 66 (64.70%) | |
| X2 | 5.345 | | | |
| P-value | 0.020 | | | |

Table 2. Prevalence of Babesia and Anaplasma sp. infection detected microscopically and by PCR in camels of the present study.

The chi-square statistic is 5.345. the *P*-value is 0.020 significant at p < 0.05.

| Table 3. | Risk factors | associated w | rith Babesia a | nd Anaplasma | sp. infections | detected in | camels of the | present study | |
|----------|--------------|--------------|----------------|--------------|----------------|-------------|---------------|---------------|--|
| | | | | 1 | | | | | |

| T- | -1 | Total samples | Babesia (+ ve) | Anaplasma (+ve) |
|---|--------------------------------------|---------------------------|-----------------|-----------------|
| Fac | ctor | =n (%) | =n (%) | =n (%) |
| A 20 (200220) | ≤5 | 39/102 (38.2%) | 13/39 (33.33%) | 23/39 (58.97%) |
| Age (years) | >5 | 63/102 (61.8%) | 6/63 (9.52%) | 24/63 (38.09%) |
| То | ıtal | 102/102 (100%) | 19/102 (18.62%) | 47/102 (46.07%) |
| X2 | | 6.3 | 392 | |
| P-value | | 0.0 | 041 | |
| The chi-square statistic is 6.392. the <i>P</i> -value is 0.041 significant at $p < 0.05$ | | | | |
| Condor | Male | 37/102 (36.3%) | 11/37 (29.73%) | 27/37 (72.97%) |
| Gender | Female | 65/102 (63.8%) | 8/65 (12.31%) | 20/65 (30.77%) |
| То | ıtal | 102/102 (100%) | 19/102 (18.62%) | 47/102 (46.07%) |
| X2 | | 7.3 | 358 | |
| P-value | | 0.0 |)25 | |
| The chi-square statistic is | s 7.358. the <i>P-value</i> is 0.025 | significant at $p < 0.05$ | | |
| Course | Local | 97 (95.10%) | 16/97 (16.49%) | 43/97 (44.33%) |
| Source | Imported | 5 (5%) | 3/5 (15.80%) | 4/5 (80%) |
| Total | | 102/102 (100%) | 19/102 (18.62%) | 47/102 (46.07%) |
| X2 | 3.046 | | | |
| P-value | 0.218 | | | |
| The chi-square statistic is 3.046. the <i>P</i> -value is 0.218 non-significant at $p < 0.05$. | | | | |

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Fig 1. Light micrograph of camels' blood smear showing Babesia sp. (A) and Anaplasma sp. (B) of an infected erythrocyte. (100x)



Fig 2. A 1.5% Agarose gel stained with ethidium bromide showing PCR product (265 bp) (A) and (428 bp) (B) of MAR1bB2R of A. marginale and small 18S rRNA gene fragment targeting Babesia sp., respectively. * Lower and higher bands are non-specific. Lane M: Low molecular weight marker (50-1500 bp).

blood samples from other countries, i.e. Pakistan (MK792346.1, MK792345.1, MK792344.1) (equine), South Africa (KU647720.1, KU647719.1) (cattle), Mexico (AF112480.1, AF111197.1, AF111195.1) USA (AF110808.1, AF348137.1, AF221693.1) and India (*Bos taurus*) MH476205.1. Sequence relationship with other most related neighboured sequences was constructed in rectangular cladogram as shown in Fig 3 A & B. On the other hand, the blast analysis of the present selected sequence of *Babesia* sp. was in relation to the same species found in blood samples from other countries, such as isolates in Goat-KAK13 in Turkey (MT498196.1), *Homo sapiens* (KY052789.1, KY052788.1, KX590752.1), cattle (MN901958.1, MN901956.1,

MN900525.1, MN900524.1) and *Rhipicephalus microplus* (MH208614.1, MH208613.1) in China (Fig 3 C & D).

Discussion

Despite the efforts made to reduce the transmission of tick-borne diseases in animals, haemopathogens are still prevalent throughout the world. Babesiosis and Anaplasmosis are distributed throughout the world affecting the livestock population (Berggoetz *et al*, 2014; De La Fuente, 2017). There is insufficient data on tick-borne diseases especially *Babesia* and *Anaplasma* sp. in the Taif region in Saudi Arabia. Most of the previous studies investigated their prevalence in cattle and other



Fig 3. FASTA sequence of part of major surface protein-1β encoding gene and small 18S rRNA gene of *A marginale* (A) and *Babesia* sp. (C), respectively. Their relationship with other reference sequences from NCBI GenBank using a phylogenetic tree of A. marginale (B) and *Babesia* sp. (D). GenBank sequences were shown by their accession numbers. Bar scale represents 0.00003 nucleotide substitution per site.

species, but very few studies have investigated the prevalence of these parasites in camels.

The cumulative infection rate of Babesiosis and Anaplasmosis was found to be 18.62% and 46.10%, respectively as estimated from the examination of 102 camels in the present study area. The present results were consistent with previous studies in Egypt, in which they have recorded infection rates of *Babesia* (11.8%) and *Anaplasma* sp. (47.4%) (El-Naga and Barghash, 2016). On the contrary, another study in Somalia have recorded the overall prevalence of *Babesia* (52.2%) and *Anaplasma* sp. (13.2%) (Abdalla *et al*, 2017) that is not in agreement with the findings of present study. This may be explained by the husbandry practices in desert areas where all livestock share common inhabitancy and wandering in pasture lands with continuous migration.

Other studies in Saudi Arabia have reported prevalence of *Babesia* sp. in the Riyadh region (13.17%) (Swelum *et al*, 2014) and *Anaplasma marginale*, *Candidatus Anaplasma camelii* in Riyadh and Makkah regions and Asir Province as 40.50 and 2%, respectively (Ismael *et al*, 2016; Alshahrani *et al*, 2020). Yet, another study didn't record any *Babesia* infection

in all camels they had tested in Riyadh (Alanazi *et al*, 2020) and Asir provinces (Alshahrani *et al*, 2020). This may be due to the isolation of the locality from *Babesia* infection or to the animals having been treated against *Babesia*. However, Ghafar and Shobrak (2014) have reported high prevalence of *Anaplasma* sp. closely related to *A. marginale* (99% identity) in camels, cattle, sheep, foxes, and Dabb lizards in the Taif region.

It was clear from the results that polymerase chain reaction gave better findings of the DNA of the pathogens than microscopic method, hene it was a more accurate and sensitive method than microscopy. It was paralleled with many studies that have used molecular tools to screen and identify Babesia and/or Anaplasma worldwide in camel hosts and their tick vectors as a more sensitive technique for the diagnosis of haemoparasitic infection (Belkahia et al, 2015; Abdalla et al, 2017; Ibrahim et al, 2017; Sharifiyazdi et al, 2017; Azeem et al, 2019; Selmi et al, 2019; Mirahmadi et al, 2022). In the present study, 18S rRNA and major surface protein-1 β encoding genes were targeted for Babesia and A. marginale detection. The 18S rRNA gene is widely used in Babesia research for better identification and comparison (Bahrami et

al, 2017; Yue *et al*, 2020). The major surface proteins are considered as useful markers in *A. marginale* molecular epidemiology (Molad *et al*, 2009). There are six major surface proteins of *A. marginale* that are well characterised and are antigenically responsible for antibodies production in infected animals (Wei *et al*, 2020).

The present study has reported a high prevalence of *Babesia* (18.62%) and *A. marginale* (46.10%) in dromedaries of Saudi Arabia based on PCR evaluation. These findings are consistent with result of Junsiri *et al* (2020) who have recorded a high prevalence of *A. marginale* in cattle blood samples (10.30%) in Thailand based on PCR of the major surface proteins-4 gene. Moreover, they have observed a high degree of genetic diversity in the analysed *A. marginale* population according to their major surface proteins 2, 4, and 5 clones.

The short amplicons size (428 bp) of the 18S rRNA gene and (265 bp) of major surface protein–1 β of *Babesia* and *A. marginale* obtained in PCR screening limits their deposition in GenBank. Also, in our previous studies, we have detected that those selected samples harbour other pathogens such as *Trypanosoma* (Al Malki and Hussien, 2022a), *Theileria* (Al Malki and Hussien, 2022b), and *Toxoplasma* (Al-Malki, 2022), making it more interfering in recovering targeted genes of near full-length using nested PCR (Wei *et al*, 2020).

Isolates of 18S rRNA and major surface protein-1 β genes have shown phylogenic relationships with other isolates of *Babesia* and *A. marginale* in different hosts of other countries, as previously reported (Junsiri *et al*, 2020; Morikawa *et al*, 2021 and Wei *et al*, 2020). However, sequencing more isolates with larger amplicon sizes could be useful for the relationship assessment of those selected pathogens in the blood of camels found in Taif governorate, Saudi Arabia.

The present study showed a significantly higher percentage of *Babesia* (33.33%) and *Anaplasma* sp. (58.97%) infection among young camels (\leq 5 years) than older animals 9.52% and 38.09%, respectively. Recently, we have detected *Theileria* sp. in the same samples with higher prevalence in young camels than older animals (Al Malki and Hussien, 2022b). There is a co-infection of tick-borne pathogens (Anaplasmosis, Babesiosis and Theileriosis) in the same animal, because pathogens can share the same route of tick transmission (Lee *et al*, 2020). This could be due to poorly developed immune system to combat pathogen infection (Ahmed *et al*, 2008) or higher care

for adult animals by the owner. Moreover, a lower infection prevalence in older animals may be due to the development of concomitant immunity due to their recurrent infections throughout their lifetime (Ilhan et al, 1998; Gharbi and Darghouth, 2014). On the other hand, there is a significant increase of Babesia (29.73%) and Anaplasma sp. (72.97%) infection in males than female camels 12.31% and 30.77%, respectively. This was in agreement with the result of Alanazi et al (2020), who reported a non-significant increase of Babesia (3.48%) and Anaplasma sp. (7.96%) infection in male cattle than female samples (1.24% and 3.11%) in four regions (Riyadh, Al-Kharj, Al-Hasa and Al-Qassim) of Saudi Arabia. The lower prevalence rate in female camels than males could be attributed to more care from their owners as female camel are source of milk during lactation and caring for their young ones.

In conclusion, the present study confirmed the prevalence of babesiosis and anaplasmosis in *Camelus dromedarius* of the Taif region, Saudi Arabia.

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Declarations

Ethics approval and consent to participate

Data and samples were collected from veterinarians as per their periodic examination according to ministerial recommendation. We obtained a permission letter from the Ministry of Environment, Water and Agriculture (KSA) to collect cattle and camel samples from different locations in Taif for our research study with the number 106082/1074/1442, date 21-02-1442H. Sample collection and all experimental procedures were performed in accordance with a national ethical requirement. National Committee of Bioethics (NCBE) at King Abdulaziz City for Science and Technology (KACST) with number: 10023117, valid till 01 October 2023.

Availability of data and materials

All data generated or analysed during this study are included in this published article.

Competing interests

The authors declare that they have no competing interests.

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COMPARATIVE ANATOMY OF THE OPHTHALMIC DIVISION OF THE TRIGEMINAL NERVE IN CAMEL AND SHEEP WITH SPECIAL REFERENCE TO ITS CLINICAL IMPORTANCE

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ABSTRACT

The aim of this study was to describe the topographic anatomy and the distribution pattern of ophthalmic division of the trigeminal nerve in 5 dromedary camels and 3 sheep. In both species, the origin and the primary branches of the ophthalmic nerve were similar, but they differed in the pattern of distribution. The primary branches included were zygomaticotemporal nerve, frontal nerve, frontal sinus branch and nasociliary nerve. The study would help deciding the sites of this nerve block in these species.

Key words: Camel, cornual nerve, frontal nerve, infratrochlear nerve, ophthalmic nerve, sheep, supraorbital nerve

The ophthalmic branch is the smallest of the three divisions of the trigeminal nerve, purely sensory and innervates the cilliary body, the cornea and the iris; to the lacrimal gland and conjunctiva (Shankland, 2001). Anaesthesia of these nerves is sometimes necessary for eyelid and conjunctival biopsies and other minor surgeries (Michau, 2005). Furthermore, this nerve blockade is preferred for some minor ophthalmic operation in the eye and/or the upper eyelid (Badawy and Eshra, 2015). The cornual nerves are involved in the analgesic preferred technique for dehorning in ruminants (Hall *et al*, 2001).

The ophthalmic division of the trigeminal nerve is well described in other species, namely, equine, bovine and canines (Levine *et al*, 2008) but the clinical anatomy of this nerve in dromedaries and ovine is scarcely reported.

This study was aimed to describe the topographic anatomy and distribution pattern of ophthalmic division of the trigeminal nerve in dromedary camel (*Camelus dromedarius*) and sheep (*Ovis aries*).

Materials and Methods

This study was performed in accordance with the ethical guidelines approved by the Institutional

Animal Care and Use Committee of the Faculty of Veterinary Medicine, Benha University, Egypt. The study was conducted on 10 heads from apparently healthy mature males (5 camels, 3 sheep) which were obtained immediately after slaughter from Toukh and Qalioube abattoir, Egypt. One camel skull was used for demonstrating the foramina of the nerve exit in this species. Each head was frozen at -18° C, until these were used for this study. Nomenclature used in this study was written according to the Illustrated Nomina Anatomica Veterinaria (Schaller, 2011) and Smuts and Benzuidenhout (1987).

Results

Ophthalmic nerve

Origin and distribution: In camels and sheep, the ophthalmic nerve originated intracranially (at level of foramen lacerum) from the trigeminal ganglion in a common trunk with the maxillary nerve (Fig 1a, b). It exited the cranium through the orbitorotundum foramen (Fig 1a, b). In camels, it was divided immediately after its origin within the cranial cavity to give its primary branches (Fig 1a). However, in sheep, the division occurred just at the foramen of exit (orbitorotundum) (Fig 1b). In the two species, the ophthalmic nerve gave off the

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following branches, from the lateral to the medial: the zygomaticotemporal nerve, which was the most lateral branch, the frontal nerve, the fronal sinus branch and the nasociliary nerve, which was the most medial branch (Fig 1a, b).

Frontal sinus branch: In camel, it arose either from the ophthalmic or the frontal nerve (Fig 1a, b). In sheep, it originated from the ophthalmic nerve in close association to the frontal nerve. In the two species, it coursed along the upper border of the dorsal rectus muscle, until it left the orbit through a small foramen, which led into the frontal sinus.

Zygomaticotemporal nerve: In camels, it detached the lacrimal nerve just as it emerged from the orbitorotundum foramen. It then coursed rostral on the dorsolateral part of the orbit, along the medial border of the lateral rectus muscle. It pierced the periorbital fat pad until it reached the angle of junction between the zygomatic process of the frontal bone and the zygomatic process of the temporal bone (Fig 2a). At this junction, it ended by division into medial and lateral branches. The medial branches ran under the frontoscutularis muscle, where it gave branches to the skin of the temporal region. The lateral branches ended in malaris muscle and the skin of this facial region.

In sheep, the course and distribution of the zygomaticotemporal nerve were similar to those in camels, except for its terminal branches. The division into medial and lateral branches was not clear in sheep; however, ventral to the lacrimal gland the nerve left the periorbita accompanied with the cornual vein. It then turned caudomedially to run under the frontoscutularis muscle, where it gave off branches to the skin of the temporal region, and finally divided giving the cornual nerves (Fig 2b). The latter distributed at the lateral and caudal sides of the base of the horn (Fig 2b).

Frontal nerve: In the camel, it was divided into two branches, i.e. the supraorbital and the infratrochlear nerves. The latter left the orbit through the orbital fissure, while, the supraorbital nerve continued the course of the frontal nerve and proceeded rostrodorsally within the periorbita until it reached the orbital rim, namely at the level of the supraorbital notch, where it pierced the skin of the upper eye lid (Fig 2a). In sheep, the supraorbital nerve exited the skull through the supraorbital foramen, and distributed within the skin of the upper eyelid, whereas the infratrochlear nerve arose from the nasociliary nerve.

Nasociliary nerve: In camel, after it emerged from the the orbitorotundum foramen, it coursed

between the dorsal oblique and the medial rectus muscles (Fig 3a). During its course, it gave muscular branches to these muscles and the levator palpebrea superiorus, the long cilliary nerve and the communicating branch to the cilliary ganglion. It then terminated by giving the ethmoidal and the frontal nerve. The latter was the continuation of the nasociliary nerve in camel.

The nasociliary nerve had similar origin and course in sheep (Fig 3b). However, it gave two to three long cilliary nerves, instead of the single branch found in camels (Fig 3c). In addition, the infratrochlear nerve was the continuation of the nasociliary nerve in sheep.

In camel and sheep, the infratrochlear nerve as its name implies, passed below the pulley (the trochlea) of the obliques dorsalis muscle. In camel only it left the orbit through the orbital fissure. In both species, the infratrochlear coursed caudomedially under the frontalis muscles to give cutaneous branches to the frontal region. In sheep, it also gave cornual branches, which supply the lateral and the rostral sides of the base of the horn.

In the two species, the ethmoidal nerve was the smaller branch of the nasociliary nerve. It penetrated the ethmoidal foramen to gain access the nasal cavity, where it coursed on the dorsolateral border of the nasal septum. Finally, the ethmoidal nerve terminated in the mucous membrane covering the cranial part of nasal septum and the dorsal nasal concha.

Clinical importance:

In the camel the site of needle insertion for supraorbital nerve block was at the level of the supraorbital notch, where the nerve exited the skull (Fig 4 a, b, c). However, in sheep, the needle was inserted at the foramen of exit, i.e., the supraorbital foramen (Fig 5 a, b).

To achieve local anaesthesia of the horn in sheep, the cornual nerves of the zygomaticotemporal nerve and the infratrochlear nerve must be desensitised. For the blockade of the cornual branches of the zygomaticotemporal nerve, the needle was inserted just caudal to the frontal process of the zygomatic bone, closer to the root of the supraorbital process (Fig 5 a, b). However, for blocking the cornual branches of the infratrochlear nerve the needle was inserted dorsomedially close to the orbital margin (Fig 5 a, b).

Discussion

The present study demonstrated the branching pattern of the ophthalmic division of the trigeminal



Fig 1. An illustration showing branching of the ophthalmic nerve in camel (a) and sheep (b), showing: Trigeminal ganglia (a), orbitorotundum foramen (b), maxillary nerve (c), ethmoidal foramen (d), lacrimal gland (e), supra orbital notch (f), zygomaticotemporal n. (1), lacrimal n. (1a), medial branch of zygomaticotemporal nerve (1b), lateral branch of zygomaticotemporal nerve (2), cornual branches of zygomaticotemporal nerve (2), long cilliary nerve (2a), ethmoidal nerve (2b), infratrochlear nerve in sheep (2c), cornual branches of infratrochlear nerve (2c), frontal nerve (3), frontal sinus branch (4), supraorbital nerve (5).

nerve in camels and sheep with special reference to the clinical importance. The origin and the primary branches of the ophthalmic nerve are similar, but the primary division occurs intracranial in the camel (Ahmed, 1979), and not at the foramen of exit as in sheep and the other ruminants (Sisson and Grossman, 1975). They also differ in the pattern of distribution of these branches. The zygomaticotemporal nerve in camels ended by division into medial and lateral branches. However, in sheep these medial and lateral branches were not clear and instead the zygomaticotemporal nerve left the periorbita and finally, divided giving the cornual nerves. The infratrochlear nerve arose from the frontal nerve in camels, while in sheep it arose from the nasociliary nerve. The frontal sinus branch usually arose from the frontal nerve in camels, but in sheep it arose from the ophthalmic nerve itself. The nasociliary nerve continued as the frontal nerve in camel, whereas in sheep it continued as the infratrochlear nerve. It also gave off a single long cilliary nerve in the camels, but in sheep as well as other small ruminants it gave two-three long cilliary nerves. The above-mentioned anatomical differences were similar to those described in camels (Ahmed, 1979; Smuts and Benzuidenhout, 1987) and in small ruminants (Sisson and Grossman, 1975; Dyce *et al*, 1996).

Comparing with other ruminants, the camel orbit had special anatomical features (Badawy and Eshra, 2018), this may explain the difference of



Fig 2. Camel (a) and sheep (b) heads (dissected), showing: supraorbital process (1), supraorbital nerve (2), upper eyelid reflected (3), notice that the supraorbital nerve terminates in the subcut. Of the upper eyelid, Frontoscutularis muscle (4), temporal fossa (5), zygomatic arch (6), zygomaticotemporal nerve (7), cornual vein (8), base of the horn (9).

foramina of exits between camel and other ruminants. In camels, the supraorbital foramen was absent and instead there was a supraorbital notch, at which the supraorbital nerve left the orbit. On the other hand, the infratrochlear nerve exited the camel skull through the orbital fissure, while in sheep it directly pierced the periorbita and gave the cornual branches. These observations in camels cause in agreement with those described by Ahmed (1979) and Smuts and Benzuidenhout (1987) in camel, and disagreed with Shahid and Kausar (2005), Monfared (2013) and Almayahi (2014) who reported that the infratrochlear fissures (orbital fissures) were the exit of the supraorbital nerve.

Regarding the clinical importance, the sites used in this study for needle insertion cause in agreements with those used for nerve blockade in sheep (Hall *et*



Fig 3. Camel (a) and sheep (b) heads (dissected), showing: camel orbit (eyeball removed) (1), medial rectus muscle (2), nasociliary nerve (3), retractor bulbi (4), maxillary nerve (5), lacrimal nerve (6), lacrimal artery (7), lacrimal gland (8), supraorbital process (excised) (9), eyeball (10), obliqus dorsalis muscle (11), long cilliary nerves (two nerves) (12).

al, 2001), and camel (Badawy and Eshra, 2015). For cornual nerve block in sheep, palpation of the nerves is done by rolling the skin and subcutaneous muscles



Fig 4. Site of needle insertion for supraorbital nerve block in the camel: camel bony orbit (skull) (a), camel head (b), dissection at sites of the needle insertion (c): orbitorotundum foramen (1), optic foramen (2), supraorbital process (3), supraorbital notch (4), orbital fissure (exit of infratrochlear nerve) (5), zygomatic process of frontal bone (6), zygomatic process of temporal bone (7), site of needle placement of supraorbital nerve, at level of supraorbital notch (8), upper eyelid (9), site of needle placement of supraorbital nerve (dissected) (10), supraorbital nerve located just at the level of supraorbital notch (11), upper eyelid reflected (12).



Fig 5. Sheep head showing: Site of needle placement of supraorbital nerve, at supraorbital foramen (1), site of needle placement of cornual branch of zygomaticotemporal nerve (2), site of needle placement of cornual branch of infratrochlear nerve (3).

over them before inserting the needle. Similarly, the supraorbital nerve can easily be located at the level of supraorbital foramen in sheep, and at the supraorbital notch in camels.

Conclusion

The origin and primary branches of ophthalmic nerve were similar; however, the secondary branches and pattern of distribution were different. The clinically important nerves described in the study were the supraorbital nerve in camel and sheep, and the cornual nerves of the zygomaticotemporal nerve and the infratrochlear nerve. The sites of nerve block for these nerves were demonstrated.

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COMPARISON OF SOME HORMONAL AND BIOCHEMICAL CONSTITUENTS IN FOLLICULAR FLUID OF PREDOMINANT FOLLICLE COEXIST WITH OVERSIZED FOLLICLE AND ITS COUNTERPART PRESENT IN THE ABSENCE OF OVERSIZED FOLLICLE IN CAMELS (Camelus dromedarius)

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ABSTRACT

This study was aimed to compare between some hormonal and metabolic constituents in follicular fluids and serum of predominant follicles coexisting with oversized follicles and its counterpart present in absence of oversized follicle in camels (*Camelus dromedarius*). Follicular fluids and sera were collected from animals who had follicles size 0.5–1.0 cm (small; n = 10), >1.0–1.6 cm (medium; n = 10) and >1.6–2.0 cm (large; n = 10) which were present in absence or presence of oversize follicles. Follicular fluids and sera were subjected to biochemical and hormonal analysis. Results revealed increased concentrations of oestradiol 17- β (E2) of follicular fluid from the various size antral predominant follicle which existed in the absence of oversize follicle. A significant (P<0.01) high concentration of P4 present in the follicular fluid of small size predominant follicle coexisted with the oversize follicle. A highly significant cortisone concentration was recorded in follicular fluid of small, medium and large predominate existing in absence of oversize follicles. The insulin like growth factor II (IGF-II) and general thyroxine in the follicular fluid from the small follicles that coexisted with the oversize follicle. Ultra-sensitivity triiodothyronine concentrations were significantly high in follicular fluid collected from predominant small and medium size follicle (P<0.001) and P<0.0001, respectively) existing in absence of oversize follicle. In conclusion, the presence of an oversize follicle alters hormonal and biochemical constituents of follicular fluid of predominant follice coexist with it.

Key words: Camel, oestradiol 17-β, follicles, hormones, metabolites

Dromedary camels display a distinguishing reproductive pattern among different domestic animal species. The single hump camels have been classified as induced ovulatory animal (Wilson, 1984; Tibary and Anouassi, 1997). The ovulation mainly occurs in response to coitus (El-wishy, 1987; Ismail, 1987). The camels' oestrous cycle has no luteal activity (Musa and Abusineina, 1978; Skidmore *et al*, 1995). Accordingly, the dromedary oestrous cycle is described as a 'follicular wave pattern (Skidmore *et al*, 1996; Tibary and Anouassi, 1996; Tibary and Anouassi, 1997; Skidmore *et al*, 2013). Follicles mature in six days, maintain their size for 13 days and regress in 8 days (Musa and Abusineina, 1978). In absence of mating, the fate of the mature follicle follows one of two possible paths: atresia and vanishing in the ovarian stroma or cystic degeneration (Tibary and Anouassi, 1996). The ovarian cysts have been reported in the dromedary (El wishy, 1987), Ilama and alpaca (Bravo *et al*, 1993). In dromedary camels, there is inconsistency about the incidence of ovarian cysts. If the female camel is not bred, 30 to 40% of them are predisposed to develop some forms of cystic ovaries (Tibary and Anouassi, 1996). Abattoir survey revealed that the incidence of the ovarian cyst was 6.9% (Al-Afaleq *et al*, 2012). Rectal examination indicated that the frequency of ovarian cyst in the camel is 4.7% (Ali *et al*, 2010). The effect of ovarian cysts on camel fertility is uncertain (Ghoneim *et al*, 2013). Some authors (Tibary and Anouassi, 1997) suggested that

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ovarian cysts are a physiologic variation of follicular dynamics and do not affect the fertility (Tinson and McKinnon, 1992). Based on the size, camel ovarian cysts were considered to be pathologic (Ali *et al*, 2010). Camels' oversized follicles are accompanied by infertility problems in the form of repeat breeding, nymphomania and anoestrus (Waheed *et al*, 2017). As the biochemical metabolites of follicular fluids are vital for the maturation and fertilisation of the oocyte, the changes in these metabolites may influence the growth and quality of the oocyte. The goal of the present study is, therefore, to compare some hormonal and biochemical composition of the predominant antral follicle coexisting with oversized with its counterpart present in absence of oversized follicle.

Materials and Methods

During the breeding season (October-April), 219 genitalia were recovered from clinically healthy adult (6-15 years of age) non-pregnant female camels (Camelus dromedarius) at a local abattoir in the eastern province of the Kingdom of Saudi Arabia. The reproductive history of those animals was unknown. A 10 mL blood sample was collected from each animal during exsanguinations into nonheparinised tubes. After slaughtering, the genitalia were macroscopically examined to confirm that these were clinically normal. Immediately after collection, selected ovarian pairs and blood samples were transported to the laboratory in an icebox within one-hour post-slaughter. In the laboratory, ovaries were washed twice in cooled 0.9% NaCl and blotted dry. Paired ovaries bearing functional corpus luteum were excluded from the investigation. Both predominant antral follicles coexisting with thin wall oversized follicle (>20 mm in diameter; Tibary and Anouassi, 1997) and from ovaries which have no oversized follicles were considered for measuring using a Vernier caliper. Based on follicle diameter, 3 follicle categories were considered for puncture: 0.5-1.0 cm (small; n = 10), >1-1.6 cm (medium; n = 10) and >1.6-2.0 cm (large; n=10). Follicular fluids of the predominant follicle were aspirated using sterilised 22-gauge hypodermic needles and syringes. The follicular fluid was centrifuged at 1250X g at 4°C for 10 minutes. The supernatant was harvested and stored at -20°C pending analysis. Blood sera from selected animals were separated and stored at -20°C until analysis.

Hormonal and biochemical analysis

Enzyme immune assay kits purchased from Mybiosource® (USA) were used for estimation

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of the concentrations of camel oestradiol 17-Beta-Dehydrogenase (E2; pg/mL; Catalog No. MBS9381137), camel progesterone (P4; ng/mL; Catalog No. MBS7606970), camel cortisone (ng/mL; Catalog No. MBS062065), camel insulin-like growth factor-II (IGF-II; ng/mL; Catalog No. MBS058122), camel ultra-sensitivity triiodothyronine (nmol/L; Catalog No. MBS056436), general thyroxine (ng/mL; Catalog No. MBS056436), general thyroxine (ng/mL; Catalog No. MBS289276) and vit C (µg/ml; Catalog No. MBS2700398).

The laboratory reported intra- and inter-assay coefficient of variances of the studied hormonal and biochemical constituents were 4.4% and 5.1% for oestradiol, 2.3% and 4.8% for progesterone, 4.4% and 5.1% for cortisone, 3.1% and 3.9% for insulin-like growth factor-II, 2.3% and 4.1% for ultra-sensitivity triiodothyronine, 3.2% and 5.3% for general thyroxine, 3.9% and 7.4% for vitamin C, respectively. The kits did not validate before the use with camel follicular fluid or serum. The sensitivity of assays for oestradiol 17-Beta-dehydrogenase, progesterone, cortisone, insulin-like growth factor-II, ultra-sensitivity triiodothyronine, general thyroxine and vit C were 0.1 ng/ml, 0.188 ng/ml, 1.0 ng/ml, 1.0 ng/ml, 0.1 nmol/L, 0.0975 ng/ml and 173.5 µg/ml, respectively. All measurements were carried out according to the manufacturers' guidelines. The optical densities were measured using an ELISA reader (Absorbance Microplate Reader ELx800TM, BioTek®, Highland Park, VT, USA and Microplate Strip Washer (ELx800 TM, BioTek®, Highland Park, VT, USA).

Statistical analysis

The data of hormonal and biochemical constituents are presented as the means ± SEM. Analyses were conducted by Student's t-test (t)using INSTAT software 3.1 (2017).

Results

The mean concentrations of oestradiol, cortisone and vitamin C in follicular fluid from the small follicles that exist in the absence of the oversized follicles were found higher as compared with that of the small follicles that coexist with the oversized follicles (P<0.0001; Table 1). The concentrations of progesterone were lower in the follicular fluid harvested from the small follicles that exist in the absence of oversized follicles that to versized follicle (P<0.01). The IGF-II and general thyroxine in the follicular fluid from the small follicles that exist in the absence of the oversized follicles were lower compared with that of the small follicles that coexisted with the oversized follicle (P<0.0001). There was no difference in the concentration of oestradiol and cortisone in the serum of camels bearing small follicle which exist in absence of oversized follicle and serum of camels bearing small follicle coexist with oversized follicle (P>0.05; Table 2). The mean concentration of progesterone in the serum of camels bearing small follicle exist in absence of oversized follicle was significantly lower than that bearing small follicle coexist with oversized follicle (P<0.0001; Table 2).

The IGF-II levels in the serum of camels bearing small follicle exist in absence of oversized follicle was significantly higher (P<0.0001) than that bearing small follicle coexist with oversized follicle. The serum of camels bearing small follicle exist in absence of oversized follicle had significantly lower (P<0.0.05) concentration of ultra-sensitivity triiodothyronine than that bearing small follicle coexist with oversized follicle. Likewise, the general thyroxine concentration was lower (P<0. 001) in the serum of camels bearing small follicle which existed in absence of oversized follicle than that bearing small follicle which coexisted with oversized follicle. However, the vitamin C concentration was significantly higher (P<0. 0.0.05) in the serum of camels bearing small follicle exist in absence of oversized follicle than that bearing small follicle coexist with oversized follicle.

Oestradiol, cortisone, IGF-II and ultrasensitivity triiodothyronine concentrations were

| Table 1. | Concentrations of some hormonal and biochemical constituents (mean ± SEM) in the follicular fluid of predominant small |
|----------|--|
| | follicle which coexisted with oversize follicle and its counterpart present in the absence of oversize follicle in camels. |

| Hormonal and biochemical constituents | Fluid from small follicle exist in absence of oversize follicle | Fluid from small follicle coexist with oversize follicle | P-value |
|---|---|---|----------|
| Oestradiol 17-β (pg/ml) | 703.0 ^a ± 51.96 C.I.* 585.48 – 820.52 | 24.9 ^b ± 1.12 C.I.* 22.37 – 27.43 | P<0.0001 |
| Progesterone (ng/ml) | 0.07 ^a ± 0.02 C.I.* 0.035 - 0.105 | $0.014^{b} \pm 0.002$ C.I.* 0.009 – 0.019 | P<0.01 |
| Cortisone (ng/ml) | 0.40 ^a ± 0.02 C.I.* 0.36 - 0.44 | 0.004 ^b ± 0.0004 C.I.* 0.003 - 0.005 | P<0.0001 |
| Insulin-like growth factor-II (ng/ml) | 83.48 ^a ± 0.45 C.I.* 82.47 – 84.49 | 111.57 ^b ± 0.45 C.I.* 110.55 – 112.59 | P<0.0001 |
| Ultra-sensitivity triiodothyronine (nmol/L) | 4.70 ^a ± 0.02 C.I.* 4.67 - 4.73 | $4.32^{b} \pm 0.09$ C.I.* 4.13 – 4.52 | P<0.001 |
| General thyroxine (ng/ml) | 9.24 ^a ± 0.02 C.I.* 9.20 – 9.28 | 9.80 ^b ± 0.01 C.I.* 9.79 – 9.81 | P<0.0001 |
| Vitamin C (µg/ml) | 15.54 ^a ± 0.32 C.I.* 14.81 – 16.27 | 11.95 ^b ± 0.63 C.I.* 10.52 – 13.38 | P<0.0001 |

Means with dissimilar superscripts are significantly different; *Confidence Interval

Table 2. Concentrations of some hormonal and biochemical constituents (mean \pm SEM) in the serum of the camels bearing predominantsmall follicle which coexisted with oversize follicle and its counterpart present in the absence of oversize follicle.

| Hormonal and biochemical constituents | Serum of camels bearing small follicle exist in the absence of oversize follicle | Serum of camels bearing small follicle coexist with oversize follicle | P-value |
|--|---|--|----------|
| Oestradiol 17-β (pg/ml) | 1.51 ± 0.48 C.I.* 13.42 – 15.58 | 1.90 ± 0.60 C.I.* 13.04 – 15.76 | 0.8977 |
| Progesterone (ng/ml) | $\begin{array}{c} 0.041^{a} \pm 0.002 \\ \text{C.I.*} \ 0.037 - 0.045 \end{array}$ | $0.069^{b} \pm 0.005$ C.I.* 0.057 – 0.081 | P<0.0001 |
| Cortisone (ng/ml) | 0.002 ± 0.0003 C.I.* 0.002 - 0.003 | 0.002 ± 0.0003 C.I.* 0.001 - 0.003 | 0.2098 |
| Insulin-like growth factor- II (ng/ml) | 111.14 ^a ± 0.77 C.I.* 109.39 – 112.89 | 92.99 ^b ± 2.32 C.I.* 87.75 – 98.24 | P<0.0001 |
| Ultra-sensitivity triiodothyronine (nmol/L) | $4.25^{a} \pm 0.01$ C.I.* $4.23 - 4.27$ | 5.29 ^b ± 0.39 C.I.* 4.41 – 6.17 | P<0.05 |
| General thyroxine (ng/ml) | 8.88 ^a ± 0.005 C.I.* 8.87 – 8.89 | $9.14^{b} \pm 0.059$ C.I.* 9.01 – 9.27 | P<0.001 |
| Vitamin C (µg/ml) | 22.56 ^a ± 0.05 C.I.* 22.45 – 22.68 | 20.33 ^b ± 0.85 C.I.* 10.41 – 22.25 | P<0.05 |

Means with dissimilar superscripts are significantly different; *Confidence Interval

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higher in follicular fluid obtained from the medium follicles that existed in the absence of the oversized follicles compared with that of the medium follicles that coexisted with the oversized follicles (Table 3). Significant differences were not reported in the values of the progesterone and vitamin C between the follicular fluid harvested from the medium follicles that existed in the absence of oversized follicles and that collected from the medium follicles that coexisted with oversized follicle. The general thyroxine concentrations in follicular fluid from medium follicles that existed in the absence of the oversized follicles were higher (P<0.01) compared with that of the medium follicles that coexisted with the oversized follicles.

Oestradiol, cortisone and vitamin C didn't vary significantly between serum of camels bearing medium follicles which existed in the absence of oversized follicle and the serum of camels bearing medium follicles which coexisted with the oversized follicles (Tabel 4). Progesterone and general thyroxine concentrations were significantly higher (P<0.01) in the serum of the animals bearing medium follicles coexisted with the oversized follicle than in the serum of the animals bearing medium follicles exist in the absence of oversized follicle. The IGF-II concentrations were higher (P<0.0001) in the serum of the camels bearing medium follicles existed in the absence of oversized follicle than in the serum of the camels bearing medium follicles coexist with the oversized follicle. The ultrasensitive triiodothyronine values were significantly higher (P<0.0001) in the

serum of the animals bearing medium follicles coexist with the oversized follicle than that serum of animals bearing medium follicles exist in absence of oversized follicle.

Oestradiol and cortisone were higher (P<0.0001) in the follicular fluid of large size predominant follicles which existed in the absence of oversized follicle than that in the follicular of large size predominant follicles fluid coexist with the oversized follicle (Table 5). There were no significant differences in the concentrations of the progesterone, IGF-II and ultra-sensitivity triiodothyronine between the follicular fluid of large size predominant follicles exist in the absence of oversized follicle and that fluid of large size predominant follicles which coexisted with the oversized follicle.

The concentrations of the general thyroxine and vitamin C were higher (P<0.001) in the follicular fluid of the large predominant follicles that coexist with oversized follicle than that of the follicular fluid of large size predominant follicles which exist in the absence of the oversized follicle (Table 5). There was no significant differences in the concentrations of the oestradiol, cortisone and general thyroxine between the serum of the camels bearing large size predominant follicles exist in the absence of oversized follicle and the serum of camels bearing large size predominant follicles which coexist with the oversized follicles (Table 6). The progesterone concentrations in the serum of the animals bearing large size predominant follicles coexisting with the oversized follicle were significantly higher than that detected in the serum

Table 3. Concentrations of some hormonal and biochemical constituents (mean ± SEM) in the follicular fluid of medium size predominant follicle which coexisted with oversize follicle and its counterpart present in the absence of oversize follicle in camels (*Camelus dromedarius*).

| Hormonal and biochemical constituents | Fluid from medium size predominant follicle exist in the absence of oversize follicle | Fluid from medium size predominant follicle coexist with oversize follicle | P-value |
|--|---|--|----------|
| Oestradiol 17-β (pg/ml) | 531.10 ^a ± 25.38 C.I.* 473.69 – 588.51 | 10.90 ^b ± 0.82 C.I.* 9.04 – 12.76 | P<0.0001 |
| Progesterone (ng/ml) | 0.016 ± 0.003 C.I.* 0.010 - 0.022 | 0.016 ± 0.003 C.I.* 0.008 - 0.024 | 0.9999 |
| Cortisone (ng/ml) | 0.28 ^a ± 0.02 C.I.* 0.24 – 0.33 | $0.004^{b} \pm 0.0009$ C.I.* 0.002 - 0.006 | P<0.0001 |
| Insulin-like growth factor- II (ng/ml) | 100.19 ^a ± 1.84 C.I.* 96.02 – 104.36 | 88.98 ^b ± 1.35 C.I.* 85.93 – 92.03 | P<0.0001 |
| Ultra-sensitivity triiodothyronine (nmol/L) | 4.67 ^a ± 0.02 C.I.* 4.63 – 4.71 | $3.20^{b} \pm 0.03$ C.I.* $3.14 - 3.25$ | P<0.0001 |
| General thyroxine (ng/ml) | 10.22 ^a ± 0.28 C.I.* 9.58 – 10.87 | $9.28^{b} \pm 0.02$ C.I.* $9.23 - 9.34$ | P<0.01 |
| Vitamin C (µg/ml) | 12.38 ± 0.08 C.I.* 12.21 - 12.55 | 12.28 ± 0.41 C.I.* 11.35 – 13.21 | 0.8150 |

Means with dissimilar superscripts are significantly different; *Confidence Interval

of the animals bearing large size predominant follicles whih exist in the absence of oversized follicle (P<0.01). The IGF-II was significantly elevated (P<0.001) in the serum of the animals bearing large size predominant follicles coexisting with the oversized follicle than those animals bearing large size predominant follicles exist in the absence of oversized follicles. The ultra-sensitive triiodothyronine concentrations were significantly raised in the serum of the camels bearing large size predominant follicles coexisting with the oversized follicle than those animals bearing large size predominant follicles which existed in the absence of oversized follicle (P<0.0001). The vitamin C concentrations were significantly higher in the serum of the camels bearing large size predominant follicles exist in the absence of oversized follicles than those animals bearing large size predominant follicles coexisting with the oversized follicles (P<0.0001).

Discussion

The assessment of some hormonal and biochemical composition of the predominant antral follicle coexisting with oversized with its counterpart present in absence of oversized follicle were the goals of this study. Follicular fluid holds different biochemical metabolites that are derived from serum or synthesised locally in the follicles and shared in the metabolic activities of follicular cells (Edwards, 1974; Gérard *et al*, 2002). The constituents of the follicular fluid change through the growth and development of each follicle (Wise, 1987). This study reported a significant increase in the concentrations of oestradiol of follicular fluid from the various size antral predominant follicle that exist in the absence of oversize follicle. The ability of antral follicles to produce large amounts of oestradiol is a distinctive sign of follicle health status (Kobayashi et al, 2006). The prsent study demonstrated no significant change in the level of oestradiol either in the serum of camels bearing large follicle existing in absence of oversize follicle or in serum of camels bearing large follicle coexisting with the oversize follicle. The presence of the oversize follicle does not associate with a significant increase in serum oestradiol (Ghoneim et al, 2013). The present study recorded a significant high progesterone in the follicular fluid of small size predominant antral follicle coexist with the oversize follicle. Granulosa and theca cells secret large amounts of progesterone which act as a precursor for androgen and subsequently estrogen production (McNatty et al, 1984). Progesterone promotes the production of proteolytic enzymes essential for the collapse of follicles at ovulation (Iwamasa et al, 1992). The source of the significant high peripheral progesterone concentrations reported in camels bearing different size predominant follicles which coexisted with oversized follicle may be the adrenal cortex (Asher et al, 1989). Glucocorticoids in follicular fluid are derived from the general circulation (Lewicka et al, 2003). The glucocorticoid status of ovarian follicular fluid is prognostic to oocyte quality (Lewicka et al, 2003). The 11beta-hydroxysteroid dehydrogenases convert cortisol to its inactive metabolite cortisone and vice versa (Quinkler et al,

Table 4. Concentrations of some hormonal and biochemical constituents (mean ± SEM) in the serum of the camels bearing medium size predominant follicle which coexisted with oversize follicle and its counterpart present in the absence of oversize follicle.

| Hormonal and biochemical constituents | Serum of camels bearing medium size predominant follicle exist in absence of oversize follicle | Serum of camels bearing medium size predominant follicle coexist with oversize follicle | P-value |
|--|--|---|----------|
| Oestradiol 17-17-β (pg/ml) | 2.51 ± 0.71 C.I.* 10.59 – 13.81 | 3.37 ± 1.07 C.I.* 7.89 – 12.71 | 0.1553 |
| Progesterone (ng/ml) in serum | 0.069 ^a ± 0.003 C.I.* 0.063 - 0.075 | 0.083 ^b ± 0.003 C.I.* 0.077 - 0.089 | P<0.01 |
| Cortisone (ng/ml) in serum | 0.001 ± 0.0002 C.I.* 0.0009 - 0.002 | 0.002 ± 0.0002 C.I.* 0.002 - 0.003 | 0.0652 |
| Insulin-like growth factor- II (ng/ml) | 102.50 ^a ± 7.60 C.I.* 85.31 – 119.69 | 48.49 ^b ± 1.87 C.I.* 44.27 – 52.72 | P<0.0001 |
| Ultra-sensitivity triiodothyronine (nmol/L) | 4.35 ^a ± 0.05 C.I.* 4.23 - 4.47 | $4.70^{b} \pm 0.04$ C.I.* $4.60 - 4.80$ | P<0.0001 |
| General thyroxine (ng/ml) | 9.17 ^a ± 0.02 C.I.* 9.13 – 9.21 | 10.35 ^b ± 0.34 C.I.* 9.59 – 11.11 | P<0.01 |
| Vitamin C (µg/ml) | 24.16 ± 0.67 C.I.* 22.64 - 25.68 | 22.00 ± 1.13 C.I.* 19.45 – 24.55 | 0.1172 |

Means with dissimilar superscripts are significantly different; *Confidence Interval

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2003). This study reported a high significant cortisone concentration in follicular fluid of small, medium and large predominate by existing in absence of oversize follicles wherever, there were no recorded significant changes in peripheral cortisone in animals that had or had not oversize follicles. Cortisol inhibits the ovarian steroidogenesis (Michael *et al*, 1993) and stimulate oocyte maturation (Fateh *et al*, 1989; Jimena *et al*, 1992). IGF-II concentrations in the follicular fluid of the predominant small follicles coexisting with the oversize follicle were significantly high. On the other hand, the follicular fluid of the predominant medium size follicle existing in the absence of an oversize follicle had significantly high concentration

of IGF-II. IGF-II concentrations in the serum of camels bearing small, medium and large size predominant follicle which existed in absence of oversize follicle were significantly high. In primate species, IGFII is the predominant circulating and intraovarian form of IGFs (Giudice, 2001; Tkachenko *et al*, 2021). IGFII stimulates granulosa steroidogenesis (Giudice, 2001). Parallel with the results of Tabatabaei *et al* (2011), ultrasensitive triiodothyronine concentrations were significantly high in follicular fluid collected from predominant small and medium size follicle existing in absence of oversized follicle. General thyroxine concentrations were significantly high in the follicular fluid of predominant small and large

 Table 5. Concentrations of some hormonal and biochemical constituents (mean ± SEM) in the follicular fluid of the camels bearing large size predominant follicle which coexisted with oversize follicle and its counterpart present in the absence of oversize follicle.

| Hormonal and biochemical constituents | Fluid from large follicle exist in absence of oversize follicle | Fluid from large follicle coexist with oversize follicle | P-value |
|--|--|---|----------|
| Oestradiol 17-β (pg/ml) | 664.10 ^a ± 13.26 C.I.* 634.11 - 694.09 | 9.00 ^b ± 1.08 C.I.* 6.57 – 11.43 | P<0.0001 |
| Progesterone (ng/ml) | 0.017 ± 0.003 C.I.* 0.009 - 0.025 | 0.017 ± 0.003 C.I.* 0.009 – 0.025 | 0.9999 |
| Cortisone (ng/ml) | 0.28 ^a ± 0.02 C.I.* 0.23 - 0.32 | 0.009 ^b ± 0.001 C.I.* 0.007 – 0.011 | P<0.0001 |
| Insulin-like growth factor- II (ng/ml) | 93.28 ± 2.07 C.I.* 88.61 - 97.95 | 91.55 ± 2.10 C.I.* 86.81 – 96.29 | 0.5639 |
| Ultra-sensitivity triiodothyronine (nmol/L) | 3.66 ± 0.16 C.I.* 3.31 - 4.01 | 3.73 ± 0.08 C.I.* 3.55 – 3.92 | 0.6952 |
| General thyroxine (ng/ml) | 8.88 ^a ± 0.23 C.I.* 8.37 – 9.39 | 10.60 ^b ± 0.29 C.I.* 9.94 – 11.26 | P<0.001 |
| Vitamin C (µg/ml) | 9.61 ^a ± 0.29 C.I.* 8.95 – 10.27 | 11.26 ^b ± 0.19 C.I.* 10.82 – 11.70 | P<0.001 |

Means with dissimilar superscripts are significantly different; *Confidence Interval

 Table 6. Concentrations of some hormonal and biochemical constituents (mean ± SEM) in the serum of the camels bearing large size predominant follicle which coexisted with oversize follicle and its counterpart present in the absence of oversize follicle.

| Hormonal and biochemical constituents | Serum of camels bearing large follicle exist in absence of oversize follicle | Serum of camels bearing large ollicle coexist with oversize follicle | P-value |
|--|---|---|----------|
| Oestradiol 17-β (pg/ml) | 17.60 ± 1.04 C.I.* 15.26 – 19.94 | 15.30 ± 0.92 C.I.* 13.22 – 17.38 | 0.1140 |
| Progesterone (ng/ml) | 0.059 ^a ± 0.001 C.I.* 0.057 - 0.061 | 0.069 ^b ± 0.002 C.I.* 0.064 - 0.074 | P<0.01 |
| Cortisone (ng/ml) | 0.002 ± 0.0003 C.I.* 0.0008 - 0.002 | 0.002 ± 0.0003 C.I.* 0.0009 – 0.003 | 0.8364 |
| Insulin-like growth factor- II (ng/ml) | 55.84 ^a ± 1.93 C.I.* 51.47 - 60.21 | 73.98 ^b ± 3.61 C.I.* 65.82 - 82.14 | P<0.001 |
| Ultra-sensitivity triiodothyronine (nmol/L) | 4.75 ^a ± 0.007 C.I.* 4.73 – 4.77 | $4.95^{b} \pm 0.007$ C.I.* $4.93 - 4.97$ | P<0.0001 |
| General thyroxine (ng/ml) | 8.55 ± 0.20 C.I.* 8.09 – 9.92 | 8.30 ± 0.077 C.I.* 8.13 - 8.47 | 0.2650 |
| Vitamin C (µg/ml) | 23.18 ± 0.22 C.I.* 22.68 - 23.68 | 15.49 ± 0.72 C.I.* 13.86 – 17.12 | P<0.0001 |

Means with dissimilar superscripts are significantly different; *Confidence Interval

size follicles that coexist with the oversize follicle. The follicular fluid of predominant medium size follicle that exist in absence of oversize follicle had a significant high concentration of general thyroxine. The concentrations of general thyroxine in the serum of camels bearing small and medium size follicles coexist with oversized follicle were significantly high. The majority of thyroxine present in follicular fluid appear to be derived from peripheral blood and enter follicles through theca interna cells (Cai et al, 2019). Thyroid hormones control the growth, differentiation, and metabolism in almost all somatic tissues (Ingbar and Wieber, 1981). Moreover, thyroxine affects the folliculogenesis (Ashkar et al, 2010; Verga Falzacappa et al, 2012; Zhang et al, 2013; Fedail et al, 2014) and ovarian steroidogenesis (Cecconi et al, 1999). In this study, Vitamin C concentrations were significantly high in follicular fluid of small size predominant follicle exists in absence of oversized follicle and in follicular fluid of large size predominant follicle which coexisted with the oversized follicle. The serum of camels bearing small and large size predominant follicle exist in absence of oversized follicle had a significant high concentration of Vitamin C. The ovaries store high amounts of ascorbic acid within the granulosa, thecal, and luteal cells (Deane, 1952). Ascorbic acid endorses steroidogenesis (Sanyal and Datta, 1979), acts as an antioxidant (Goralczyk et al, 1992; Luck et al, 1995) and assets in remodeling the basement membrane during follicular growth (Murray et al, 2001).

The current study revealed significant differences in some hormonal and biochemical constituents between follicular fluids from predominant follicle which coexisted with the oversized follicle and its counterpart present in the absence of the oversized follicle. Relying on these outcomes we can hypothesise that the presence of an oversize follicle alters some hormonal and biochemical constituents of follicular fluid of predominant follicle which coexist with it.

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PROTEIN PROFILE AND GLYCOSIDASE ACTIVITIES OF PROSTATE AND BULBOURETHRAL GLANDS SECRETION IN CAMELS (Camelus dromedarius)

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ABSTRACT

This study was aimed to investigate protein profiles and glycosidase activities of bulbourethral and prostate glands secretion in dromedary camels. Sixteen healthy male camels (5-13 years old) were slaughtered and both glands were collected. The obtained secretions of both glands were used for determination of protein profile by 7-20% gel electrophoresis. Activities of β -N-acetylglucosaminidase, α -N-acetylgalactosaminidase and α -L-fucosidase were also determined. The current findings showed 11 (175.7, 129.3, 126.8, 94.9, 77.8, 74.4, 71.1, 53.3, 21.8, 15.9 and 9 kDa) and 15 (124.6, 89.7, 81.1, 75.5, 72.1, 60, 54.4, 48.9, 43.3, 40, 32.5, 24, 17.8, 13.3 and 9 kDa) protein bands in secretion of bulbourethral and prostate gland, respectively. Three (77.8, 53.3 and 9 kDa) and 6 bands (81.1, 75.5, 48.9, 17.8, 13.3 and 9 kDa) showed higher staining intensities in bulbourethral and prostate secretion, respectively. Both secretions shared a band of 9 kDa with higher intensity in bulbourethral secretion. Activities of glycosidase in bulbourethral and prostate secretions were verified and were higher in bulbourethral than in prostate secretion. α -L-fucosidase showed higher activity in glands secretions compared to other enzymes. Conclusively, bulbourethral and prostate secretions and glycosidases.

Key words: Accessory sex glands, bulbourethral, camels, electrophoresis, glycosidases, prostate, proteins

Dromedary camels display a distinguishing anatomical and physiological pattern among different domestic animal species. Male dromedaries have two accessory sex glands, prostate and bulbourethral glands and they do not have seminal vesicles (Elwishy, 1988; Hafez and Hafez, 2001). Camel semen has been characterised as very viscous and forms coagulum directly after collection (Lichtenwalner et al, 1996; Bravo et al, 1997; Zeidan et al, 2000). The reproductive efficiency in camelids is low (Tibary, 1997; Skidmore, 2003). The viscosity in camel semen hinders the sperm motility (Tibary, 1997; Aminu and Sahani, 2000) and does not permit the semen to blend well with the diluents until it is completely liquefied (Wani, 2009). From the other side, glycosidases are a group of hydrolytic enzymes originate from lysosome and catalyse the hydrolysis of glycoproteins, glycolipids and glycosaminoglycans (Miller et al, 1993; Hahn et al, 2001; Jóźwik et al, 2003). Glycosidases

play an important role in different reproductive events such as cumulus cells expansion (Takada *et al*, 1994), sperm capacitation (Taitzoglou *et al*, 2007), sperm oviductal epithelial cells interaction (Lefebvre *et al*, 1997), sperm zona pellucida binding (Miranda *et al*, 2000; Zitta *et al*, 2006), polyspermy block (Miller *et al*, 1993) and early embryos development (Tsiligianni, 2018). The present study was aimed to determine the protein profile and activities of some glycosidases (β -N-acetylglucosaminidase, α -N-acetylgalactosaminidase and α -L-fucosidase) of the bulbourethral and prostate glands secretions in dromedary camel.

Materials and Methods

Animals and samples

A total of 16 mature healthy male camels (5-13 years old) with unknown reproductive history were slaughtered in the local abattoir in Al-Ahsa

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Governorate during the breeding season (November to March). After slaughtering, the prostate and bulbourethral glands were collected and transferred in an ice tank to the laboratory within half an hour. For each male the bulbourethral and prostate glands were dissected in a petri dish and squeezed using a metal squeezer to obtain their secretion. The collected fluid was centrifuged at 1500 g for 10 min and the supernatant were stored at -80°C pending analysis.

Analysis of enzymes

Three enzymes were estimated in the bulbourethral and prostate secretion using ELISA reader (Absorbance Microplate Reader ELx 800TM BioTek®, USA; Microplate Strip Washer ELx 50TM BioTek®, USA) and commercial ELISA diagnostic kits (My Biosource®). These enzymes were camel β -N-acetylglucosaminidase (Catalog # MBS094638), camel α -N-acetylgalactosaminidase (Catalog # MBS053019) and camel α -L-fucosidase (Catalog # MBS092780). The procedures for analysis and calculation were adopted according to the manufacturer instruction.

Sodium dodecyl-sulfate polyacrylamide gel electrophoresis (SDS-PAGE) fractionation of proteins in glands secretion

Five samples of bulbourethral gland secretions each containing 100µg of protein were pooled. The same procedures were carried out with 5 samples of prostate gland secretion. The protein concentration in the pooled samples of each gland secretions was determined by using QuantiProTM BCA Assay kit (Sigma Chemical Company, UK) and stored at -20°C. The pooled samples of each gland secretion were subjected to one dimensional SDS-PAGE gradient gel electrophoresis (Laemmli, 1970) on 7-20% gradient gel as follow: 50µg protein of each pool was diluted with an equal volume of Bio-Rad Laemmli sample buffer, Cat. No. 161-0737 [62.5mM Tris-HCl (pH 6.8), 2% SDS, 0.01% Bromophenol blue, 25% glycerol, 5% β -mercaptoethanol], heated to 100°C for 5 min and loaded onto a 4% stacking polyacrylamide gel which was overlaid on top of a 7-20% resolving gel. A total of 5µl of pre-stained protein ladder of molecular weights ranged from 10-200 kDa (Cell Signaling Danvers, MA, USA) was loaded in a separate well. Gels were run at room temperature at 150V for one hour then at 100V until completion overnight. Coomassie Blue stain was used for visualisation of the gel protein-banding pattern. A calibration curve based on the molecular weight markers was constructed and used to calibrate the molecular weight of individual proteins in the secretion. For permanent records, the

gel was rinsed in distilled water and photographed and documented using gel documentation system (Gel DocTMXR System, Bio-Rad).

Statistical analysis

Data are presented as means \pm SEM for bulbourethral and prostate secretion, and compared by t-test using SPSS program, version 16.0 (Inc, 2007). Two-way analysis of variance (ANOVA) was used to compare the activities of the relevant enzyme activities in the same gland secretion.

Results

SDS-PAGE fractionation of bulbourethral and prostate gland secretion revealed a pattern of 11 and 15 protein bands, respectively when stained by Commassie blue stain (Fig 1 and 2) (Table 1 and 2). The molecular weight of these bands were 175.7, 129.3, 126.8, 94.9, 77.8, 74.4, 71.1, 53.3, 21.8, 15.9 and 9 kDa in bulbourethral gland secretion (Fig 1; Table 1). The molecular weight of protein bands of prostate gland secretion were 124.6, 89.7, 81.1, 75.5, 72.1, 60, 54.4, 48.9, 43.3, 40, 32.5, 24, 17.8, 13.3 and 9 kDa (Fig 2; Table 2). One band (9 kDa) was common in both glands secretion, however, this band showed higher intensity in bulbourethral gland secretion compared

 Table 1. SDS-PAGE fractionation of bulbourethral gland secretion visualised by Coomassie blue stain.

| No of band (from up to down) | Molecular weight (kDa) | No of band (from up to down) | Molecular weight (kDa) |
|------------------------------------|------------------------------|------------------------------------|------------------------------|
| 1 | 175.7 | 7 | 71.1 |
| 2 | 129.3 | 8 | 53.3 |
| 3 | 126.8 | 9 | 21.8 |
| 4 | 94.9 | 10 | 15.9 |
| 5 | 77.8 | 11 | 9 |
| 6 | 74.4 | | |

Table 2. SDS-PAGE fractionation of prostate gland secretion visualised by Coomassie blue stain.

| No of band (from up to down) | Molecular weight (kDa) | No of band (from up to down) | Molecular weight (kDa) |
|------------------------------------|------------------------------|------------------------------------|------------------------------|
| 1 | 124.6 | 9 | 43.3 |
| 2 | 89.7 | 10 | 40 |
| 3 | 81.1 | 11 | 32.5 |
| 4 | 75.5 | 12 | 24 |
| 5 | 72.1 | 13 | 17.8 |
| 6 | 60 | 14 | 13.3 |
| 7 | 54.4 | 15 | 9 |
| 8 | 48.9 | | |





Fig 1. Protein profile of Bulbourethral gland secretion on 7-20% polyacrylamide gel stained by Coomassie blue. Lane 1-Molecular weight markers. Lane 2- Bulbourethral gland secretion.

to that of prostate gland (Fig 1 and 2, respectively) (Table 1 and 2, respectively). Three bands (77.8, 53.3 and 9kDa) showed the higher staining intensities in bulbourethral gland secretion (Fig 1). Six bands (81.1, 75.5, 48.9, 17.8, 13.3 and 9kDa) showed the higher staining intensities in prostate gland secretion (Fig 2). The activities of β -N-acetylglucosaminidase, α -N-acetylglactosaminidase and α -L-fucosidase enzymes increased significantly (P<0.05) in

Fig 2. Protein profile of Prostate gland secretion on 7-20% polyacrylamide gel stained by Coomassie blue. Lane 1- Molecular weight markers. Lane 2- Prostate gland secretion.

bulbourethral compared to that of prostate gland secretion (Table 3). The activity of α -L-fucosidase was significantly higher than that of other studied glycosidases (β -N-acetylglucosaminidase, α -Nacetylgalactosaminidase) in both bulbourethral and prostate gland secretion (Table 3). The dominance of glycosidases activities was to α -L-fucosidase followed by β -N-acetylglucosaminidase and finally by α -Nacetylgalactosaminidase (Table 3).

 Table 3. The activities of glycosidase enzymes in prostate and bulbourethral glands secretion of dromedary camels (mean ± SEM), (n=16).

| Enzymes | Units | Bulbourethral | Prostate | P-value |
|-----------------------------------|-------|---------------------------|-------------------------|----------|
| Camel β-N-acetylglucosaminidase | ng/ml | 2.18 ± 0.10^{Ya} | 1.43 ± 0.07^{Yb} | 0.000006 |
| Camel α-N-acetylgalactosaminidase | ng/ml | 2.35 ± 0.07^{Xa} | 2.12 ± 0.08^{Xb} | 0.021598 |
| Camel α-L-fucosidase | ng/ml | 13216.84 ± 10.92^{Wa} | 9663.16 ± 6.56^{Wb} | 0.000009 |

a-c within rows, means \pm SEM with different superscripts differ significantly (P < 0.05). w-y within columns, means \pm SEM with different superscripts differ significantly (P < 0.05).

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Discussion

As far as we know this is the first study that evidenced the role of proteins and glycosidases in the viscosity and coagulation process of semen of camels. Many proteins from seminal plasma had been related to either fertility, like in bull (Killian et al, 1993), boar (Flowers, 1998), stallion (Brandon et al, 1999) and buffalo (Harshan et al, 2009), freezability, as in bulls (Asadpour et al, 2007) or viability of spermatozoa, like in bulls and rams (Barrios et al, 2000). Addition of plasma proteins to semen probably improved the function of semen extenders and consequently, fertility. There is very little information available about the seminal plasma protein profile or its functions in camelids. The most notable feature in the anatomy of the internal genitalia of camelids was the absence of vesicular glands (Tibary and Anouassi, 1997); they only possessed a prostate and two bulbourethral glands. In most mammalians, secretion by the vesicular glands accounts for all the major seminal plasma proteins (Bergeron et al, 2005). Moreover, bovine seminal plasma proteins, secreted by vesicular glands, mediate sperm recognition and binding to the oviductal epithelium to form a reservoir (Gwathmey et al, 2006). During ejaculation, spermatozoa mixed with bovine seminal plasma proteins. These proteins removeed some cholesterol from the plasmatic membrane and subsequently bind to choline phospholipids. This replacement process did not allow free movement of phospholipids, and consequently stabilised the plasmatic membrane (Villemure et al, 2003). The current findings revealed the presence of 11 proteins bands in bulbouretheral gland secretion of male dromedary camels. The molecular weight of these bands were 175.7, 129.3, 126.8, 94.9, 77.8, 74.4, 71.1, 53.3, 21.8, 15.9 and 9 kDa. Previous study (Apichela et al, 2014) indicated the presence of 8 protein bands in bulbouretheral gland secretion of male llama by using one dimension 8-18% gradient SDS-PAGE and the molecular weight of these bands were 254, 231, 203, 169, 148, 130, 118 and 49 kDa. As displayed in the result study, the number and molecular weight of bands in dromedary camels were different from that detected in llama (Apichela et al, 2014). This difference mainly attributed to species difference, type of separated gel and/or the type of used molecular weight marker. The result study demonstrated that the bulbourethral and prostate glands secreted several proteins that may facilitate sperm adhesion to the oviduct in camelids. At least 11 or 15 protein bands had been found in bulbourethral and prostate glands secretion, respectively that were

and hence, they would prolong spermatozoa life in the female genital tract. This differed dromedary from other species, such as boar, in which bulbourethral secretions did not contain proteins (they were not detected electrophoretically or by gel filtration) (Schellpfeffer and Hunter, 1970). By means of mass spectrometry, four seminal plasma proteins have been identified in alpaca (Kershaw-Young and Maxwell, 2012). One of them, Mucin 5B, was a gel-forming protein produced by the bulbourethral glands and had been related to semen viscosity. Mucin 5B could be responsible for the laminar substance that entraps spermatozoa in the sperm reservoir following mating. This protein probably degraded by some mechanism of sperm release triggered by the oviduct, although allowing spermatozoa ascend to the site of fertilisation. The results indicated that the camels' bulbourethral and prostate glands seemed to produce protein molecules with particular functions and needed to be identified. The introduction of semen into the female tract orchestrated striking molecular and cellular changes that facilitated conception and pregnancy. Seminal plasma contained many molecules bind to cognate receptors on target cells in the female reproductive tract, activating changes in gene expression leading to modifications in the cellular composition, structure and function of local tissues and of tissues distal to the reproductive (Robertson, 2005). In the present study, 3 (77.8, 53.3 and 9kDa) and 6 bands (81.1, 75.5, 48.9, 17.8, 13.3 and 9kDa) showed higher staining intensities in bulbourethral and prostate gland secretion, respectively. In addition, both secretions shared a band of 9 kDa but higher intensity was recorded in bulbourethral secretion. Previously, Stelletta et al (2021) demonstrated that the concentration of 15-18 kDa molecular weight (MW) proteins showed a positive correlation with sperm concentration and foal rate in horses. They concluded that a strong positive correlation was found between sperm concentration and 23-28 kDa MW proteins (r=0.77). In addition, the volume of 19-22 kDa MW proteins was negatively correlated with pregnancy and foal rate. Similarly, the volume of high MW proteins (173-385 kDa) correlated negatively with sperm motility and foal rate (Stelletta et al, 2021). The current study may give explanation for relation between fertility and protein profile of bulbourethral and prostate glands secretions including the role of the shared band and the other bands of higher intensities in both bulbourethral and prostate gland secretion.

secreted by these glands. Some of them seem related to the ability of sperm to form an oviductal reservoir,

Glycosidases were engaged in several reproductive events such as cumulus cells expansion (Takada *et al*, 1994), sperm capacitation (Taitzoglou *et al*, 2007), sperm oviductal epithelial cells interaction (Lefebvre *et al*, 1997), sperm zona pellucida binding (Miranda *et al*, 2000; Zitta *et al*, 2006), polyspermy block (Miller *et al*, 1993) and early embryos development (Tsiligianni, 2018). The activity of glycosidases (β-N-acetylglucosaminidase, α -N-acetylgalactosaminidase and α -L-fucosidase) has been verified in the uterine luminal fluid of the dromedary camels (Ghoneim *et al*, 2021), cattle (Tsiligianni *et al*, 2007; Tsiligianni, 2018), sheep (Tsiligianni *et al*, 2003; Samartzi *et al*, 2020) and mares (Reilas *et al*, 2000).

Previous study of Jauhiainen and Vanha-Perttula (1986) demonstrated that in the fractionation with gel filtration on Sepharose 6B, the beta-Nacetylglucosaminidase (beta-NAG) activities derived from bull testis and caput epididymidis had smaller molecular weights than did the secretory enzymes in seminal plasma, seminal vesicle secretion and cauda epididymidis. Maximum activity of all beta-NAG isoenzymes was observed at pH 5.0 (Jauhiainen and Vanha-Perttula, 1986). This study explained the presence of glycosidase activities in bulbourethral and prostate glands secretions of dromedary camels. As indicated recently for uterine fluid (Ghoneim *et al*, 2021), the current findings explains that β -Nacetylglucosaminidase, α-N-acetylgalactosaminidase and α -L-fucosidase in bulbourethral and prostate glands secretions may play a role in carbohydratemediated events in the uterus of dromedary camels. Glycosidases played an important role in different reproductive events; one of them was sperm capacitation (Taitzoglou et al, 2007). Parallel to that, in the present study the activities of α-L-fucosidase were reported to be significantly higher than that of other studied glycosidases in both bulbourethral and prostate gland secretion. This may indicate the major role of this enzyme in sperm capacitation besides other studied enzymes. Presence of the glycosidases in uterine luminal fluid of the dromedary camel had also been documented (Ghoneim et al, 2021). However, the activities of α -L-fucosidase reported to be higher significantly than that of other studied glycosidases in the uterine fluid of dromedary camels (Ghoneim et al, 2021). The current study concluded that bulbourethral and prostate gland secretions may be involved in viscosity and coagulation processes of dromedary semen owing to their contents of secretory proteins and glycosidases.

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MAGNETIC RESONANCE IMAGING OF THE DROMEDARY CAMEL STIFLE

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ABSTRACT

The objective of the present investigation was to develop a high-field magnetic resonance imaging (MRI) protocol for assessment of the dromedary camel stifle region and to describe normal MRI appearance of the stifle by comparing MRI images with their corresponding anatomic slices. Twelve cadaveric hind limbs were obtained from 6 clinically sound adult dromedary camels without hind limb lameness. Cadaveric stifles were scanned by 1.5 Tesla MRI system using T1-weighted, T2-weighted, proton density gradient echo and short Tau inversion recovery sequences in 3 planes. After imaging, stifles were frozen at – 18°C for 2 weeks, then sectioned in sagittal, dorsal or transverse planes. Optimal MRI images from different sequences and planes were evaluated and correlated to their corresponding gross anatomic slices. Descriptive findings of the articular cartilage, subchondral bone, cruciate ligaments, menisci, menisco-tibial and menisco-femoral ligaments, long digital extensor tendon, and patellar ligament were reported. The high-field MRI protocol described in this study provided high spatial and contrast resolution of the osseous and soft tissue structures of the dromedary camel stifle joint. Data obtained in this study could be used as normal reference standards for evaluation of the dromedary camel stifle in clinical situations.

Key words: Dromedary camel, imaging, MRI, stifle

Diagnosis of stifle injuries is routinely based on physical examination followed by radiography and/or ultrasonography (Bourzac *et al*, 2009; Beccati *et al*, 2013). Radiography is classically used to diagnose osteochondral injuries of the stifle joint of equines, although some osteochondral defects of the femoropatellar and femorotibial joints could not be detected radiographically (Barr *et al*, 2006; Nelson *et al*, 2016). Advanced imaging through of stifle joint in camels has been done by Sangwan and Gahlot (2015).

The stifle joint of dromedary is very important as many lameness imaging of hind quarter originate from this joint. Lameness of hind quarter involving stifle joint is well reported (Gahlot, 2007; Al-Juboori, 2013; Ramadan,1994) The anatomy of sifle joint is different than other large animals as it has absence of the medial patellar ligament in camels (Krishnamurthy *et al*, 1979). Lameness in stifle joint has been caused by upward fixation of patella (Gahlot *et al*, 1991; Krishnamurthy *et al*, 1992; Mistry *et al*, 1991), ruptured cranial cruciate ligament (Pearce and Hurtig, 1999) and arthritis (Shoieb and Sayed-Ahmed, 2016).

Magnetic resonance imaging (MRI) is a noninvasive modality that allows combined

evaluation of articular cartilage, subchondral bone, and soft tissue structures associated to the joint in equines (Santos *et al*, 2015). Many researchers have done studies on Magnetic Resonance Image (MRI) of the digits (El-Shafey and Abd Al-Galil, 2012), tarsus (Al Mohamad *et al*, 2021), fetlock joint, pastern and coffin joints (Irahim *et al*, 2019 a,b), carpal joint (Ibrahium and Shaker, 2018), temporomandibular joint (Arencibia *et al*, 2012), cranioencephalic structures (Arencibia *et al*, 2005), head structures (Emam *et al*, 2020) and normal brain (Arencibia *et al*, 2004) of camels. However, MRI of stifle joint in camels has not been reported previously.

The purpose of the present study was, therefore, to carry out the normal magnetic resonance imaging of stifle in dromedary camel. A corroborative interpretation of MRI images was done by the sagittal, transverse and dorsal cryosections of hindlimbs used for MRI imaging.

Materials and Methods

Right and left stifles were collected from 6 adult camels (3 males and 3 non pregnant females; age range, 7-16 years; and weight, 450-625 kg) that were clinically sound and free from any pathology or lameness.

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Immediately after death, limbs were disarticulated at the hip joint and maintained in normal position. The limbs were placed in the central bore of a 1.5 Tesla Ingenia MRI system (Philips Ingenia 1.5T MRI; Philips GmbH, Hamburg, Germany) with the lateral aspect as the dependent portion and the long axis of the limb parallel to the MRI table (to simulate the limb of a camel in lateral recumbency), then scanned in transverse, sagittal and dorsal planes. Sagittal images were produced by orienting slices parallel to the medial and lateral margins of the femur and tibia at the level of the medial collateral ligament. Dorsal images were produced by orienting slices parallel to the longitudinal axis of the femorotibial joint on sagittal images. The transverse plane was acquired by orienting slices perpendicular to the medial collateral ligament and parallel to menisci and joint space on sagittal images. The scanning sequences were T1weighted (T1), T2-weighted (T2), Proton Density (PD) gradient echo and Short Tau Inversion Recovery (STIR). Acquisition settings were: repetition time, 3,160 milliseconds; echo time, 14 milliseconds; echo number, 1; excitation number, 1 matrix size, 512; and slice thickness, 4 mm. Representative images at various levels that best correlated with the gross anatomic slices were selected.

After imaging, the specimens were frozen at – 18 °C for 2 weeks. Frozen stifles were sectioned transversely, sagittally or dorsally by means of an electric band saw into 1 cm slice thickness. The cut surfaces of each section were rinsed, numbered and photographed. Anatomic slices were used to facilitate an accurate interpretation of the anatomical structures and were correlated to their corresponding MRI images for identification and confirmation of each anatomical structure and its signal intensity.

Results and Discussion

The MRI images acquired in this study accurately represented the gross specimen evaluation of all structures, including the menisci, meniscotibial and meniscofemoral ligaments, and the cruciate ligaments of the dromedary camel stifle joint (Smuts and Bezuidenhout, 1987). MRI images in stable joint of present study showed a differential and tomographic details of cartilage, cortical bone, subchondral bone, trabecular bone, cancellous bone, menisci, ligaments, tendons and muscles. The obtained results were in agreement with the previous reports in horses confirming that MRI offers the best evaluation technique of all anatomical structures of the stifle joint particularly the soft tissue structures (Peterfy *et al*, 1994; Widmer *et al*, 2000; Nagy and Dyson, 2011). Results of the present study showed that MRI enabled investigation of intra-articular structures of stifle joint that would facilitate detection and diagnosis of stifle injuries in dromedary camel.

In present study, representative anatomic structures were identified on MRI images and frozen sections (Figs 1, 2 and 3). The sagittal and dorsal plane images allowed evaluation of articular alignment, synovial fluid and synovial membrane while transverse plane images provided the most detailed evaluation of cruciate ligaments. Use of high-field 1.5 Tesla magnet and pulse sequences of a gradient echo in T1, T2, PD and STIR produced excellent anatomic delineation of the bony, articular, ligamentous, and tendinous structures of the dromedary camel stifle joint. T1 and PD sequences produced images with high definition and good signal intensity and provided high anatomical details. The T2 sequence demonstrated the synovial structures and had a good contrast between synovial fluid, soft tissues, bones and cartilaginous structures. STIR sequence was valuable for identification of areas with high fat content. The MRI protocol and sequences used in this study were in general accordance with reports in horses (Tucker and Sampson, 2007; Daglish et al, 2018). However, MRI of the equine stifle was difficult depending on patient size (Holcombe et al, 1995; Judy, 2011).

Soft tissue structures comprising the stifle joint were consistently identified including medial collateral ligament, cranial and caudal cruciate ligaments, patellar ligament, medial and lateral cranial meniscotibial ligaments, meniscofemoral ligament, popliteal tendon, joint capsule and synovial fluid. Similar data were reported in horses (Holcombe *et al*, 1995; Tucker and Sampson, 2007), except that lateral collateral ligament and medial and lateral patellar ligaments are absent in camels (Smuts and Bezuidenhout, 1987).

The medial collateral ligament appeared more lobulated and generally was well-defined, had low signal intensity on all image sequences and surrounding by higher signal intensity fatcontaining soft tissues that was evident on STIR images. The cranial and caudal cruciate ligaments had homogeneous very low signal intensity on PD, T2 and STIR images. The medial and lateral menisci had moderate signal intensity on T1 and PD sequences, and low signal intensity on STIR and T2 images. On



Fig 1. Midline sagittal cryosection (A) and T1 weighted (B) and T2 weighted (C) MRI images at the level of the tibial intercondylar eminence. Cranial is to the right, proximal to the top. 1, femur; 1a, lateral femoral condyle; 2, tibia; 2a, tibial tuberosity; 2b, intercondylar eminence of tibia; 3, patella; 4, femoropatellar articulation; 5, femorotibial articulation; 6, lateral meniscus; 7, meniscofemoral ligament; 8, caudolateral bundle of cranial cruciate; 9, caudal cruciate ligament; 10, patellar ligament; 11, fat; 12, lateral patellar retinaculum; 13, rectus femoris muscle; 14, fibularis longus muscle 15, common tendon of the long digital extensor and fibularis tertius muscles; 16, long digital flexor muscle; 17, lateral head of gastrocnemius muscle; 18, semimembranosus muscle.



Fig 2. Transverse cryosection (A) PD MRI image at the level of the menisci and tibial intercondylar eminence. Cranial is to the right, medial to the top. 1, patellar ligament; 2, fat; 3, insertion tendon of gluteobiceps muscle; 4,; combined tendons of long digital extensor and fibularis tertius muscles 5, medial femoral condyle; 6, lateral femoral condyle; 7, tibial intercondylar eminence; 8, medial collateral ligament; 9, origin of popliteus muscle; 10, medial patellar retinaculum; 11, lateral meniscus; 12 medial meniscus; 13, cranial lateral meniscotibial ligament; 14, cranial medial meniscotibial ligament; 15, caudal cruciate ligament; 16, intermeniscial ligament; 17, popliteus muscle; 18, superficial digital flexor muscle; 19, lateral head of gastrocnemius muscle; 20, medial head of gastrocnemius muscle; 21, gluteobiceps muscle; 22, semitendinosus muscle; 23, semimembranosus muscle.

T1 - weighted images, signal intensity was similar to articular cartilage, but on other images they have lower signal than cartilage. Tendons and ligaments of the stifle joint had homogenous low signal intensity on all sequences. Synovial fluid in the surrounding sheaths and in the joint had high signal intensity on PD and T2 sequences and low signal intensity on T1 images. The muscles supporting the stifle joint had intermediate to high signal intensity on PD images and moderately low signal intensity on T1, T2 and STIR images. The boundaries of muscles were seen with slightly higher signal intensity on T1 and STIR images, slightly lower signal intensity on PD images. The same was reported in horses (Santos *et al*, 2015) and dogs (Przeworski *et al*, 2016). In camels, femoropatellar and medial and lateral



Fig 3. Middle dorsal cryosection (A) and T1 weighted and T2 weighted MRI images at the level of the medial collateral ligament. Medial is to the left and proximal to the top. 1, femur; 1a, medial femoral condyle; 1b, lateral femoral condyle; 1c, femur cancellous bone; 1d, femur trabercular bone; 1e, articular cartilage of femur; 2, tibia; 2a, tibial plateau; 2b, articular cartilage of tibia; 3, lateral meniscus; 4, medial meniscus; 5, caudal cruciate ligament; 6, cranial cruciate ligament; 7, tendon of the popliteal muscle; 8, medial collateral ligament; 9, common origin of fibularis tertius and lateral digital extensor muscles; 10, cranial tibial muscle; 11, medial head of gastrocnemius muscle; 12, lateral head of gastrocnemius muscle; 13, vastus lateralis muscle; 14, rectus femoris muscle.

femorotibial compartments are communicated (Smuts and Bezuidenhout, 1987), while in horses the medial and lateral femorotibial compartments are separated by a synovial membrane (Budras *et al*, 2011).

In all sequences, the articular cartilage, subchondral bone, cortical bone, cancellous bone with its trabercular structure was consistently visualised. On T2 and PD images, articular cartilage was recognised as a layer of homogenous intermediate to high signal intensity with a smooth osteochondral junction and was clearly defined from the bone underneath it in all joints by the differences in signal intensity. On T1, PD and T2 images, cancellous bone had intermediate to high signal intensity, representing the fat content of the bone. Subchondral bone had homogenous low signal intensity with regular osteochondral junction. Cancellous bone had heterogeneous signal intensity with a well-defined trabecular pattern. On STIR images, cancellous bone had homogeneous low signal intensity, there was no distinct definition between the cortical and cancellous bones as both had low signal intensity, articular cartilage was barely visible and was recognised as a very thin layer of intermediate signal intensity. Our protocol allowed MRI examinations of all stifles and anatomical structures as well as signal intensities of each individual structure were completely delineated in accordance with reports for human knees (Chien *et al*, 2020) and equine stifle joint (Santos *et al*, 2015).

The present study provided a depiction of the normal MRI features of dromedary camel stifle joint associated with its corresponding gross anatomical sections. In this study, freezing of limbs in the same position as the MRI examination allowed exact matching between gross anatomical sections and MRI images which facilitated evaluation and identification of various structures of the stifle joint. This study provided an anatomic and MRI reference for the dromedary camel stifle joint, which can be used as a guide for interpretation of clinical cases and as a reference for other research projects.

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ECHOBIOMETRY OF EYES OF DROMEDARY CAMELS (Camelus dromedarius)

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ABSTRACT

Transcorneal ultrasonographic scanning of 12 adult healthy camels of both sex were performed using linear array transducer on B-mode. The ultrasonographic appearance of the eye was described and ocular dimensions were recorded. The echo-biometric studies on four parameters i.e. anterior chamber depth (ACD), lens thickness (LT), vitreous chamber depth (VCD) and axial length (AL) were recorded. The ultrasonography showed that the eyes of camels were appeared as slightly ovoid structures with anechoic contents such as anterior chamber, vitreous chamber and lens. The cornea, anterior and posterior lens capsule, iris, granula iridica/corpora nigra and sclera-retinal rim appeared as hyperechoic. Non-significant differences were found in all parameters when compared between right and left eyes of male and female camels. However, the anterior chamber depth in male camels were significantly higher than female camels $P \le 0.05$. The present study provides echo-morphometric view of the intra-ocular structure in adult healthy eyes of camels.

Key words: Camel eye, Echobiometry, Ultrasonography

The ophthalmic ultrasonography is a reliable tool to quantify the ocular dimensions and it is safe and non-invasive procedure (Dudea, 2011). Ocular ultrasound biometry was used in different animals, i.e. cat (Mirshahi et al, 2014), goat (Ribeiro et al, 2009), horse (Gialletti et al, 2018; Sorouri et al, 2009) and dromedary camel (Kelawala et al, 2015). Ultrasonographic measurements of the Bulbous oculi of the camel were done in terms of corneal thickness, anterior chamber depth, lens thickness, vitreous chamber depth, axial length and optical axis (Khan and Türker, 2021). Echobiometry of eye usually provides direct dimensions (Kelawala et al, 2015; Osuobeni and Hamidzada, 1999; Yadegari et al, 2013) but indices are more reliable than diameters because they are independent of the size (Kara et al, 2011).

Camels are vulnerable to a variety of ophthalmic problems, including corneal and eyelid laceration, panophthalmos, corneal opacity, and descematocele etc (Bishnoi and Gahlot, 2001). Ocular ultrasonography of camel eye is well studied previously (Tharwat and El-Omar, 2021; Yadegari *et al*, 2013). Ultrasonography of the eye provides a detailed examination of the interior of the eye.

Echobiometry of the eyes of dromedary camels is least studied, hence present study was undertaken to perform echobiometry of eye of camels by transcorneal ultrasonographic scanning.

Materials and Methods

Twelve live healthy adult camels with the clear cornea and without any ocular pathology were selected (6 male and 6 female) for ocular ultrasonography. Camels were restrained in sternal recumbency and mild sedation was given by xylazine hydrochloride¹ (at the dose rate of 0.2 mg/Kg body weight) by intravenous route. B- mode transcorneal ultrasonography (Edan U2 prime edition) was done by using a linear array transducer of frequency 8-13 MHz. Coupling gel was applied over the transducer and probe was placed gently over the corneal surface perpendicular to the centre of the cornea (vertical plane, Fig 1). Ocular echobiometric measurements were recorded in the vertical plane image. After the procedure excess coupling gel was wiped off with cotton, and the eye was rinsed with normal saline.

Diverse ocular echobiometric parameters measured in both left and right eyes of all the camels were - anterior chamber depth (ACD), lens thickness (LT), vitreous chamber depth (VCD) and Axial length (AL). Statistical analysis, student's t test was used for comparing the left and right eyes and between male and female camels under the study.

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Results

On B-mode ultrasonography camel eye appeared as slightly ovoid in structure. Cornea, anterior chamber, lens, iris, ciliary body, vitreous chamber and sclera-retinal rim were well visualised ultrasonographically (Fig 2). Corneal stroma, anterior chamber, vitreous chamber, lens cortex and nucleus appeared as an anechoic area and anterior and posterior corneal layer, iris, ciliary body, anterior and posterior lens capsules and scleraretinal rim appeared as hyperechoic images. The cornea appeared as three-layered, two hyperechoic convex lines with an anechoic area in between. Iris was located adjacent to the anterior lens capsule and ciliary body. Granula iridica/ corpora nigra appeared as a hyperechoic structure in the anterior chamber from the dorsal side of the iris which was well visualised sonographically in all the camels. The sclero-retinal rim appeared as a concave hyperechoic line in the posterior globe wall and its 3 layers could



Fig 1. Vertical plane ultrasonography in camel eye will a linear array transducer.



Fig 2. Sonogram of camel eye (AC-anterior chamber, CNcorpora nigra, CB- ciliary body, ALC- anterior lens capsule, Po LC-posterior lens capsule, VC-vitreous chamber, OD-optic disc).

not be differentiated ultrasonographically. The optic disc was not a consistent finding in the study and it appeared as raised or depressed hyperechoic structure in the posterior wall. The nerve tract showed mixed echogenic shadow, which started from the posterior margin of the sclero-retinal layer.

The various echobiometric parameters recorded are summarised in table 1 and table 2. There was no significant difference noted in any of the ocular components between the left and right eyes of male and female camels. However, the overall values of ACD were significantly higher in male camels than female camels ($P \le 0.05$).

Table 1. Ultrasonographic measurements (Mean \pm SE) of the
ocular structures of the left and right eye of dromedary
camels (n=12).

| Ocular structures | Left eye (in mm) | Right eye (in mm) | |
|-------------------|------------------|-------------------|--|
| ACD | 5.65±0.31 | 5.8±0.41 | |
| LT | 10.53±0.45 | 10.21±0.41 | |
| VCD | 17.84±0.57 | 17.72±0.51 | |
| AL | 34.33±0.59 | 34.07±0.66 | |

Table 2. Ultrasonographic measurements (Mean \pm SE) of the
ocular structures of the male (n==6) and female (n==6)
adult camels (* indicate P \leq 0.05).

| Ogular shru shuros | Sex (Mean ± SE) in mm | | | |
|--------------------|-----------------------|------------|--|--|
| Ocular structures | Male | Female | | |
| ACD | 6.15*±0.33 | 5.3*±0.39 | | |
| LT | 10.07±0.6 | 10.68±0.26 | | |
| VCD | 18.12±0.5 | 17.43±0.58 | | |
| AL | 34.78±0.3 | 33.62±0.95 | | |

Discussion

Ocular sonography is an easy, non-invasive diagnostic procedure used to identify ocular pathology. An early diagnosis of eye disease is crucial for the success of the treatment.

In present study the ultrasonography of camel eye was done by B mode using linear array transducer. Khan and Türker (2021) also used ultrasound B-mode technique for ocular measurements of the hybrid camel and it showed amplitude of returned echoes as dots (Mirshahi *et al*, 2014). A probe of the B-scan can also generate charismatic image of the eye as it transmits multiple sound waves (Solarte and Shaikh, 2007). Another crucial component of these devices is transducer and generally, linear transducers having 7.5 to 10 MHz frequency are used for ocular measurements (Dudea, 2011). The assessment of ocular dimensions is crucial for ophthalmic surgeons and must be determined before any ophthalmic interference (Grinninger *et al*, 2010). Ultrasonography was performed under xylazine sedation in the current study and other researchers also did it under xylazine sedation (El-Tookhy *et al*, 2012 and Abedellaah *et al*, 2017). A standoff pad is usually required to visualise the cornea (Hager *et al*, 1987). However, standoff pad was not used in the present study instead a copious amount of coupling gel was used, which obviate the use of a standoff pad. The ultrasonographic appearances of ocular structures were similar to previous observations in camel eyes (El-Tookhy *et al*, 2012; Yadegari *et al*, 2013; Kelawala *et al*, 2015; Abedellaah *et al*, 2017).

The ocular components of camel eyes were identical to buffalo (Assadnassab and Fartashvand, 2013), horse (Reef, 1998; Tripathi et al, 2018), cattle (El-Maghraby et al, 1995; Potter et al, 2008; Tripathi et al, 2018), goat (Ribeiro et al, 2009; Athar et al, 2021a), sheep (Athar et al, 2021b) and dog (Kumawat and Jhirwal, 2021). The structure resembling granula iridica described in the equine eye (Diaz, 2004; Valentini et al, 2010) was also well developed and observed in camels in this study and similar observations were made by other researchers also (El-Tookhy et al, 2012; Kelawala et al, 2015). These structures help them of case of direct exposure to sunlight into the eye (Samuelson, 2007). Khan and Türker (2021) recorded ultrasonographic details of eyeballs of hybrid camels and these showed 95% confidence intervals for measurements as corneal thickness (CT) (1.56-1.87), ACD (2.33-4.27), LT (6.81-10.00), VCD (23.01-24.44), AL (35.13-38.60) and Optical axis (OA) (34.89-37.24). The value of ACD/AL was found bigger while VCD/AL of adult one-humped camel were found smaller in size by Kassab (2012), Kelawala et al (2015) and Yadegari et al (2013) as compared to the hybrid camel (Khan and Türker, 2021). Transcorneal method of ocular sonography was used in this study and a similar method was also used by others (Kassab, 2012; EL-Tookhy et al, 2012; Yadegari et al, 2013 and Kelawala et al, 2015). Parrot has higher values for ACD/AL and LT/AL but very much smaller optical axis index (OA/AL) (Lehmkuhl et al, 2010) than the camel (Khan and Türker, 2021).

Good quality US images were obtained in vertical plane (longitudinal) positioning of the probe in the present study which was in agreement with others researchers (El-Magharaby *et al*, 1995; Ribeiro *et al*, 2010). No significant difference was detected between left and right eyes echobiometry in dromedary as also reported by others (Yadegari *et al*, 2013 and Kelawala *et al*, 2015). However a significant difference was noted between male and female camels ACD. A higher ACD was noted in male camels than females, and the higher mean values may be attributed to the small sample size and difference in breed and age of the animal under the present study.

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INTRAVITREAL INJECTION OF GENTAMICIN IN DROMEDARY CAMEL WITH UVEITIS

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ABSTRACT

This study was aimed to evaluate intravitreal injection of gentamicin in cases of uveitis in camels. Eighteen camels that suffered from anterior, posterior or panuveitis were included in the present study. Complete ophthalmic examinations were performed before and following the treatments and these were treated with a 4 mg gentamicin which was injected intravitreally together with topical antibiotics for one week, and topical nonsteroidal anti-inflammatory drugs over the course of 2-6 weeks based on each camel's individual response to therapy. One third camels (33%) affected with uveitis had poor vision before the treatments, while vision was not improved by 10% after six months improvement of vision was seen from 41-75% after one year of intraocular injection of gentamicin. The results of this study showed that the intravitreal gentamicin injection in camel affected with anterior uveitis, posterior uveitis and panuveitis help in healing and improved the vision.

Key words: Camel, gentamicin, intravitreal, ophthalmology, uveitis

Ocular affections in camels, like in most other livestock, can cause a debilitating condition that can severely affect animal productivity (Bishnoi and Gahlot, 2004; Fahmy *et al*, 2003; Kumar *et al*, 2016). However, camels are prone to eye injuries while browsing from trees and thorny weeds and it results into corneal wounds and injuries to the outer parts of the eye (Abdella *et al*, 2018; Bishnoi and Gahlot, 2004). Moreover, camels suffer from a wide range of ophthalmic affections, which causes anterior and posterior eyes infection (Abdella *et al*, 2018; Fahmy *et al*, 2003; Gebreyohanes and Assen, 2017). Occasionally, damage to the eye can be severe enough and may lead to blindness (Abdella *et al*, 2018).

Uveitis is characterised by exceptionally wide heterogeneity, regarding both oetiology and symptoms (Laven and Lawrence, 2006; Malalana *et al*, 2017). The pathophysiology and course of the disease are complex and multifactorial associated with various symptoms (Rojas-Carabali *et al*, 2021). The classic signs of uveitis are episcleral congestion, epiphora, corneal oedema, blepharospasm, aqueous flare and fibrin in the anterior chamber (Fingerhut *et al*, 2019; Rojas-Carabali *et al*, 2021). The chronic from of uveitis may lead to irreversible complications (Fischer *et al*, 2019; Rojas-Carabali *et al*, 2021). Few reports described uveitis in camels (Abdella *et al*, 2018; Fahmy *et al*, 2003; Gahlot, 2000; Madany *et al*, 2006) and there

are no specific treatments reported for uveitis in camels except local and systemic anti-inflammatory treatment (Bishnoi and Gahlot, 2004; Madany *et al*, 2006). Recently, uveitis is being treated in veterinary medicine in many surgical procedures like pars plana vitrectomy in horses, dogs and non-human primates (Fingerhut *et al*, 2019; Fruhauf *et al*, 1998; Hirashima *et al*, 2022; Hopster *et al*, 2013; Tshilenge *et al*, 2016). However, intravitreal injection of gentamicin in horses (Fischer *et al*, 2019), suprachoroidal injection of triamcinolone in horses (Gagnon *et al*, 2021) and cidofovir injection in dogs with chromic glaucoma (Low *et al*, 2014) has been reported.

Several recent studies indicated the good efficacy of gentamicin in equine recurrent uveitis (ERU) (Fischer *et al*, 2019; Kleinpeter *et al*, 2019; Launois *et al*, 2019).

This study was, therefore, aimed to evaluate the efficacy of single-dose intravitreal injections of gentamicin in cases of uveitis of camels.

Materials and Methods

Ethical approval

The study was approved for research purposes by the Ethics Committee at King Faisal University in Saudi Arabia (Approval number: KFU-REC-2021-OCT-EA00010).

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Animals

Camels (aged 2-18 years) with uveitis (n=18; male=7, females=11) brought to the Veterinary Teaching Hospital, College of Veterinary Medicine, King Faisal University were selected. The uveitis was unilateral (n=9) and bilateral (n=9). Further clinical examination revealed panuveitis (n=12), anterior uveitis (n=2) and posterior uveitis (n=4). Complete history, clinical examination, ocular examinations using ophthalmoscope and ultrasound were performed in Veterinary Teaching Hospital. The clinical signs of uveitis were conjunctival congestion, miosis, epiphora, blepharoedema or blepharospasm, aqueous flare, photophobia, fibrin in the anterior chamber, equatorial vesicular cataracts, capsule adhesions, lens vitreous body opacifications, and retinal detachment. This study was conducted from March 2020 to January 2022.

Ocular examination

After history and clinical examination, complete ophthalmic examinations were performed to differentiate between anterior (Fig 1B) and posterior and panuveitis (Fig 1A) by evaluation (dazzle, and pupillary light reflexes (PLR)), slitlamp biomicroscope (Kowa SL-15) (Kowa Company Ltd., Tokyo, Japan) and a subjective clinical vision assessment (menace response) and neuro-ophthalmic indirect ophthalmoscopy (Heine Beta 200 and Heine Omega 500; Heine Optotechnik, Herrsching, Germany). Aqueous flare was graded as follows: 0 (none), 1 (faint), 2 (moderate), 3 (severe) or 4 (blood



Fig 1. (A) Five-year old camel presented for a persistent chronic panuveitis of the left eye with an accumulation of fibrin in the anterior and posterior chamber, blepharospasm and miosis were present. (B) Twelve-year old camel affected with anterior uveitis with epiphora, corneal oedema, and blepharospasm. (C) This image shows the place of intravitreal injection, where the yellow dashed line indicates the distance between the upper part of the cornea and the place of injection (10 mm); the white arrow showed the position of injection. (D) This image shows the intravitreal injection after opening the eye using a Barraquer eyelid speculum; the injection is done using a 30-gauge needle/syringe combination.



Fig 2. (A) Twelve-year old camel before the intravitreal injection presented with anterior uveitis with corneal oedema and overall cloudiness. (B) Four weeks after injection: Slight reduction in cloudiness and fibrin in the anterior chamber. (C) Six months after injection: reduced corneal oedema (by 50%), cloudiness with improved vision. (D) One year after injection: more reduced cloudiness than six months ago; the vision was restored to a moderate degree.

or fibrin present in the anterior chamber) (Lam *et al*, 2015). Fundus images were obtained by Kowa Genesis (Kowa Company Ltd., Tokyo, Japan) in camels with posterior segment abnormalities, whenever possible.

Sedation and intravitreal gentamicin injection

Each camel was sedated with intravenous injection of xylazine 2% (0.1 mg/kg bodyweight; Rompun, Bayer Health Care), and an auriculopalpebral nerve block (1.5 mL lidocaine SC, 2% Lidocain inj., Teva) was performed on the respective eye. Topical oxybuprocaine (Novesine 0.4% eyedrops, OmniVision) was used for topical corneal analgesia. However, eyelids were held open manually. The ocular surface was first irrigated with 0.5% povidone-iodine solution (Betadine, Egis) and then rinsed with saline. Following sedation, the camel's head was positioned atop a pair of pads placed on a ground to increase stability. The conjunctival fornices were irrigated with 1.0 ml of baby shampoo solution (0.1% dilute in saline solution), 1.0 ml of a 1.0% dilute iodine solution, and 1.0 ml of balanced saline solution (Brooks et al, 2017). Dorsal globe exposure was facilitated with prototype evelid retractor, and further enhanced by rotating the camel's head away from the examiner to exaggerate ventral globe rotation. Camels were treated with a 4 mg injectable gentamicin solution containing preservatives (Genta80; 80 mg/ml) which was drawn up in a 30- gauge needle/syringe combination (12mm length, 1.0 ml insulin syringe) (Fig 1D). The injection site was 10 mm posterior to the limbus at 12 o'clock (Fig 1C). Due to the difficulty of accurately measuring and determining the injection point with calipers, the injection point was roughly estimated by the examiner immediately before the injection. The injection was facilitated by applying gentle but steady pressure while slowly and deliberately rotating the needle in a clockwise manner with the needle directed toward the optic nerve head to avoid inadvertent contact



with the lens. Same fluid quantity from vitreous was withdrawn using a second insulin syringe with 23-gauge needle at either the 11:00 o'clock (left eye) or 1:00 o'clock (right eye) positions in order to keep the same fluid pressure in the ocular and this fluid was used for more investigations (Fig 3C).

Post-injection therapy and Follow-up examination

Post intravitreal injection, a medical therapy consisting of topical antibiotics (Oxytetracyclin) q12h for one week, and topical nonsteroidal antiinflammatory drugs (NSAIDs) that were gradually tapered over the course of 2-6 weeks based on each camel's individual response to therapy. Systemic Flunixin-meglumine @ 1.1mg/kg, q24h was also administered intravenously for 7 days. Camels were monitored weekly for the first month. Subsequent follow-up examinations were spaced further apart based on the camel's individual response to treatment. Inflammation was markedly reduced which was evident by absence of signs of uveitis (Fig 2A, B, C, D and Fig 3A, B).



Fig 3. (A) Three-year old camel before the intravitreal injection presented with chronic panuveitis with secondary keratitis.
(B) Six months after injection: Uveitis remained controlled without medical treatment; the keratitis was reduced. (C) This image shows the intravitreal fluid withdrawn from the right eye at 1:00 o'clock after opening the eye using a Barraquer eyelid speculum; the aspiration was done slowly using a 23-gauge needle/ syringe combination.



Fig 4. Changes in vision after intravitreal gentamlcin injection.

Statistical analysis

The obtained data was recorded in Excel spreadsheets and imported into Graph Pad Prism 7 (GraphPad Software, San Diego, CA, USA) software for further analysis. Graphs, calculations, and

| Time (deve) | Camala Evac | Errog | Unilateral/ bilateral | Improvements eyes (%) | | | |
|---------------------------|-------------|-------|--------------------------|-----------------------|----------|----------|--|
| Time (days) | Cameis | Eyes | | Good | Moderate | Poor | |
| Pre-injection (0 days) | 18 | 27 | 9/9 | 11 (41%) | 7 (26%) | 9 (33%) | |
| Post-injection (7 days) | 18 | 27 | 9/9 | 11 (41%) | 5 (18%) | 11 (41%) | |
| Post-injection (14 days) | 18 | 27 | 9/9 | 13 (49%) | 5 (18%) | 9 (33%) | |
| Post-injection (21days) | 18 | 27 | 9/9 | 13 (50%) | 7 (25%) | 7 (25%) | |
| Post-injection (28 days) | 18 | 25 | 9/8 | 14 (56%) | 6 (24%) | 5 (20%) | |
| Post-injection (60 days) | 16 | 24 | 8/8 | 15 (63%) | 5 (21%) | 4 (16%) | |
| Post-injection (90 days) | 15 | 22 | 8/7 | 14 (64%) | 4 (18%) | 4 (18%) | |
| Post-injection (120 days) | 15 | 22 | 8/7 | 15 (67%) | 5 (22%) | 2 (11%) | |
| Post-injection (150 days) | 15 | 22 | 8/7 | 15 (67%) | 4 (18%) | 3 (15%) | |
| Post-injection (180 days) | 14 | 20 | 8/6 | 16 (80%) | (10%)2 | 2 (10%) | |
| Post-injection (360 days) | 8 | 12 | 4/4 | 9 (75%) | 1 (8%) | 2 (15%) | |

Table 1. Subjective visual assessment pre- and post-intravitreal gentamicin injection (days).

statistical analyses were performed using GraphPad Prism software.

Results and Discussion

The information is limited about treatment of uveitis in camels; therefore. the main goal of this study was to conduct clinical trial of the intravitreal injection of gentamicin to treat the uveitis by minimising ocular inflammation and restoration of vision to a varying degree (Fischer et al, 2019; Gerding and Gilger, 2016; Wollanke et al, 2022). However, the pharmacodynamics of gentamicin in the all types or stages of uveitis remains enigmatic (Fischer et al, 2019; Gan et al, 2001; Kleinpeter et al, 2019; Wollanke et al, 2022). Romeike et al (1998) reported that the primary mechanism of action of gentamicin could suppress or block the activation of specific T-cell that are identified to play a significant role in autoimmune uveitis. While, many studies in recent years reported successful treatments of equine recurrent uveitis affected with Leptospira using intraocular gentamicin injection due to the direct effect of gentamicin on gram-negative bacteria and improvement was noticed within days of starting treatment (Fischer et al, 2019; Voelter et al, 2020; Wollanke et al, 2022).

In present study, no difficulties were found in intraocular injection in camels under sedation and local anesthesia except the posterior movement of the eye, which was more than described in horses or humans (Ganapathy *et al*, 2018; Jose-Vieira *et al*, 2021; Yi *et al*, 2008). In animals of present study, the eye was pushed and fixed it in the anterior part of the orbital cavity directly before the injection by applying pressure in medial side of the zygomatic process to expose the eye in order to facilitate the injection process. A difficulty was noticed in withdrawing the vitreous humor samples using the 30-gauge needle but fluid withdrawal was easy and safe with 23-gauge needle as in equine (Ackermann *et al*, 2021). One of the limitations of this study was the difficulty in follow up of the treatment with the owners, especially keeping the camel in the shade during the first days after treatment, which may have an impact on the results of the treatment.

In present study, 62% of eyes of affected camels had panuveitis, while the incidence of posterior and anterior uveitis were 27% and 11%, respectively. However, studies are scarce about the type of uveitis in camels (Kumar et al, 2016; Madany et al, 2006). A similar increased percentage of panuveitis type was recorded in horses (Ackermann et al, 2021; Fischer et al, 2019; Wollanke et al, 2022), while a higher percentage for anterior uveitis was reported in humans (Roche et al, 2021; Silvestri et al, 2020). The results of this study showed that the intravitreal gentamicin injection in camel affected with anterior uveitis, posterior uveitis and panuveitis helped in healing and improved the vision (Fig 2 and 3). On the other hand, three eyes in two camels developed cataracts, retinal degeneration and loss of vision after intraocular injection. Therefore, the risks of injection cannot be ignored, and must be discussed in detail with the owner before starting the treatment options (Fischer et al, 2019; Launois et al, 2019). In this study, nine eyes (Table 1 and Fig 5) (33%) affected with uveitis had poor vision before the treatments, while the vision decreased to 10% after six months of intraocular injection of gentamicin which was in agreement with result of Fischer et al (2019) and Kleinpeter et al (2019) for treatments of equine recurrent uveitis. The increased percentage of good vision improvement of eyes was from 41% to 75%

after one year of treatment indicated the effectiveness of intravitreal injections of gentamicin in animals of present study (Fig 2D). The stability of equine recurrent uveitis with reduction of ophthalmological symptoms and an improvement in vision after intravitreal injection with a single low dose of gentamicin was seen (Fischer *et al*, 2019; Kleinpeter *et al*, 2019; Wollanke *et al*, 2022). However, two camels of present study suffering from unilateral panuveitis continued to have poor vision even after one year of the treatment (Table 1).

In conclusion, intravitreal injection in camels affected with uveitis can be treated by intervitseal injection of gentamicin. However treatment and after care protocol needs more attention.

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SELECTED RESEARCH ON CAMELID IMMUNOLOGY

(Hard Bound, 392 pages, few figs coloured, Edition 2016)

In 1989 a group of biologists led by Raymond Hamers at the Free University Brussels investigated the immune system of dromedaries. This discovery was published in Nature in 1993. Based on their structure, these peculiar camelid antibodies have been named Heavy Chain Antibodies (HCAb), as they are composed of heavy chains only and are devoid of light chains. Sera of camelids contain both conventional heterotetrameric antibodies and unique functional heavy (H)-chain antibodies (HCAbs). The smaller size and monomeric single domain nature make these antibodies easier to transform into bacterial cells for bulk production, making them ideal for research purposes. Camelid scientists world over were greatly fascinated by a new field of research called "Camelid Immunology". Significant research has been done on camelid immunology in recent decade. In order to benefit future camelid immunology researchers, this book was planned in the series of "Selected Topics" by Camel Publishing House with a title- "Selected Research on Camelid Immunology" edited by T.K. Gahlot, U. Wernery and Serge Muyldermans. This book is a unique compilation of research papers based on "Camelid Immunology" and published in Journal of Camel Practice and Research between 1994-2015. Research on this subject was done in 93 laboratories or institutions of 30 countries involving about 248 scientists. In terms of number of published papers in JCPR on the immunology the following countries remain in order of merit (in parenthesis), i.e. Iran (1), India and UAE (2), China and Saudi Arabia (3), Sudan (4), Kenya and Belgium (5), USA (6), Germany (7) and so on. The book contains 11 sections and is spread in 384 pages. The diverse sections are named as overview of camel immune system; determinates of innate immunity, cells, organs and tissues of immune system; antibodies; immunomodulation; histocompatibility; seroprevalence, diagnosis and immunity against bacteria, viruses, parasites and combination of other infections; application of camel immunoglobulins and applications of immune mechanisms in physiological processes. The camelid immunology has to go a long way in its future research, therefore, this reference book may prove quite useful for those interested in this subject. Book can be seen on www.camelsandcamelids.com.



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INVESTIGATION OF LAMENESS IN RACING DROMEDARY CAMELS (*Camelus dromedarius*) AND ASSOCIATED OXIDATIVE STRESS BIOMARKERS

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ABSTRACT

In racing camels, lameness is measured to be a major health issue and an economically important problem for many camel owners. This study aimed to investigate different oxidative stress and antioxidant biomarkers in the blood of racing lamed dromedary camels. Moreover, to highlight their role in lameness diagnosis, pathogenesis and to emphasise its role to monitor treatment response. Thirty five out of 315 racing camels exhibited clinical lameness. The serum levels of malondialdehyde (MDA) and nitric oxide (NO) in lame dromedary camels with different perceived causes of lameness (punctured foot, traumatic injury) were remarkably over than those detected in the control healthy dromedary camels. However, lame dromedary camels had significantly lower levels of serum superoxide dismutase (SOD), reduced glutathione (GSH), catalase (CAT), and total antioxidant capacity (TAC) when compared with the control healthy camels. The serum levels of MDA, NO, SOD, GSH, CAT, and TAC markers in lame dromedary camels pre-and post-treatment were measured in this study. An obvious decline was detected in serum levels of MDA and NO of lame camels after 10 days of treatment, whereas, the levels of antioxidant markers (SOD, GSH, CAT, and TAC) were significantly increased toward normal values. The ROC curves were created. The AUCs were assessed to evaluate the accuracy of each variable to distinguish diseased and healthy camels. Based on the ROC curves and AUCs; MDA, SOD, GSH, CAT, TAC, and NO were considered highly diagnostic and predictive biomarkers of lame dromedary camels. Moreover, the addition of antioxidants to the treatment protocol of lameness may enhance the treatment response in camels.

Key words: Camel, catalase, glutathione, lameness, malondialdehyde, super oxide dismutase

A variety of factors and widely varied causes can lead to camel lameness, including direct trauma, nutritional problems, punctured foot, abnormal limb conformation, and infectious disease (Gahlot and Chouhan, 1992; Ramadan, 1994; Gahlot, 2007; Al- Juboori, 2011a; Al-Juboori, 2011b; Al-Juboori, 2010; Mostafa and Khalil, 2018; Mostafa, 2020). Lameness in camels is characterised by partial or non-weight bearing by one or more limbs, swelling of the joints, pain upon palpation, protruding toes, shivering while sitting, and an asymmetrical pelvis (Gahlot, 2007). In addition to decreased milk production, decreased reproductive performance, growth retardation, and culling from farms or competition, lame camels also suffer from diminished physiological vitality and need additional treatment and care costs (Manefield and Tinson, 1997; Al-Ani, 2004 and Al-Juboori, 2010). Camel lameness differs from that of cattle and horses owing to its unique

anatomy, biomechanics, geoclimatic adaptations, and use (Gahlot, 2000). There is increasing evidence that oxidative damage contributes to many diseases, such as atherosclerosis, cancer, liver damage, rheumatoid arthritis, immunological incompetence, neurodegenerative disorders, and aging (Dalle-Donne *et al*, 2003; Habif *et al*, 2001). Oxidative stress (OS) is defined as RONS (Reactive Oxygen/Nitrogen species) that exceed the body's antioxidant capacity (Finaud *et al*, 2006).

The body produces RONS as a result of its normal metabolic processes and through exposure to an array of environmental and physiological stressors. The tissue's specific antioxidant defenses and the specific macromolecules targeted by RONS will determine the degree of damage and disease generation that may accompany OS. The total antioxidant capacity of the body provides protection against the excessive production of reactive oxygen

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and nitrogen species (RONS) by cells (Bloomer and Fisher-Wellman, 2008). Endogenous and exogenous compounds contribute to antioxidant capacity (Halliwell and Gutteridge, 1999; Possamai *et al*, 2007). The former recognised antioxidant compounds include uric acid, superoxide dismutase, catalase, and glutathione peroxidase. Over the last decade, various tests for the measurement of OS have been developed to assess the oxidative status of an individual under normal or pathological conditions or after any kind of intervention. By measuring the levels of markers for ongoing oxidative damage in serum and plasma samples, we can get a complete picture of the OS state in the body (Argqelles *et al*, 2004).

There have only been a few studies comparing antioxidant capacity and OS in domestic animals, particularly in racing dromedary camels (Mousa *et al*, 2006). Our study measured (malondialdehyde) MDA as well as nitric oxide (NO) (as markers of OS), super oxide dismutase (SOD), reduced glutathione (GSH), catalase (CAT), and total antioxidant capacity (TAC) levels (as markers of antioxidant status) in lame racing dromedary camels and healthy ones. Moreover, the study monitored the oxidantantioxidant status in lame dromedary camels after 10 days of treatment.

Materials and Methods

Camels' selection and sampling protocol

A total of 315 racing dromedary camels, aged 5.5–8.1 years, were investigated between January and September 2019 in one camel herd in the eastern region of Saudi Arabia. A total of 35 out of 315 racing camels exhibited clinical lameness. Punctured feet and traumatic injuries were diagnosed as lesions responsible for clinical lameness in these racing camels. Bovine hoof testers and walking on sandy, pebbled or hard tracks were used to diagnose lame camels (Gahlot, 2000 and 2007). Moreover, 20 clinically healthy racing dromedary camels were carefully chosen as a control group.

Whole blood samples were collected from clinically lame dromedary camels (N = 35) and the control healthy group (N = 20) for further biochemical analysis. Lame dromedary camels were subjected to a treatment protocol which included the use of non-steroidal anti-inflammatory drugs (NSAIDS) (2.2 mg flunixin per kg of camel body weight, IV injection), cleaning, and disinfection of lesions for five consecutive days, with complete rest of the affected camels.

Evaluation of oxidative stress and antioxidant biomarkers

With the help of commercial ELISA kits (Cayman, USA), malondialdehyde, reduced glutathione, catalase, and superoxide dismutase activities were determined in serum. After nitrate has been reduced to nitrite by the Griess reagent, nitric oxide (NO) is determined as the nitrite concentration in serum. Using sodium nitrite as a standard, the reaction was measured at nm (Ding et al, 1988). A commercial test kit (Bayer diagnostics) was used to measure total serum protein concentration. The NO concentration in serum was measured using a Nmol/mg protein unit. Beers and Sizer (1952) method, CAT activity was measured in the RBC hemolysate. CAT activity was measured by measuring the difference in absorbance per min/mg Hb following the decomposition of H_2O_2 . Spectrophotometric analysis of TAC was conducted using kits supplied by Biodiagnostic®, Egypt.

Data Analysis

All parameters were expressed as mean ± SD. Comparisons in mean were performed by Kruskal-Wallis ANOVA on Ranks followed by Dunn's multiple comparisons. The different means were significant at P<0.05. Statistical analysis was performed using JMP software version 11.0.0 (SAS Institute, Cary, NC, USA). Spearman's rank correlation test was used to investigate the correlation between parameters. Each assay's diagnostic accuracy was evaluated by creating the ROC (receiver operator characteristics) curve and determining the area under the curve (AUC). An AUC of 0.7 to 0.9 was considered moderately accurate, an AUC of >0.9 highly accurate, and an AUC of 1 perfect.

Results

The serum levels of MDA and NO in lame dromedary camels with different causes were remarkably (P 0.0001) higher than those detected in the control healthy dromedary camels (Fig 1). However, we found that lame dromedary camels had significantly lower levels of serum SOD, GSH, CAT, and TAC when compared with the control healthy camels. (Fig 1). The serum levels of MDA, NO, SOD, GSH, CAT, and TAC markers in lame dromedary camels pre-and post-treatment were measured in this study. A significant decline was detected in serum levels of MDA and NO of lame camels after ten days of treatment, whereas the levels of antioxidant markers (SOD, GSH, CAT, and TAC) were significantly increased towards normal values (Fig 2). Spearman's correlation was estimated for the study biomarkers in clinically lame camels and healthy ones and in lame camels before and after 10days of treatment (Table 1). There was a significant appositive correlation between TAC, SOD, GSH, and CAT. However, significant negative correlations were observed between OS markers (MDA and NO) and all tested antioxidants (TAC, SOD, GSH, and CAT) in camels under investigation.1

The diagnostic test characteristics of OS and parameters in racing dromedary camels with clinical lameness were explored in table 2. The ROC curves were created. The AUCs were assessed (Fig. 3) to evaluate the accuracy of each variable in distinguishing diseased and healthy camels. Based on the ROC curves and AUCs, MDA (AUC = 0.910), SOD (AUC = 0.922), GSH (AUC = 0.901), TAC (AUC

Table 1. Correlation matrix using spearman test among different oxidative stress biomarkers in racing dromedary camels with clinical lameness.

| | sMDA | CAT | GSH | SOD | NO | TAC |
|------|--------|--------|--------|--------|--------|-----|
| sMDA | 1 | | | | | |
| CAT | -0.557 | 1 | | | | |
| GSH | -0.527 | 0.524 | 1 | | | |
| SOD | -0.542 | 0.497 | 0.556 | 1 | | |
| NO | 0.589 | -0.613 | -0.515 | -0.558 | 1 | |
| TAC | -0.557 | 0.633 | 0.518 | 0.64 | -0.597 | 1 |

Serum malondialdehyde (sMDA), catalase (CAT), reduced glutathione (GSH), super oxide dismutase (SOD)

= 1), and NO (AUC = 0.994) were similarly highly diagnostic and predictive for treatment response in lame dromedary racing camels.



Fig 1. Box plots displaying variability of malondialdehyde (MDA); catalase (CAT), reduced glutathione (GSH); super oxide dismutase (SOD), nitric oxide (No) and total antioxidant capacity (TAC) in healthy and lame dromedary racing camels.



Fig 2. Box plots elucidating changeability of malondialdehyde (MDA); catalase (CAT), reduced glutathione (GSH); super oxide dismutase (SOD), nitric oxide (NO) and total antioxidant capacity (TAC) in lame dromedary racing camels before and after treatment.

| Table 2. | Diagnostic test characteristics of oxidative stress |
|----------|---|
| | parameters in racing dromedary camels with clinical lameness. |

| Parameters | Threshold | AUC |
|------------------------|-----------|-------|
| sMDA (nmol /g protein) | ≥ 13.48 | 0.910 |
| CAT (U/mg Hb) | ≤ 14.40 | 0.958 |
| GSH (mmol / L) | ≤ 6.05 | 0.901 |
| SOD (U/mg Hb) | ≤ 4.35 | 0.922 |
| NO (nmol/g protein) | ≥ 0.24 | 0.994 |
| TAC (Mm/L) | ≤ 1.15 | 1.00 |

Serum malondialdehyde (sMDA), catalase (CAT), reduced glutathione (GSH), super oxide dismutase (SOD).

Discussion

The clinical signs of lame camels in this study are in concurrence with the clinical picture of lame camels reported in other studies (Gahlot, 2007; Al-Juboori, 2011a and Al-Juboori, 2011b; Al-Juboori, 2013; Mostafa and Khalil, 2018; Mostafa, 2020).

There are several types of stress that athletes of all species encounter, including OS. According to the results presented in this study, circulating OS is generated by increased free radical generation (increased NO levels), lipid peroxidation enhancements (increased MDA levels), combined



Fig 3. Receiver operating characteristic (ROC) curve analysis of malondialdehyde (MDA); catalase (CAT), reduced glutathione (GSH); super oxide dismutase (SOD), nitric oxide (NO) and total antioxidant capacity (TAC) in healthy and lame dromedary racing camels.

with abnormalities of antioxidant status (reduced GSH, SOD, CAT, and TAC) in racing dromedary camels clinically affected by lameness. As far as we know, this study is the first to describe OS status in lame dromedary racing camels. It is known that OS is involved in the pathogenesis of lameness in dairy cows (Al-Qudah and Ismail, 2012; Zhao *et al*, 2015).

In particular, polyunsaturated lipids are prone to oxidation. Biomarkers of lipid peroxidation are considered the best indicators of OS since lipids are one of the most vulnerable substrates to free radical damage (Georgieva, 2005).

During the radical-induced breakdown of polyunsaturated fatty acids, MDA forms. The reaction between MDA and thiobarbituric acid produces thiobarbituric acid reactive substances (TBARS), which facilitates the measurement of these substances by spectrophotometry (Janero, 1990). In this study, increased levels of serum MDA and NO in lame racing dromedary camels under the same environment, diet, training management, and feeding regimen proved that OS influences lameness in dromedary racing camels. In addition, significantly reduced levels of tested antioxidants (SOD, GSH, CAT, and TAC) markers were observed in lame racing dromedary camels, providing yet another support for the notion that oxidative damage may be involved in lameness pathogenesis.

OS is any disturbance in the normal redox state of cells that will cause veritably bad effects due to the yield of peroxides, and free radicals, leading to damage of all factors in the cell, including proteins, lipids, and DNA (Kowaltowski and Vercesi, 1999). Accordingly, OS can cause disturbances in normal mechanisms of the cellular capability to detoxify the reactive interceders or to repair the cell damage (Kowaltowski and Vercesi, 1999). As proved previously and verified in this study, a complex association exists between OS and inflammation. Moreover, OS is a consequence of the imbalance between reactive oxygen species (ROS) and product and antioxidant capacity. This can be because of either heightened ROS generation detected, a disturbed antioxidant system, or a combination of both (as perceived in this study). In the presence of OS, uncontained ROS attacks modify and denature functional and structural molecules, leading to cell injury (Vaziri, 2008).

Comparable to our findings, it was reported that MDA levels were increased in varieties of inflammatory conditions in dromedary camels like acute, and chronic cystitis (Abd Ellah, *et al*, 2012; El-Deeb and Buczinski, 2015), liver abscess (El-Deeb *et al*, 2014), *Coxiella burnetii* infection (El-Deeb *et al*, 2019) and *Trypanosoma evansi* infection (Saleh *et al*, 2009; El-Deeb and Elmoslemany, 2015; El-Bahr and El-Deeb, 2016).

The NO levels in lame dromedary racing camels' cases compared to those in the control group, a statistically highly significant increase (P<0.0001) was observed. NO and peroxynitrite are free nitrogen derivatives among the reactive nitrogen species (RNS) (Tabakoglu and Durgut, 2013). Yarim et al (2006) described NO as a free radical that mediates both physiological and pathological events in the body. Despite its primary role in defending against bacteria, viruses, and parasites, NO has been reported to suppress the immune system. Accordingly, NO may protect or damage tissues depending on its concentration (Bozukluhan et al, 2013). In the presence of bacterial infections, macrophages produce large amounts of nitric oxide and exhibit antibacterial properties (Bozukluhan et al, 2016). A different viewpoint suggests that nitric oxide has anti-inflammatory property (Miranda et al, 2001). A major component of inflammatory diseases is peroxynitrite, a strong oxidising agent in tissues and organs. Sezer and Keskin (2014) described peroxynitrite as a highly toxic form of nitric oxide. According to a other research study, neutrophils released from diseased animals produce high levels of NO and myeloperoxidase, which ultimately leads to nitrotyrosine formation (i.e., protein damage) (Wessely-Szponder et al, 2004).

As detected in this study, increased NO production was also reported in humans with other inflammatory skin diseases and cutaneous infections (Serarslan *et al*, 2005; Bickers and Athar, 2006). In

harmony with our findings, synovial fluid NO levels were significantly higher in 20 arthritic calves than in the control group (Yurdakul and Sartas, 2013). According to Yarim *et al* (2006) and Bozukluhan *et al* (2013) serum NO levels were higher in cattle with foot-and-mouth disease than in the control group, which was attributed to NO release and immune system stimulation.Conclusively, the increase in NO levels in this study suggests that it contributes actively to the development of racing dromedary camel lameness.

Since SOD catalyses the dismutation of superoxide to hydrogen peroxide (Halliwel *et al*, 1993), it is an important first line of defense against pro-oxidants. In this study, the levels of SOD, GSH, CAT, and TAC were significantly decreased in lame camels when compared with controls. Observed reductions in SOD, and CAT activities in the serum of lame racing camels in our study correlate with lower glutathione levels in the serum. The levels of tested antioxidants significantly increased toward normal values following the lameness treatment protocol. The present study provides evidence that levels of examined antioxidants can be used to evaluate the state of OS in lame camels, and to guide the treatment response.

Several methods have been developed to determine total antioxidant capacity (TAC) because it is difficult to measure each antioxidant component separately and their interaction within the plasma. The antioxidant capacity is based on the cumulative effect of all antioxidants present in plasma, and body fluids (Ghiselli *et al*, 2000). In this study, we detected that TAC is significantly decreased in lame dromedary camels and that it positively correlates significantly with all tested antioxidants, which gives a new and easy tool to evaluate the antioxidant status in lame camels, and to monitor treatment response.

The antioxidant state is the product of numerous distinct chemicals and systemic metabolic interactions interacting together (Ghiselli *et al*, 2000). TAC, as a single metric, provides useful information about the dynamic equilibrium between pro-oxidants and antioxidants in the plasma compartment (Ghiselli *et al*, 2000; Cao and Prior, 1998). Comparable to our results, TAC is an effective method for assessing stress in transported calves (Pregel *et al*, 2005). To conclude, evaluating TAC in camels may be a more precise and efficient indicator of camel lameness than measuring a single metric, which may reveal individual variances.

Present investigation has established a link between OS and lameness. Compared with our

results, OS biomarkers were similarly higher in sheep with hoof disorders (Talukder *et al*, 2015). Several inflammatory pathways are known to be activated by changes in the redox state of cattle (Sordillo and Aitken, 2009; Shi *et al*, 2015).

In present investigation it was revealed that the levels of MDA (AUC = 0.910) and antioxidant biomarkers (AUCs ranged from 0.901-1) were considered sensitive and specific biomarkers for differentiating lame camels from healthy ones and this might help monitoring the progress of treatment. This study found that lame camels have higher levels of MDA and NO biomarkers and lower serum levels of SOD, GSH, CAT, and TAC than healthy camels. The results of this study suggest that the measurement of MDA, NO, and antioxidant biomarkers in addition to physical examinations of camels with lameness may be a putative diagnostic and predictive tool for lameness in racing dromedary camels. Moreover, the addition of antioxidants to the treatment protocol may enhance the treatment progress in lame camels.

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PATHOLOGICAL STUDY OF VARIOUS LIVER LESIONS PREVALENT IN CAMELS OF RAJASTHAN

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ABSTRACT

Tissue samples of liver (n=80) were examined from carcasses of camels of either sex, irrespective of age groups and breeds during post-mortem examination from July 2017 to June 2018. Out of these, 36 samples showed gross lesions were processed for subsequent histopathological examination. An overall incidence of liver lesions in camel recorded was and these 45 per cent (36 out of 80). Diverse pathological lesions in liver were abscess, cirrhosis, fatty changes, haemorrhages, haemosiderosis, hepatitis, hydatidosis, hydropic degeneration and necrosis showing occurrence as 2.50, 8.75, 5.00, 6.25, 1.25, 5.00, 5.00, 3.75 and 7.50 per cent, respectively. Cirrhosis (8.75 per cent) and haemosiderosis (1.25 per cent) were reported as the most prevalent and least prevalent pathological conditions, respectively, affecting liver of camels during the study period.

Key words: Camel, liver, lesions, pathology

The Camel is generally considered resistant animal and suffers only few diseases compared to other livestock species (Narnaware et al, 2021). Hepatocellular injury is one of the pathologic condition affecting domestic animals including camels (Belina et al, 2015). The causes of liver lesions in camel are numerous but primarily liver is affected by toxic substances, infectious diseases, parasitic hepatitis, tumours etc. which contribute to hepatobiliary disease, such as hepatic insufficiency (Kitila, 2016). Mehta et al (2012) reported maximum mortality (41.39%) in camel due to involvement of digestive system. Björklund (2014) and Tornquist et al (1991) reported hepatitis and hepatic lipidosis is common pathological findings in camelids. Tharwat et al (2012) performed ultrasound guided hepatic biopsy to diagnose liver pathology in camels.

Various types of pathological lesions found in liver of camel included hepatitis, cirrhosis (El-Mahdy *et al*, 2013; Thrwat, 2020), fibrosis (Hegazy *et al*, 2010) necrosis (Abu Damir *et al*, 1993), non specific hepatic degeneration and fibrosis (Hegazy *et al*, 2010), liver abscess (Aljameel *et al*, 2014) and haemosiderosis. Miscellaneous conditions like degenerative changes as fatty changes, hydropic degeneration and various circulatory disturbances as hyperaemia, oedema and haemorrhages are also common. The frequent pathological findings in various diseases of camel comprise of the involvement of liver. In many instances, such lesions in liver are of great value in diagnosis of camel diseases. The pathological conditions of liver in camel have not so far been studied extensively. Thus study was undertaken to find out gross and histopathology of various liver lesions of camels prevalent in Rajasthan.

Materials and Methods

For the present study, 80 tissue samples of liver were examined from carcasses of camels of either sex, irrespective of age groups and breeds during post-mortem examination from July 2017 to June 2018. Out of these, 36 samples of liver showed gross lesions these were further processed for histopathological examination. All the representative tissue samples were collected in 10% buffered formalin for histopathological examination. The tissues were processed mechanically for paraffin embedding by acetone and benzene technique (Lillie, 1965). The tissue sections of 4-5 microns or micrometer thickness were cut and stained with haematoxylin and eosin staining method as a routine. Van Gieson's special staining method was used for demonstration of collagen fibres (Culling, 1974). The detailed histopathological observations were recorded.

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Results and Discussion

Various liver lesions recorded in present study are placed in Table 1. An overall incidence of various pathological conditions affecting liver was recorded as 45 per cent (36 out of 80) which corresponded well with the findings of Hamza *et al* (2017) which was 45.7 per cent. Liver showed higher incidence of inflammatory conditions, degenerative changes, circulatory disturbances and parasitic infestation.

| S. No. | Type of condition | No. of samples | Percentage | |
|-----------|-----------------------|-------------------|------------|--|
| 1. | Abscess | 2 | 2.50 | |
| 2. | Cirrhosis | 7 | 8.75 | |
| 3. | Fatty changes | 4 | 5.00 | |
| 4. | Haemorrhages | 5 | 6.25 | |
| 5. | Haemosiderosis | 1 | 1.25 | |
| 6. | Hepatitis | 4 | 5.00 | |
| 7. | Hydatidosis | 4 | 5.00 | |
| 8. | Hydropic degeneration | 3 | 3.75 | |
| 9. | Necrosis | 6 | 7.50 | |
| | Total | 36 | 45.00 | |

 Table 1. Incidence of various liver lesions recorded in present study.

Abscess

This condition was recorded in 2.50 per cent cases in present study. A higher incidence was reported by Aljameel *et al* (2014) as 13.5 per cent. Grossly, multiple small white foci containing whitish caseous pus along with congestion and haemorrhages were observed. Microscopically, focal area of necrosis enclosed by thick capsule along with polymorphonuclear leucocytic infiltration (Fig 1) was seen. These changes were in agreement with earlier findings of El-Mahdy *et al* (2013), Belina *et al* (2015) and Terab *et al* (2021).

This condition might be due to pyogenic bacterial infections or fascioliasis and secondary bacterial complication (Belina *et al*, 2015). Liver abscesses are found in CLA or pseudotuberculosis infection (Terab *et al*, 2021).

Cirrhosis

The occurrence of cirrhosis was 8.75 per cent in present study whereas Jamshidi and Zahedi (2014) found it as 10 per cent.

Grossly, affected liver was reduced in size and was firm and difficult to cut. Microscopically, presence of chronic fibrosed inflammation confined to the areas extending only a short distance beneath the capsule (Fig 2), presence of fibrous bands running in between parenchyma along with little lymphocytic infiltration and perivascular fibrosis mainly in portal area was observed. These findings were in close approximation to the observations reported by Singh (1998) and Ibrahim *et al* (2021).

Cirrhosis was frequently noticed concomitant with parasitic condition, however, in many cases contributory factors could not be incriminated. Ibrahim *et al* (2021) reported severe fibrosis in hepatic torsion in camels.

Fatty Changes

This condition was recorded in 5.00 per cent cases. A higher incidence was (20%) observed by El-Mahdy *et al* (2013). Grossly, liver appeared pale, soft and greasy with rounded edges. Histopathologically, the hepatic cells showed fatty changes with presence of fat droplets as clear round spaces and granular cytoplasm (Fig 3) were in agreement with earlier findings of Singh *et al* (2006) and Zakian *et al* (2016).

Ketosis may be one of the possible causes of fatty changes. Other factors involved copper sulphate poisoning (Damir *et al*, 1993) or PPR infection (Zakian *et al*, 2016) or Brucellosis (Abdirahman, 2020).

Haemorrhages

This condition was recorded in 6.25 per cent cases. A lower incidence (2.91%) was reported by Singh (1998). Grossly, large and irregular superficial areas and pin-point haemorrhagic areas of variable sizes were seen on liver. Microscopically, severe haemorrhages replaced the hepatic parenchyma along with congestion, necrosis and presence of inflammatory infiltration in adjacent parenchyma were in agreement with observations of Singh (1998) and Ibrahim *et al* (2021).

This condition might be due to trauma or Aflatoxin B1 residues (Al-Gabri, 2013) or hepatic torsion (Ibrahim *et al*, 2021).

Haemosiderosis

This condition was recorded in 1.25 per cent cases which corresponded well with the findings of Singh (1998) who found it 1.45 per cent. Grossly, the liver showed brownish tinge due to the presence of haemosiderin in hepatic cells. Microscopically, haemosiderin as golden coloured pigment filled in phagocytes (Fig 4) was in agreement with Singh (1998) and Ibrahim *et al* (2021).

This condition might be observed in scars, in areas where haemorrhages had occurred or in chronic



Fig 1. Microphotograph of liver abscess showing focal area of necrosis enclosed by thick capsule along with polymorphonuclear leucocytic infiltration. H&E 100X.



Fig 2. Microphotograph of liver showing red coloured fibrous tissue along with thickened glisson's capsule. Van Gieson's 100X.



Fig 3. Microphotograph of liver showing fatty changes indicating fat droplets as clear round spaces. H&E 200X.



Fig 4. Microphotograph of liver showing haemosiderin as golden coloured pigment filled in phagocytes. H&E 400X.



Fig 5. Microphotograph of liver showing multiple cysts with eosinophilic lamellated wall and presence of faint pink homogenous substance along with hepatocellular degeneration. H&E 100X.



Fig 6. Microphotograph of liver showing hydropic degeneration as small clear vacuoles along with cellular infiltration. H&E 200X.

passive hyperaemia (Runnels *et al*, 1976). Ibrahim *et al* (2021) reported this condition in hepatic torsion in camel.

Hepatitis

This condition was recorded in 5.00 per cent cases. A higher incidence (20%) was reported by El-Mahdy *et al* (2013). Grossly, the liver was markedly enlarged and centres of lobules were opaque, grayish or yellowish. Microscopically, infiltration of lymphocytes and few neutrophils along with areas of hepatocellular degeneration was seen. These changes were in agreement with earlier findings of Seboussi *et al* (2009), El-Mahdy *et al* (2013) and Tavella *et al* (2018).

The inflammation of liver might be caused by various conditions including toxicity of diminazene aceturate (Homeida *et al*, 1981) or selenium toxicity (Seboussi *et al*, 2009).

Hydatidosis

This condition was recorded in 5.00 per cent cases. Almost similar findings were reported by Mirzaei *et al* (2016) as 4.54 per cent. Grossly, grayish white detectable hydatid cysts of variable sizes were located either single or multiple on the surface and embedded in the hepatic parenchyma which was in agreement with earlier report of Osman (2008). Microscopically, cyst wall appeared as outer eosinophilic lamellated layer with presence of faint pink homogenous substance within the lumen (Fig 5) was in harmony with those mentioned by Tantawy (1992) and Borai *et al* (2013).

Hydatidosis in liver might be due to the fact that liver possesses great capillaries site encountered by the parasite, which adopt the portal vein route and primarily hepatic filtering system sequentially (Kebede *et al*, 2009). Nourani and Salimi (2013) reported hydatid cyst as the most common hepatic lesion in liver of camels.

Hydropic degeneration

This condition was recorded in 3.75 per cent cases. A higher incidence (18.67%) was recorded by El-Mahdy *et al* (2013). Microscopically, the liver cells increased in size due to accumulation of fluid. Small clear vacuoles seen within the cytoplasm along with hepatocellular degeneration and cellular infiltration (Fig 6) which were in agreement with Singh *et al* (2006), El-Mahdy *et al* (2013) and Tavella *et al* (2018).

This condition might occur due to pathogenic infections such as Hepatitis E virus 8 infection (Wang

Necrosis

This condition was recorded in 7.50 per cent cases and a higher incidence (18.1%) was reported by Salem and Azza (2011). The gross findings were presence of grayish necrotic foci on surface. The involved hepatocytes showed dense, granular and opaque cytoplasm with coagulative necrosis. Similar findings were reported by Borai *et al* (2013) and Zakian *et al* (2016).

This presumably may be due to involvement of some toxins in feed possibility fungal, bacterial or plant toxins or chemicals playing some role in causing the condition.

Groom *et al* (1995) reported hepatic-necrosis in an alpaca which was associated with halothane anaesthesia possibly due to hepatotoxic effect of halothane on liver.

In present study the tumours of liver were not seen. However, intrahepatic cholangiocarcinoma in an 18-year-old male camel has been reported and it was composed of gland-like structures and/or solitary islands of neoplastic cells in the tumoural stroma (Birincioglu *et al*, 2008).

Most of the pathological conditions of liver in camels are diagnosed during postmortem examination. However, a more detailed study of liver lesions is required to identify these pathological conditions during clinical examination through modern diagnostic tools.

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EPIDEMIOLOGICAL INVESTIGATION ON GENITAL MYIASIS OF BACTRIAN CAMELS IN PARTS OF INNER MONGOLIA, CHINA

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ABSTRACT

The incidence and prevalence of Bactrian camel genital myiasis seriously endanger the health of camels and hinder the healthy development of Bactrian camel industry. In order to further understand the epidemic situation of the disease in main production areas of Bactrian camels in Inner Mongolia, China, from May to October 2021, 3 areas with severe incidences in Alxa Left Banner, Urad North Banner and Durbed Banner were selected for epidemiological investigation. Total of 2038 female camels in 21 camel herds were investigated. The results showed that the overall prevalence rate was 26.6%, the highest incidence group reached 82.6%, while the lowest group was only 1.4%. The prevalence rates of Bactrian camel genital myiasis in Alxa Left Banner, Urad North Banner and Durbed Banner was 28.0%, 23.8% and 23.7%, respectively. The pathogen of Bactrian camel genital myiasis is *Wohlfahrtia magnifica*, and the highest prevalence often occurs in July to August in each year. The prevalence rate in female camels under 5 year-old was lower than that of in adult camels, and it was highest in female camels between 5-15 years old and give birth 2-4 times and no deaths were found. The prevalence rate in free-range female camels. Camels grazing on pastures near the lakes and riverbanks had higher morbidity than that of in camels grazing on other pastures. Therefore, the morbidity of genital myiasis in Bactrian camels is significantly affected by age, number of deliveries, feeding method, different regions and pasture types.

Key words: Bactrian camel, epidemiology, genital myiasis

Genital myiasis in Bactrian camels is caused by larva of Wohlfahrtia magnifica in the external reproductive organs of female camels. Wohlfahrtia magnifica (Diptera: Sarcophagidae) is mainly found in Southeastern Europe, southern Russia, Asia, the Middle East and northern Africa (Pirali Kheirabadi et al, 2014). W. magnifica infests a wide range of animals, infects their genital tract and other open wounds. Six flocks of sheep infested with genital myiasis have been reported in China, and the identified pathogens were all W. magnifica (Li et al, 2019). Three cases of genital myiasis in a goat, a ram and a dog have been reported in Italy (Gaglio et al, 2011). In Fars province of Iran, 61% of all animal wound myiasis were caused by larvae of W. magnifica (Rafinejad et al, 2014). A case of gingival myiasis was reported in Xinjiang, China, and the pathogen was identified as W. magnifica (Zhang, 2005).

The present study investigated the prevalence of Bactrian vaginal myiasis in some areas of Inner Mongolia, China.

Materials and Methods

Survey area

The grassland types in Alxa Left Banner, Urad North Banner and Durbed Banner are mainly desert and semi-desert steppe, with scarce water resources and sparse vegetation. The present investigations was carried out in above 3 comparable regions with similar landscape and different soil conditions and water sources.

Epidemiological survey

According to the life cycle of flies, comprehensive investigation was carried out by visiting farmers, distributing standardised questionnaires and electronic questionnaires on May to October in 2021. The content of the questionnaires include the basic information of the herdsman, the number and age of infected she-camels, and the rearing environment. All survey data was summarised and statistically analysed.

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Symptom assessment

All of the investigated camel herds were clinically examined visually, then the infected camels were subsequently restrained using ropes one by one and careful inspection was carried out to the swelling and damage of vulva, surrounding blood stains and presence of larvae in the wound and their number.

Sample collection

Five infected camels were randomly selected from each of 3 regions. Ten larvae at different stages were collected from each camel, and put them into formalin, respectively. Then, 10 third-stage larvae were collected from each of the 5 infected camel, and put them into a foam box with a length of 20 cm and a width of 10 cm that has been pre-installed with local sand, and spray a small amount of water on the surface of the sand to make the surface sand slightly wet. Finally, the box was covered with gauze, took them back to the laboratory, and cultivated it at room temperature (about 26°C), until the larvae emerged into flies.

Morphological observation

Stereo Discovery.V20 microscope was used to observe the morphology of the 1st, 2nd and 3rd stage larvae (Fig 2) and the artificially hatched adult flies from 3 different regions.

Results

Morphological observation of larva

Clinical examination showed that the larva of 3 developmental stages existed at the wound site of most infected camels. The length of 1st instar larvae was 1-3 mm, 2nd instar larvae was 3-12 mm, and 3rd instar larva was 12-20 mm (Fig 1).

The larvae had 1 pseudoscolex, 3 thoracic segments, 8-10 abdominal segments, anus and other structures. The 9th and 10th abdominal segment were located on the ventral surface of the 8th abdominal segment, which was usually not obvious, and the 10th segment was the anal plate. The pseudoscolex had a pair of downwardly curved and sharp mouth hooks, and there was a long labrum between the two mouth hooks of the first stage larvae, but the labrum of the second stage larvae has disappeared. This was consistent with the observations of An et al (2019). Ring spines were covered on the dorsal and ventral sides of the larvae at each stage, and the number of spines were decreased significantly from the 7th abdominal segment. A deep cup-shaped depression was observed on the posterior surface of the 8th abdominal segment with several pairs of conical fleshy processes at the edge of the depression.

Morphological observation of adult flies

The 3rd instars were successfully eclosioned after 15-20 days in laboratory, and their morphological characteristics were observed by Stereo Discovery.V20 stereomicroscope (Fig 3).

The adult fly was 9-13 mm in length, with naked compound eyes and dense silvery powder on parafrontalia, parafacialia and posterior eyes. When viewed from the top of the head, the width of the frons was about half that of the head, and when viewed from the side, the height of the bucca was about half that of the eye. Occiput expanded backwardly. Antennae were slightly shorter, the length of the third section was about 1.5 times that of the second section, and there were arista at the base of the third section. Thoracic segment had black background and grey powder, 3 black vertical stripes on the tergite. Lower squama was about 2 times of the upper squama. The abdomen was long and oval, with distinct black patches, and spots like water drop. The central black patches on the 3rd and 4th tergites were large and were connected to the 1st and 2nd syntergite forward, and the 5th tergite had smaller black patch. According to the characteristics of the adult fly, and its larvae were obligate parasitic warm-blooded vertebrates (Fan, 1994). The adult flies were identified as W. magnifica. The pathogen of genital myiasis of Bactrian camels in these 3 areas was W. magnifica.

Clinical manifestation

According to the local lesions of affected camels, these were grouped into lightly, moderately and heavily infected camels (Fig 4). In lightly affected camels, the vulva was slightly swollen, a small amount of blood stains could be seen in the tail and hind legs, lesions caused by larvae can be seen at or near the inner margin of the vulva mucosa, with a diameter between 1-3 cm, and no secondary infection was seen. Usually less than 100 larvae were counted per camel, and no repeated infection appeared after application of pesticide.

In moderately infected camels, the vulva was significantly swollen, accompanied by bloody and fibrinous excretion, lesions and septic wounds can be seen at the vulva, with a diameter between 3-8 cm. There were 100-200 larvae in perineal area and vaginal tissue. The camels had pain response, continuous rubbing of wound area, and partial anorexia. A small number of camels had recurrence of infection after treatment with pesticide.



Second instar Th Fig 1. The body length of larvae at each stage.



Fig 2. The larvae of each stage were observed under stereoscope.

(a) First instar, (b) Head of first instar, (c) Second instar, (d) Head of second instar, (e) Third instar, (f) Head of third instar. 1 is pseudoscolex, 2-4 is thoracic segment (usually 3 segments), 5-12 is abdominal segment (usually 8~10 segments), 13 is mouth hooks, 14 is Labrum, and 15 is Spine.

In heavily infected camels, the vulva was severely swollen, accompanied by bloody and purulent excretion, severe lesions and septic wounds were seen at the vulva, with a diameter greater than 8 cm. Usually, more than 200 larvae were found in multiple larger wounds. The genital area appeared strongly deformed and swollen. All infected camels showed obvious restlessness, loss of appetite, malnutrition, prolonged disease course, and repeated infection after treatment. Among infected camels, about 30% were lightly infected and rest of them were moderately or heavily infected camels, and most of heavily infected camels remained infected whole year.

Epidemiological Statistics

Total of 2038 she-camels were investigated in 21 camel herds, with a minimum of 23 camels, a maximum of 300 camels per herd examined. Among



Fig 3. Stereoscopic observation of artificially eclosioned fly (a) Side view, (b) Head, (c) Dorsal view, (d) Ventral view of the abdomen. (a): 1. Head, 2. Thoracic, 3. Abdomen, 4. Front legs, 5. Middle legs, 6. Hind legs, 7. Upper squama, 8. Lower squama, 9. Halter, 10. Terminalia, 11. Palpi, 12. Proboscis. (b): 1. Compound eyes, 2. Ommatidia, 3. Interfrontalia, 4. Parafrontalia, 5. Parafacialia, 6. Bucca, 7. The first section of the antenna, 8. The second section of the antenna, 9. The third section of the antenna, 10. Arista, 11. Vibrissae, 12. Inter-frontal bristles. (c): 1. Mesothorax prescutum, 2. Scutal sulcus, 3. Mesothorax postscutum, 4. Scutellar suture, 5. Scutellum, 6. 1st and 2nd abdominal segment, 7. 3rd abdominal segment, 8. 4th abdominal segment, 9. 5th abdominal segment, 9. 1st and 2nd abdominal segment, 8. 3rd sternite, 4. 4th sternite, 5. 1st and 2nd abdominal segment, 8. 5th abdominal segment, 9. Anus, 10. Spiracles.



LightModerateSevereFig 4. Clinical manifestations of lesions with different degrees of infection

them, a total of 491 camels were infected, and the prevalence rate found was 26.6% (Table 1). No deaths occurred. A total of 1151 she-camels from 14 camel herds were investigated in Alxa Left Banner, and 280 were infected, with a prevalence rate of 28.0%. A total of 747 she-camels were investigated from 4 camel herds in Durbed Banner, and 181 were infected, with a prevalence rate of 23.7%. A total of 140 she-camels were investigated from 3 camel herds. In Urad North Banner 30 were infected, with a prevalence rate of 23.8%. Therefore, the prevalence rate was similar in the 3 regions, and the earliest cases appeared in mid-May, then gradually increased in June and July, peaked in July and August, then gradually decreased in September and almost ended in mid-October.

Among the 21 camel herds surveyed, 15 were free-range camel herds on natural pastures, 5 were semi-free-range camel herds, and 1 was a completely house-raised camel herd. The highest incidence rate reached 82.6%, which was one of the free-range camel group; and the lowest incidence rate was only 1.4%, which was a semi grazing camel group. The average prevalence rate of grazing camels, semi grazing camels and completely house-raised camels



Fig 5. Average prevalence rate of female camels in different feeding methods.



Fig 6. Average prevalence rate of female camel in different grassland types.

was 31.7%±16.2%, 15.8%±9.0% and 2.9%, respectively (Fig 5).

Among the 15 free-range camel herds, 11 camel herds were distributed in the arid grasslands of the Gobi, drinking well water; 4 camel herds were distributed in desert grasslands, with plenty of natural water sources such as lakes and river beaches. The prevalence of camels distributed in desert grasslands with lakes and river beaches was generally higher than that of camels in the Gobi steppe (Fig 6).

We further analysed 277 infected camels and found that the youngest camel infected was 7 months old and the oldest was 20 years old. Three infected camels were 1 year age, 25 camels were between 1 and 5 years and 249 camels were over 5 years of age.

We further analysed the parity of 52 infected camels and found that there were 6 camels that had not produced calves, the rest were multiparous female camels, and the female camels who had given birth to 2 calves had the highest prevalence rate (Table 2).

Discussion

After artificial eclosioned and morphological observation, the maggots collected in this survey were identified as W. magnifica. This was similar with the epidemiological investigated results of vaginal myiasis of Bactrian camels by Huhe et al (1994) in Alxa Left Banner. This indicates that vaginal myiasis of Bactrian camels caused by the larva of the W. magnifica has been prevalent in these areas for a long time. A case of genital myiasis of Bactrian camel caused by Wohlfahrtia magnifica was reported in southwest of Iran (Sazmand and Joachim, 2017). An outbreak of genital myiasis was reported in 13 Bactrian camel herds in Mongolia, and the pathogen was identified as W. magnifica (Schumann et al, 1976). In 2009, Schnur et al (2009) investigated the myiasis of livestock in Israel and speculated that the pathogen of 2 cases of camels genital myiasis may be the W. magnifica.

The clinical symptoms observed in this investigation were similar to those described by Jiang (2016) who also found swollen vulva, constant discharge of blod and channels formed by fly maggots in inner wall of vagina. In this investigation, only 3 cases were found with serious genital tract infection extending to the anus, and no infection was found in male camels.

In Alxa Left Banner, a total of 1151 female camels were investigated and the average prevalence rate was 28.0%, which was about 20% lower than the result of ErD *et al* (2012).

Table 1. Statistics on genital myiasis of Bactrian camels in part areas of Inner Mongolia.

| Areas | No. of herds | Total No. of investigated | No. of infected | Average prevalence rate (%) |
|-------------------|--------------|---------------------------|-----------------|--------------------------------|
| Alxa Left Banner | 14 | 1151 | 280 | 28.0±19.2 |
| Durbed Banner | 4 | 747 | 181 | 23.7±5.2 |
| Urad North Banner | 3 | 140 | 30 | 23.8±13.5 |
| Total | 21 | 2038 | 491 | 26.6±16.7 |

Table 2. Relationship between the number of produced calves and prevalence rate.

| Number of produced calves | 0 | 1 | 2 | 3 | 4 | 5 | 6 | 7 |
|---------------------------|------|------|------|------|------|-----|-----|---|
| prevalence rate (%) | 11.5 | 15.4 | 30.8 | 17.3 | 15.4 | 5.8 | 3.8 | 0 |

The occurrence and development of myiasis are closely related to the life history of W. magnifica. It has been reported that the W. magnifica are in the form of pupae in winters and temperature is the key to their successful eclosion (Li, 2020). Hot weather from July to August and increased rainfall is ideal for the reproduction of flies, resulting in a rapid increase in the prevalence rate of genital myiasis. The average prevalence rate was higher in camels distributed near river shoals, hills and lake basins in present study. The prevalence rate of grazing female camels (31.7%) was significantly higher than that of semi grazing camels (15.8%), and this was again obviously higher than that of house raised camels (2.9%). This was mainly due to house raised camels have a small range of activities, access to clean food and water. In addition, the pens were regularly cleaned, hence there was lack of breeding conditions for flies, and the chance of camels contacting with flies was greatly reduced, thus occurrence of the disease was less.

It has been reported that the *W. magnifica* chooses to larviposition in the vagina of a female camel, which may be related to its antennae sensing surrounding chemical signals (Wang, 2019). Local farmers also said that camels with energy imbalance or postpartum vaginal inflammation were more susceptible to genital myiasis. Infection rates in juvenile camels are lower than in adult camels in most camel herds, and only 3 juvenile camels were found be infected during this investigation. This survey found that the prevalence rate of female camels over 5 years and with 2~4 parities was significantly higher than other camels.

Much attention should be paid to the prevention and control of this disease. Huhe *et al* (1994) used fly maggots powder to treat vaginal myiasis in Bactrian camels. Strengthening farmer's awareness of the disease and rational use of drugs are also helpful to control the disease and this would promote the healthy development of camel husbandry and impart economic benefits to the camel farmers.

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EPIDIDYMAL BASED CHANGES IN SPERMATOZOA OF DROMEDARY CAMELS

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ABSTRACT

This study was aimed to declare the role of epididymal passage on semen features, DNA integrity and ultrastructures changes in dromedary camel. The testes with attached epididymis of mature dromedary camels (n=50) were collected during the rutting season from December to April. The harvested spermatozoa from the three-main anatomical epididymal segments (Head, body and tail) were assessed for semen characters, DNA integrity as well as, ultra-structural changes. A significant difference in semen features (individual motility, sperm count, membrane and acrosome intactness, viability, normality, maturity, abnormalities and acrosome length and perimeter) among different epididymal segments. Spermatozoa from epididymal tail showed a significantly (p<0.05) lower DNA fragmentation than those collected from head segment while agarose gel electrophoresis revealed non-significant difference in DNA intensity between spermatozoa from the three epididymal regions. Ultra-structures of the epididymal spermatozoa showed changes in acrosome shape, sub-acrosomal space, chromatin condensation and protoplasmic droplet during epididymal passage. The protoplasmic droplets varied in size, density and position with the epididymal segments. In conclusion, epididymal passage (from the head to the tail) is an essential pre-request for dromedary camels' spermatozoa to attain high fertilising capacity through its great influence on spermatozoa characteristics and the fine cytological structures.

Key words: DNA integrity, dromedary camel, epididymis, spermatozoa, ultra-structures

Collection of epididymal spermatozoa received an increasing interest by many researchers to be adopted for several assisted reproductive techniques (El-Badry et al, 2015; Scholkamy et al, 2016). Sperm cells obtained from any epididymal segment have been assessed (Tajik et al, 2008). Epididymal spermatozoa recovery from slaughtered/dead animals, cryopreservation and subsequent IVF helps to preserve the genetic material either from highly productive animals and/or from endangered species (Martins et al, 2007a). Researchers studied acceptable motility and viability of spermatozoa recovered from the epididymis which have been maintained at room temperature or 5°C in camel (Waheed et al, 2011; Shahin et al, 2021), bull (Martins et al, 2009) and stallion (Muradás et al, 2006). However, researchers found that quality of epididymal spermatozoa varied according to breeding season (Abd and Ibrahim, 2014), temperature (Lone et al, 2011) and epididymal segment (Waheed et al, 2011; Rashad et al, 2018).

The current study was aimed to record the changes in semen features, DNA integrity and ultrastructures in relation to epididymal segment in mature dromedary camels during rutting season.

Materials and Methods

Epididymal semen collection and evaluation

Testes and epididymis (n=50) were collected from apparently healthy slaughtered camels aged 5 to 10 years during the rutting season (December - April). The epididymis was dissected, rinsed with 0.9% saline (Yu and Leibo, 2002) and epididymal anatomical segments (head, body and tail) were distinguished (Zayed et al, 2012). Each epididymal parts was incised and the spermatozoa were collected separately.

Semen evaluation

Sperm motility

The sperm individual progressive motility was determined by light microscope (×40) on a warm stage at 35°C (Melo et al, 2005).

Sperm count

Sperm count was determined with an improved Neubauer haemocytometer chamber after dilution with coloured hypertonic saline solution according to Atiq *et al* (2011).

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Sperm viability and abnormality

The sperm viability and morphology were evaluated in Eosin (5%) and Nigrosin (10%) stained film sand examined under oil immersion lens (×100) according to Skidmore *et al* (2013).

Plasma membrane integrity

Plasma membrane integrity was assessed by hypo-osmotic swelling test (HOS test) as described by Jeyendran *et al* (1984) with some modifications (Zubair *et al*, 2013). Briefly, 10 µl of each semen sample was mixed with 90 µl of a pre-warmed hypo-osmotic solution (0.735 g of sodium citrate dihydrate and 1.351 g of fructose in 100 ml of de-ionised water) and incubated at 37°C for one hour. The positive HOS cells indicated by swelling and coiling of the sperm tail (Lodhi *et al*, 2008).

Acrosome integrity evaluation

The rate of spermatozoa acrosome integrity was determined using Giemsa stain (\times 100) as described by Chowdhury *et al* (2014).

Evaluation of DNA fragmentation

Acridine orange technique

Acridine orange stain was used to assess DNA integrity of the harvested epididymal spermatozoa as described by Martins *et al* (2007b). Damaged DNA gave red or orange fluorescence and normal double-strand DNA structure gave green fluorescence (Andrazek *et al*, 2014).

Gel electrophoresis

DNA was extracted from spermatozoa collected from the three regions of epididymis according to Trommelen *et al* (1993) with some modifications (Weyrich, 2012).The concentration and purity of extracted genomic DNA were determined spectrophotometrically (BIO RAD, USA).

Transmission electron microscopy (TEM)

Small blocks for spermatozoa from each epididymal segment were initially fixed for 2-3 h with 2% glutaraldehyde in PBS, washed three times with PBS (pH 7.4) for 5 min at 4°C and re-fixed in 1% osmium tetroxide for 1-2 h at 4°C (Boonkusol *et al*, 2010). All samples were dehydrated in ascending grade of ethanol (50, 70, 90 and 100%) and propylene oxide for 1 h and embedded in epoxy resin. Ultrathin sections were cut using the Leica EM UC6 ultramicrotome and stained with uranyl acetate and lead citrate.

Statistical analysis

Data (expressed as mean \pm SE) were statistically analysed with one-way ANOVA followed by Tukey (HSD) test using IBM-SPSS for Windows (Ver. 21, 2017). The statistical significance was noted (P<0.05).

Results

Epididymal semen features

The epididymal semen characteristics in dromedary camels reorded in present study are presented in table 1.

Epididymal spermatozoa motility (P< 0.01), count (P< 0.001), membrane integrity (P< 0.0001), acrosome intactness (P< 0.005), viability (P< 0.05), maturity (P< 0.0001), normality (P< 0.0001) varied markedly between its compartments. There was a tremendous improvement in all previous mentioned parameters in epididymal tail compared with head and body parts. Moreover, the rate of sperm head (P< 0.005) and tail (P< 0.001) abnormalities greatly reduced in body and tail of epididymis in comparison with head segment. Acrosomal length and perimeter were highly significant (P<0.001) between epididymal segments.

Epididymal sperm DNA fragmentation

DNA fragmentation rate as examined by acridine orange showed a tendency (P=0.099) of variation between epididymal segment (Fig 1). Epididymal spermatozoa from head region possessed higher (P<0.05) fragmented DNA than those from the tail region.

The intensity of extracted sperm DNA did not show any variation between epididymal segments by gel electrophoresis (Fig 2).

Epididymal sperm ultra-structure

Alternations in spermatozoa ultra-structural during epididymal transit were mainly noticed in the acrosome shape, sub-acrosomal space, nuclear chromatin condensation and protoplasmic droplets (Figs 3-4). The acrosome appeared projected anteriorly at head segment, but the acrosome projection was absent at the tail segment. The sub-acrosomal space decreased progressively in spermatozoa from head to tail of epididymis (Fig 3 e, f). Plasma membrane of most spermatozoa was noticed somewhat elevated at epididymal tail region. Spermatozoa with a homogeneously densely packed nucleus were predominant in the tail of the epididymis than upper segments (Fig 4a-c). The protoplasmic droplets were numerous and dense in appearance in the head

Table 1. Epididymal spermatozoa features in dromedary camels.

| Item | Head | Body | Tail | P value |
|---|--------------------------|--------------------------|---------------------------|---------|
| Spermatozoa motility (%) | 13.33±2.25 ^c | 39.17±1.68 ^b | 58.13±2.82 ^a | 0.01 |
| Sperm cell count (×10 ⁶ /ml) | 58.75±10.87 ^b | 96.63±16.64 ^b | 224.70±24.86 ^a | 0.001 |
| Membrane integrity (%) | 70.58±2.06 ^b | 83.71±0.99 ^a | 87.28±0.87 ^a | 0.0001 |
| Acrosome integrity (%) | 90.61±0.45 ^b | 91.53±0.58 ^b | 95.68±0.99 ^a | 0.005 |
| Livability (%) | 49.95±1.35 ^c | 73.65±1.58 ^b | 82.84±2.97 ^a | 0.05 |
| Immaturity (%) | 19.08±1.06 ^a | 11.60±0.89 ^b | 8.00±0.78 ^c | 0.0001 |
| Sperm normality (%) | 47.07±2.31 ^c | 55.73±1.78 ^b | 66.67±2.47 ^a | 0.0001 |
| Head abnormality (%) | 10.21±2.50 ^a | 4.87±0.68 ^b | 2.94±0.46 ^b | 0.005 |
| Tail abnormality (%) | 41.91±1.82 ^a | 39.02±1.75 ^a | 30.38±2.24 ^b | 0.001 |
| Acrosome length (µm) | 4.76±0.13 ^a | 4.27±0.06 ^b | 4.00±0.07 ^c | 0.001 |
| Acrosome perimeter (µm) | 19.02±0.28 ^a | 17.70±0.14 ^b | 17.00±0.18 ^c | 0.001 |
| DNA fragmentation % | 1.62±0.14 ^a | 1.42±0.21 ^{ab} | 1.09±0.36 ^b | 0.005 |

Data was presented as mean ± SE (n=50). Values with different superscript letters within the same row were significantly different.

region, few and dark in the body region and few and light in the tail region. Protoplasmic droplets were situated at a higher position of sperm tail and centered around axoneme at head and body segments. Yet, few spermatozoa showed eccentric position around axoneme. Protoplasmic droplets at tail segment mostly situated at distal position and often at the mid-way of sperm tail and eccentrically placed around the axoneme (Fig 4d-e).

Discussion

The current investigation proved that progressive sperm motility radically increased from the epididymal head to tail and this came in accordance with former studies in camel (Waheed *et al*, 2011; El-Badry *et al*, 2015), bull and ram (Amann, 1987), horse (Johnson *et al*, 1980) and donkey (Contri *et al*, 2012). These findings slightly matched with that mentioned by El-Badry *et al* (2015) for the spermatozoa from the epididymal tail and body and slightly lower for spermatozoa from epididymal head. The motility percentage of spermatozoa from tail value was also close to those reported by Turri *et al* (2013).

The present study showed that epididymal sperm count was higher in tail segment than in body and head segments. These values matched with those of Ibrahim *et al* (2012), who claimed that the epididymal tail acts as sperm depot in dromedary camel. This finding was in a strong agreement with Bitto and Okpale (2006), Ahemen and Bitto (2007), Ugwu (2009) and Ibrahim *et al* (2012), but not in agreement with finding of Osman and El-Azab (1974), who indicated that the camel epididymal body incubated more spermatozoa than head and tail. The variations were perhaps due to different harvesting

method where dissection was associated with high sperm count.

In our study, there was significant difference in the sperm livability percentage among the three epididymal segments. This finding was not in agreement with Tajik *et al* (2008) and El-Badry *et al* (2015) in dromedary camel. Moreover, in the present study, live sperm percentage from epididymal tail was slightly higher than that recorded by Ziapour *et al* (2014) and El-Badry *et al* (2015). Nevertheless, the mean sperm livability rate herein was slightly lower in harvested spermatozoa from epididymal head and body than that recorded by El-Badry *et al* (2015).

The present research showed that sperm normality rate was higher in epididymal cauda than corpus and caput while the sperm deformities were higher in epididymal head and body than the tail. Tingari et al (1986) found that the percentage of spermatozoa with protoplasmic droplet was higher in epididymal head than body and tail. This finding was in a strong agreement with McKinnon et al (1994). In contrary, El-Badry et al (2015) recorded that the morphologically abnormal sperm percentage did not vary between the three epididymal segments and the proportion of spermatozoa with protoplasmic droplets was higher in the cauda than in the corpus or caput epididymis. Nevertheless, Tajik et al (2008) found no significant difference in the percentage of spermatozoa with protoplasmic droplets between three regions of the epididymis. Some authors reported that cytoplasmic droplets in sperm cells might be considered as an abnormality (Bravo et al, 1997; Flores et al, 2002), while others didn't agree with them (Tingari et al, 1986).


Fig 1. Representative photomicrograph for sperm DNA fragmentation stained with acridine orange stain and examined by florescent microscope. (A) refers to sperm with non-fragmented (emitted green fluorescence) DNA while (B) refers to sperm with fragmented DNA (emitted variable shades of fluorescence from yellow-green to red).

Former works considered the assessment of sperm plasma membrane integrity by the HOS test an indication of male fertility (Revell and Mrode, 1994; Perez-Llano *et al*, 2001). The present study showed that the proportion of sperm cells with an intact plasma membrane was higher for sperms from epididymal tail than head and body. The recorded values here were higher than that reported by El-Badry *et al* (2015) for camel epididymal sperm cells and Ziapour *et al* (2014) for camel ejaculatory sperms. This difference may be due to the method of evaluation.

The current study showed that percentage of spermatozoa with intact acrosome was higher in epididymal tail than those from body and head. These results were marginally higher than that recorded by El-Badry *et al* (2015), who noticed that there were no significant differences among spermatozoa with an intact acrosome between epididymal parts. Also, Morton *et al* (2010) recorded that large proportion of alpaca epididymal semen had an intact acrosome. Our study revealed that there was a very highly significant difference between the acrosome lengths of spermatozoa from different epididymal regions. Similar values were recorded by Osman and Plöen (1986), although these values were lower than that reported by Abdel-Raouf and El-Naggar (1965).

In this study, the epididymal sperm DNA didn't show differences in DNA intensity between epididymal compartments though nuclear





Fig 2. (A)Agarose gel stained with ethidium bromide showed sperm cell DNA extraction product. M: 100-bp ladder. Lanes: H (1-5), B (1-5) and T (1-5) represented DNA extracted from spermatozoa collected from head, body and tail of camel epididymis, respectively. Fig 2(B): Computer aided DNA band density assessment of sperm cell DNA extraction product.



Fig 3. Representative transmission electron micrographs showed sagittal sections at camel epididymal spermatozoa parts. (H) sperm head, (mp) mid piece, (ms) mitochondrial sheath, (pp) principle piece and (EP) end piece. Notice the wide sub-acrosomal space (Fig 3e) in camel epididymal spermatozoa (arrows) that became ultimately disappeared at final epididymal transit (Fig f).



Fig 4. Representative transmission electron microscopic images of the changes in camel spermatozoa nuclear DNA decondensation (a-c) and protoplasmic droplets (d-f) during epididymal passage. There was little variation in nuclear decondensation in samples obtained from the head (a) and body (b) epididymal regions. Spermatozoa from tail of the epididymis showed a homogeneously dense nucleus (c). Protoplasmic droplet appeared proximal eccentric position (d), distal eccentric position (e) and shed-off (f) as spermatozoa passed from head to body and tail segments, respectively.

fragmentation was higher in head than tail of the epididymis. These findings indicated high stability of camel sperm DNA during epididymal passage. Aberrant chromatin packing during spermatogenesis results in sperm DNA fragmentation (Gorczyca et al,1993; Sailer et al, 1995). Accordingly, El-Badry et al (2015) reported that dromedary camel epididymal spermatozoa from cauda epididymis had higher DNA integrity in comparison to corpus and caput epididymal spermatozoa. Our findings agreed with Yanagimachi (1994), who stated that the mammalian spermatozoa nuclei were very stable and highly condensed with a unique DNA organisation (a sixfold more compact than somatic cells). This unique DNA packing was important to protect the sperm cell and minimise damages caused by exogenous agents before fertilisation.

Electron microscope application in reproductive research was helpful in recognising the monomorphic and polymorphic sperm defects beside understanding of spermatozoa physiology and pathology (Moretti et al, 2016). In the current study, camel epididymal spermatozoa showed ultra-structural variations between epididymal segments in association with the maturational changes and most of these modifications were confined to acrosome, plasma membrane and protoplasmic droplet. In epididymal head, acrosome projected anteriorly with wider subacrosomal space and the protoplasmic droplets were numerous, condensed and dark in appearance at a higher position of sperm tail. On the other hand, in epididymal tail, acrosome projection faded with a very narrow sub-acrosomal space, plasma membrane was somewhat elevated and the protoplasmic droplet were few and light in colour at the midway of sperm tail and eccentrically placed around the axoneme. Osman and Plöen (1986) reported that the cytoplasmic droplet was proximal immediately behind the neck region at the initial epididymal segment and centered around the axoneme then became more eccentric, migrated distally and was eventually shed as the spermatozoa move through the camel epididymis.

Conclusions

Semen characteristics as well as spermatozoa morphology were greatly modified during epididymal passage and this was an essential prerequest for successful fertilisation by the ejaculated semen. Epididymal tail spermatozoa showed an improved fertilising capacity (cytologically and molecularly) that ensure its suitability for assisted reproductive techniques e.g., IVF or ICSI in camels.

Conflict of interest

The Authors declare that there is no conflict of interest.

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GROSS AND MORPHOMETRIC STUDY OF ADRENAL GLAND OF CAMELS (*Camelus dromedarius*)

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ABSTRACT

The investigation was carried out on adrenal glands of 6 recently died adult camels. The adrenal glands of camel located bilaterally in the retroperitoneum, cranial and above the kidney. The cranial part of the right adrenal gland was partially covered by the liver thus making an impression upon the liver. The right adrenal gland was irregular triangular in shape while the left adrenal gland was flat oval in shape and each gland was reddish-grey in colour. The right adrenal gland was heavier, longer, thicker and narrower than the left adrenal gland. Statistical differences between right and left adrenals for all recorded values have been analysed. The difference between right and left adrenal was redatistically significant.

Key words: Adrenal gland, gross, one humped camel

Adrenal glands produce hormones that help regulate your metabolism, blood pressure, immune system, response to stress and other essential functions. It regulates many physiological functions, both in foetal and postnatal life (Hill, 2007).

The adrenal glands of mammals are located near the cranial pole of the kidneys. They consist of two distinct parts, the outer cortex and inner medulla, which differ in morphology, function and origin. Morphological studies of adrenal gland of prenatal developed gland (El-Nahla *et al*, 2011) and gland of adult dromedary camels has been extensively studied (Abdalla and Ali, 1989; Nabipour *et al*, 2008; Rehan and Qureshi 2007; Osman *et al*, 2019).

The anatomical structures of adrenal gland is eventhough studied in few countries but their studies are important because it plays a pivotal role in adaptation of camels located at different geographical locations and in different extreme environments. Present study is aimed to study the morphological details of adrenal gland of dromedary camels of Rajasthan.

Materials and Methods

The adrenal glands were collected from 6 recently died adult camels from VCC, CVAS, Bikaner, Rajasthan. The recommendations of the ethical committee were followed for present research and investigation of the organs were carried out in the Department of Veterinary Anatomy, CVAS, Bikaner. Morphometrical and other gross anatomical studies of adrenal gland intended topography and morphological features, such as, weight, length and breadth were carried out. Weight was taken with the help of physical balance and length, width and thickness were measured by digital Vernier's caliper. Volume was measured by water displacement method.

Results and Discussion

The adrenal glands of camel were located bilaterally in the retroperitoneum, cranial and dorsal to the kidney (Figs 1 and 2). The finding was in partial harmony with the findings of Ye *et al* (2017) who found that the gland was located bilaterally in the retroperitoneum superior and above the kidney in Bactrian camel.

The right adrenal was found superior and medial to the right kidney, not attached to it (Fig 1). Similar findings were reported by Abubakar (2015) in camel. On the contrary, Raghavan (1964) observed that in ox the right adrenal lie in contact with the medial part of the cranial end of right kidney. Nandeshwar *et al* (2017) reported that the right

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adrenal was found in contact with the medial part of the cranial end of right kidney in goat.

The cranial part of the right adrenal gland was partially covered by the liver thus making an impression upon the liver (Fig 1). Similar observations were also made by Abubakar (2015) in camel and Barszcz *et al* (2016) in European Bison. On the contrary, Raghavan (1964) observed that in ox, the right adrenal occupied a part of the renal impression on the liver.

The right adrenal gland was situated more cranially than the left gland in animals of present study. On the contrary, in pigs, both adrenals were situated at the medial border of the corresponding kidney from the hilus forward (Sisson and Grossman, 2012).

The left adrenal gland was found to be superior medially away from the left kidney in camels of present study (Fig 2). The result was in agreement with that of Abubakar (2015) in camel. However, Raghavan (1964) observed that in ox, the left adrenal was not in contact with the left kidney but lied about 5-7.5 cm in front of it. Sisson and Grossman (2012) found that the left adrenal was medial in position in cattle and was usually longer and not in contact with the left kidney but situated about 5 cm cranial to it, in sheep.

Shape and colour

The right adrenal gland was irregular and triangular in shape while the left adrenal gland was flat oval in shape (Fig 3 and 4). Similar observations were made by Abubakar (2015) in dromedary camel, Ye et al (2017) in Bactrian camel and Kumar and Sharma (2017) in Gohilwadi goat. The present study was in contradiction with the observation of Budras and Habel (2003) who found that the right adrenal was more or less heart shaped and the left adrenal was comma-shaped in bovine. Ashok et al (2005) reported that right adrenal gland of crossbred goat was roughly triangular in shape and the left one was elongated in crossbred goat. Dangi et al (2008) stated that left gland in goat was roughly triangular and the right was elongated in shape. Karakurum et al (2008) described that the adrenal gland of donkey was almost oval or circular. Sisson and Grossman (2012) mentioned that the right gland was pyramidal in shape and left adrenal was heart shaped in cattle. In sheep, both the glands were bean shaped similar to kidney. Barszcz et al (2016) mentioned that the shape of left adrenal gland resembled that of number "1" and the right adrenal gland was triangular in shape in European Bison. Barreiro-Vázquez (2020) stated that the right adrenal gland had a typically triangular, "V" or heart-shaped appearance and the left adrenal gland was sometimes "C" or comma-shaped in Holstein Friesian Cow. Elkbashi (2020) observed that the right adrenal gland was oval or bean-shaped, whereas the left one ranged from rounded, triangular, pyramidal, to nearly heart- shaped in dromedary camel.

The adrenal glands in camels of present study were reddish-grey in colour (Fig 3 & 4). It differed in colour in other species, i.e. reddish brown in ox (Raghavan, 1964), reddish brown to dark grey in bovines (Budras and Habel, 2003), dark brown in goats (Nandeshwar *et al*, 2017) and red colour in Bactrain camels (Ye *et al*, 2017).

Right adrenal gland was more elongated than the left one (Figs 3 and 4), but the left one was usually longer in sheep (Sisson and Grossman, 2012) and goat (Dangi *et al*, 2008).

The right adrenal gland had 3 surfaces, 3 borders and 2 extremities (Figs 3 and 4). Al-Bagdadi (1968) found dorsal and ventral surfaces in right adrenal gland of dromedary camel.

The lateral surface of right adrenal gland was roughly flat (Figs 3 and 4), the medial surface was convex and the ventral surface was flat. Al-Bagdadi (1968) found that the dorsal and ventral surfaces of the right adrenal were flat in dromedary camel more or less like that of the sheep. On the ventral surface towards the cranial and caudal end, the dorsal and ventral adrenal artery entered into the gland, respectively.

The medial, dorsal and lateral borders were convex (Figs 3 and 4). On the contrary, Al-Bagdadi (1968) found that the right adrenal gland had rounded borders at their dorsal and ventral surfaces, and the inner medial surface was smooth in dromedery camels. The cranial extremity appeared broad and convex, while the caudal extremity was pointed.

The left adrenal gland had 2 surfaces, 2 borders and 2 extremities. Its dorsal surface was convex and ventral surface was flat (Figs 3 and 4). The finding was in partial harmony with the findings of Al-Bagdadi (1968) in camel who found that the dorsal and ventral surfaces of the left gland were convex. Towards the caudal end of ventral surface, the ventral adrenal artery entered. The lateral and medial borders were convex. The cranial and caudal extremities were rounded and convex.

Topography

The right adrenal gland was located between the right kidney and liver (Fig 1), which simulated the finding of Raghavan (1964) in ox, Abubakar (2015) in camel, Kumar and Sharma (2017) in Gohilwadi goat and Barreiro-Vázquez (2020) in Holstein Friesian cow.

The dorsal surface of both right and left adrenal gland faced towards the retroperitoneal part of roof of the abdominal cavity. This was in conformity with the findings of Budras and Habel (2003) in bovine.

The ventral surface of the right and left adrenal gland was close to caudal vena cava, which was also noticed by Barszcz *et al* (2016) in European Bison and it was in harmony with the finding of Barreiro-Vázquez *et al* (2020) who found a notch for the caudal vena cava on ventral surface of adrenal gland of Holstein Friesian cow.

Cranial pole of right adrenal gland was embedded into the ventral surface of the liver (Fig 1). This finding resembled with the reports of Karakurum



Fig 1. Photograph showing *in-situ* attachment of right adrenal gland of the camel. RA – Right adrenal gland, RK – Kidney, SI – Small intestine, L – Liver, FC – Fibrous cord.



Fig 3. Photograph showing the dorsal surface of the adrenal glands in camel. LA – Left Adrenal, RA – Right Adrenal, C – Cranial end, Cu – Caudal end, MB – Medial Border, LB- Lateral Border.

et al (2008) in donkey and Ye *et al* (2017) in Bactrian camel. This finding was in partial harmony with the report of Al-Bagdadi (1968) who revealed that the right adrenal was in contact with the liver at the medial border of the renal impression of the liver in camel.

The caudal pole of right and left adrenal glands was connected with the cranial pole of the corresponding kidney by a fibrous cord like structure (Fig1). The finding was in partial harmony with the findings of Wenling *et al* (2015) in Bactrian camel, who found that a novel connection between the adrenal gland and the kidney that mainly consisted of fibrous tissue, blood vessels and nerve bundles in Bactrian camel and named it fibrous tissue-blood vessels-nerve bundles (FBN bundle).

The medial border of the right adrenal gland was in contact with aorta. The lateral border was in



Fig 2. Photograph showing *in-situ* attachment of left adrenal gland of the camel. S – Spleen, LA – Left adrenal gland, R – Rumen, LK – Left kidney, FC – Fibrous cord.



Fig 4. Photograph showing the ventral surface of the adrenal glands in camel. LA – Left Adrenal, RA – Right Adrenal, C – Cranial end, Cu – Caudal end, MB – Medial Border, LB- Lateral Border.

contact with ventral surface of liver. Cranial pole of left adrenal gland was in contact with lateral surface of the spleen. The medial border was present towards abdominal aorta. The lateral border was in contact with medial surface of spleen. It was in disagreement with the finding of Barszcz *et al* (2016) who found that the medial border of left gland was positioned next to the caudal vena cava and lateral border was adjacent to the rumen in European Bison.

Weight

The average weight of the left adrenal gland was 38.19 ± 3.80 gm, ranged from 27.45 to 49.47 gm. The average weight of right adrenal gland was 46.91 ± 3.15 gm, ranged between 37.50 to 56 gm (Table 1). However, Budras and Habel (2003) observed that the weight of each adrenal gland was 15-23 gm in bovine. Dangi *et al* (2008) recorded the average weight of adrenal as 1.73 gm in goat and Ye *et al* (2017) reported that the weights of left and right adrenal were about 12.52 ± 2.24 gm and 12.39 ± 2.02 gm, respectively in Bactrian camel.

| Table 1. | Average weight | of left and | right adrenal | glands. |
|----------|----------------|-------------|---------------|---------|
|----------|----------------|-------------|---------------|---------|

| Sr. no. | Weight of left adrenal (gm) | Weight of right adrenal (gm) | |
|-------------|--------------------------------|---------------------------------|--|
| 1. | 49.47 | 56.00 | |
| 2. | 36.88 | 46.70 | |
| 3. | 27.45 | 37.50 | |
| 4. | 48.33 | 54.66 | |
| 5. | 38.12 | 47.74 | |
| 6. | 28.90 | 38.85 | |
| Mean ± S.E. | 38.19 ± 3.80 | 46.91 ± 3.15 | |

The difference was statistically significant between left and right, showed that the right adrenal gland was heavier than the left one (Table 4). Whereas, Budras and Habel (2003) in bovine, Ashok *et al* (2005) in crossbred goat, Dangi *et al* (2008) in goat, Kumar and Sharma (2017) in Gohilwadi goat and Barreiro-Vazquez *et al* (2020) in Holstein Friesian cow

Table 2. Average measurements of gross parameters of adrenal glands.

showed that the left gland was heavier than the right gland. It was contradictory to the statement of Ye *et al* (2017) that there was no significant difference in the gland weight (P > 0.05) in Bactrian camel.

Length

The length of left and right adrenals ranged between 51.37 to 56.90 mm and 62.56 to 75.46 mm, respectively. The average length of the left and right adrenal gland was 54.03 ± 0.84 mm and 68.99 ± 2.06 mm, respectively (Table 2). Al-Bagdadi (1968) found that the length of left and right gland was 48 mm and 42 mm, respectively in dromedary camels. Dangi *et al* (2008) found the average length of the adrenal gland that was 2.01 cm in goats and Ye *et al* (2017) found that the length of left and right gland was 4.20-5.60 and 5.20-7.10 cm, respectively in Bactrian camel.

The difference between left and right adrenal length was statistically significant hence the right adrenal was longer than the left adrenal (Table 4), which was in close agreement with the report of Elkbashi (2020) in camel. Contrarily, the left gland was longer than the right one in goats (Dangi *et al*, 2008) and sheep (Sisson and Grossman, 2012).

Width

The average width of the right and left adrenal glands were recorded as 34.58 ± 2.42 mm and 39.56 ± 1.79 mm, respectively that ranged between 27.55 to 44.18 mm and 34.51 to 46.46 mm, respectively (Table 2). Al-Bagdadi (1968) revealed that average width of the right and left adrenal glands were mentioned as 40mm and 35mm, respectively in camel. The average width of adrenal gland was 1.17 cm in goat (Dangi *et al*, 2008) whereas Ye *et al* (2017) observed in Bactrian camel that the width of left and right glands were 3.30-4.00 cm and 2.10-3.00 cm, respectively. The difference was statistically significant between left and right, hence the right adrenal gland was narrower than the left adrenal gland (Table 4). It was

| S. No. | Length(mm) | | Thickness(mm) | | Width(mm) | |
|-----------|------------|------------|---------------|------------|------------|------------|
| | Left | Right | Left | Right | Left | Right |
| 1. | 56.90 | 75.46 | 25.85 | 28.88 | 46.46 | 44.18 |
| 2. | 54.69 | 69.92 | 25.17 | 27.45 | 40.28 | 37.24 |
| 3. | 52.45 | 64.33 | 23.18 | 25.46 | 37.53 | 33.77 |
| 4. | 55.53 | 73.56 | 24.36 | 27.90 | 42.30 | 35.30 |
| 5. | 53.24 | 68.15 | 23.58 | 26.47 | 36.25 | 29.46 |
| 6. | 51.37 | 62.56 | 22.73 | 24.33 | 34.41 | 27.55 |
| Mean ±S.E | 54.03±0.84 | 68.99±2.06 | 24.15±0.49 | 26.75±0.68 | 39.56±1.79 | 34.58±2.42 |

in congruence with the observations of Dangi *et al* (2008) in goat.

| Sr. no. | Volume of left adrenal (ml) | Volume of right adrenal (ml) | |
|-------------|--------------------------------|---------------------------------|--|
| 1. | 45 | 53 | |
| 2. | 42 | 50 | |
| 3. | 41 | 47 | |
| 4. | 44 | 51 | |
| 5. | 41 | 48 | |
| 6. | 40 | 46 | |
| Mean ± S.E. | 42.17 ± 0.79 | 49.17 ± 1.08 | |

Table 3. Average volume of left and right adrenal glands.

 Table 4.
 Statistical analysis of biometrical observation of various parameters of adrenal glands of dromedary camel.

| Character | Adrenal | Range | Mean ± S.E. | Paired t ² test | |
|---------------------------------|---------|-----------------|-----------------|-------------------------------|--|
| Weight of | Right | 37.50- 56.00 | 46.91 ± 3.15 | 10.015 | |
| (gm) | Left | 27.45- 49.47 | 38.19 ± 3.80 | 12.013 | |
| Length of adrenal (mm) | Right | 62.56- 75.46 | 68.99 ± 2.06 | 12.075 | |
| | Left | 51.37- 56.90 | 54.03 ± 0.84 | 12.07° | |
| Width of adrenal (mm) | Right | 27.55- 44.18 | 34.58 ± 2.42 | -5.58 ^s | |
| | Left | 34.51- 46.46 | 39.56 ± 1.79 | | |
| Thickness of adrenal (mm) | Right | 24.33- 28.88 | 26.75 ± 0.68 | 0.205 | |
| | Left | 22.73- 25.85 | 24.15 ± 0.49 | 9.29 | |
| Volume | Right | 46-53 | 42.16 ± 0.79 | 19.17 ^s | |
| (ml) | Left | 40-45 | 49.17 ± 1.08 | | |

At the 5% level. NS - Non significant S – Significant

Thickness

Thicknesses of left and right adrenal glands were ranged between 22.73 to 25.85 mm and 24.33 to 28.88 mm, respectively. The average thicknesses of left and right adrenals were $24.15 \pm .49$ mm and 26.75 ± 0.68 mm, respectively (Table 2). Ye *et al* (2017) observed that the left and right adrenal gland of Bactrian camel were 1.00-1.50 cm and 1.30-1.70 cm thick, respectively.

The difference between the left and right adrenal length was statistically significant and accordingly the right adrenal was thicker than the left adrenal (Table 4). This was in accordance to the findings of Elkbashi (2020) and Al-Bagdadi (1968) in camels. Dangi *et al* (2008) mentioned that the left adrenal was thicker than the right in goat.

Volume

Average volumes of the left and right gland were estimated as 42.17 ± 0.79 ml and 49.17 ± 1.08 ml, respectively that ranged from 40 to 45 ml and 46 to 53 ml, respectively (Table 3). On the contrary, Ye *et al* (2017) found the volume of each adrenal gland of Bactrian camel was 13.01 ± 1.42 cm³. The difference between right and left adrenal volume was statistically significant hence the right adrenal had large volume than the left adrenal (Table 4).

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HISTOLOGICAL STUDY OF PRENATAL DEVELOPMENT OF THE SPLEEN IN CAMEL (Camelus dromedarius)

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ABSTRACT

Spleen development in the camel foetus was studied during the 1st, 2nd and 3rd trimesters of gestation using histological techniques. Ten spleens of camel foetuses were collected from Omran slaughterhouse, Al-Ahsa, Saudi Arabia. The samples were prepared by routine histological procedures and stained by the general histological stain (H and E) and some other special stains including Van Geison's for collagenous fibres, Verhoff's for elastic fibres, Gordon and Sweet for reticular fibres. At the 1st trimester, the spleen capsule was composed of fine connective tissue fibres, in the 2nd trimester the capsule and trabeculae showed thick connective tissue, while in the 3rd trimester the capsule also showed smooth muscle fibres and surrounded with large amount of adipose tissue. The parenchyma, at the 1st trimester consisted of randomly distributed lymphocytes and macrophages. At the 2nd and 3rd trimesters, it was arranged as white and red pulps. Megakaryocytes observed previously in the red pulp of adult dromedary camel were seen in the red pulp at the 1st, 2nd and 3rd trimesters of gestation. It was concluded that the spleen showed very important histological developmental changes throughout the three gestational stages.

Key words: Camel, development, foetus, gestational stage, histology, spleen

The mammalian spleen develops as gathering of mesenchymal cells in the dorsal mesogastrium. The mesenchymal cells differentiate and form the splenic capsule and connective tissue (McGeady *et al*, 2017). The histomorphological structure of the spleen has been reported by many authors (Bello *et al*, 2019; Jaji *et al*, 2019; Zidan, 2000a, Maina *et al*, 2014).

It has been stated that the spleen is surrounded by a capsule from which fibrous trabeculae emerge (Dijkstra and Veerman, 1990; Alshamarry, 2010). The spleen of the one humped camel consists of a thick capsule and parenchyma consists of splenic pulp, which is composed of white pulp packed with lymphocytes and red pulp consisted of threedimensional reticular network and splenic sinuses (Zidan *et al*, 2000a).

Bello *et al* (2016) stated that the spleen of dromedary foetus had red and white pulps of variable shape and size and special feature of connective tissue inter-digitations of variable sizes into the parenchyma along the whole surface at second and third trimester. However, there was paucity in the literature on the development of the spleen in camel foetus. Therefore, the aim of this study was to provide more information about the histological structure of the prenatal development of spleen of the dromedary camel foetus.

Materials and Methods

Ten spleens of camel foetuses were collected from Omran slaughterhouse, Al-Ahsa, Saudi Arabia. The Research Ethics Committee, Deanship of scientific research, King Faisal University approved all experiments number: KFU-REC-2022-JAN-EA000343. Depending on the gestational age (GA), the foetuses were divided into three groups: first (0-130 days), second trimester (131-260 days) and third trimester (261-423.5 days). The age of the foetus was determined using the equation of crown vertebralrump length (CVRL) GA = (CVRL + 23.99)/0.366

Small pieces (about 1cm^3 thick) were taken, then were fixed in 10% buffered formalin. The specimens (5 µm thick) were processed by routine histological procedures and stained with (H&E) and some special stains including Van Geison's for collagenous fibres, Verhoff's for elastic fibres, Gordon and Sweet for reticular fibres (Bancroft and Stevens, 2008).

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Results and Discussion

The histological details of foetal spleen obtained at different GA were noted. The foetal spleen obtained at 1st trimester was surrounded by a thin capsule of fine loose connective tissue fibres or mesenchymal connective tissue from which connective tissue trabeculae extended in the parenchyma (Fig 1). At the second trimester, the connective tissue capsule and the trabeculae became thickened in foetal spleen. The diffuse collagen connective tissue into the parenchyma was observed at the stage of 2nd trimester (Fig 2). At the third trimester, the foetal spleen capsule consisted of dense regular connective tissue with few smooth muscle fibres that also extended in the trabeculae and the spleen was surrounded with large amount of adipose tissue (Fig 3). However, at the late stages of the third trimester, the smooth muscle fibres were clearly visible in the trabeculae (Fig 3, d).

At the first trimester, the white and red zones of the foteal spleen were not clearly differentiated and the parenchyma showed large amount of randomly distributed B &T lymphocytes and large spherical macrophages with oval nuclei and eosinophilic cytoplasm (Fig 1). Giant cells (Megakaryocytes) with lobulated nuclei and highly eosinophilic cytoplasm were also observed (Fig 1).

At the 2nd trimesters, the foetal spleen parenchyma began to differentiate in a white and a red pulp. The megakaryocytes were clearly shown in the red pulp with lobulated nuclei (Fig 2).

At the 3rd trimesters, the foetal spleen parenchyma was differentiated in white and red pulps. The white pulp showed splenic corpuscles which consisted of lymphatic nodules (B-dependent zone) surrounding the central artery and periarterial sheath of non-nodular lymphoid tissue (T-dependent zone). The red pulp fills the spaces between the capsule, the trabeculae and the white pulp. The red pulp was formed of splenic venous sinuses and splenic cords in-between the sinuses that was composed of reticular net fixed to it, reticular cells and suspended aggregates of red blood cells, B & T lymphocytes and macrophages (Fig 3). In addition, the megakaryocytes were observed at the 3rd trimesters of gestation in the red pulp only (Fig 3). The number of megakaryocytes cells were increased at the 3rd trimester and some of them showed binucleated nuclei (Fig 3, c).

The present study showed that the foteal spleen at the 1st trimester of GA was surrounded with

capsule which start with fine connective tissue fibres and send fine connective tissue trabeculae in the parenchyma, then at the 2nd trimester capsule and trabeculae appeared thicker. At the stage of the 3rd trimester of GA the capsule became thick and the smooth muscle fibres were surrounded with large amount of adipose tissue. The present study agreed with some previous studies (Bello et al, 2016) which stated that trabecular connective tissue and capsular thickness increase depending on the developmental stages. According to Jaji et al (2019) the capsule in the spleen of the dromedary camel foetus had an inner smooth muscle and an outer predominant connective tissue layer. However, in present study the most of the salient features of the postnatal spleen were already evident in the first growth phase and became more developed by the second phase.

In the present study, the splenic corpuscles were observed clearly at the 3rd trimester of GA where lymphatic nodules surrounded the central artery and a non-nodular zone was seen. The red pulp is formed of splenic venous sinuses, splenic cords, reticular cells, blood cells and macrophages. The splenic cords were suspended by reticular cells net with aggregates of blood cells and macrophages. According to Veerman and van Ewijk (1975) and Steiniger (2015) the composition of the white pulp of some animal species consisted of periarteriolar lymphatic sheath (PALS), follicles and marginal zone. There were three compartments, each had their specific lymphoid and non-lymphoid cells. Reticular cells and reticulin fibres, although found in all three compartments, they formed a characteristic pattern in each compartment.

The arrangements of the spleen parenchyma was also described previously in some species (Eurell and Frappier, 2006 and Steiniger, 2015). The spleen consisted of the white pulp embedded in the red pulp. In the white pulp, T and B lymphocytes formed accumulations, the periarteriolar lymphatic sheaths located around intermediate-sized arterial vessels, the central arteries. The red pulp was a reticular connective tissue containing all types of blood cells (Steiniger, 2015). In this study a large amount of randomly distributed B and T lymphocytes, macrophages and erythrocytes, megakaryocytes were shown in Ist trimester. In the 3rd trimester splenic corpuscles the white pulp consisted of lymphoid tissue formed of lymphatic nodules was surrounded the central artery.

The number of the megakaryocytes in the red pulp of adult dromedary camel decreased with



Fig 1. Photomicrographs showing spleen of camel foetus during the 1st trimester of gestation; connective tissue capsule (C) and fine connective tissue trabeculae (T), randomly distributed lymphocytes, macrophages and megakaryocytes were seen (arrows), binucleated megakaryocyte were present (green arrow). (a & c) Haematoxylin and Eosin (X20) (b) Gordon and Sweet (X20), (d) Haematoxylin and Eosin (X40), (e & f) Haematoxylin and Eosin (X100).



Fig 2. Photomicrographs showing spleen of camel foetus during the 2nd trimester of gestation; connective tissue capsule (C) connective tissue trabeculae (T) Especially collagen fibres. (a), (b) and (c); Megakaryocytes (arrows). (a), (b) and (c) Van Gieson's (X20, X20, X63 respectively), (d), Gordon and Sweet (X63).



Fig 3. Photomicrographs showing spleen of camel foetus during the 3rd trimester of gestation; (a) white pulp (WP) surrounded central artery (A). (b), red pulp consists of venous sinuses (VS) at the margin of white pulp, marginal zone (MZ). Capsule (C) and trabeculae (T) consisted of smooth muscle fibres. (c and d); Megakaryocytes had lobulated nuclei (black arrows), binucleated megakaryocyte were present (green arrow). Haematoxylin and Eosin. (a) and (b): (X20), (c): (X40), (d): (X100).

age (Zidan *et al*, 2000b). However, megakaryocytes observed in the red pulp of foetal spleen of present study at the 1st, 2nd and 3rd trimesters increased in their numbers during the three GA. Binucleated megakaryocytes were observed at the 3rd trimester of GA.

The results of present study showed that the development of the spleen in 1st GA showed ordinary mesenchymal cells and undifferentiated zones of white and red pulps which later developed into differentiated zones of white and red pulps. In addition, the capsule and trabeculae developed from fine connective tissue to well-developed connective tissue. This development followed the advancement in subsequent GA from 1st to 3rd trimester.

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"LA CAMELERIE"- FIRST DAIRY CAMEL FARM IN FRANCE

The first dairy camel farm "La Camelerie" producing, and processing camel milk is open in North of France close to Belgium border. It has 70 camels (dromedaries, Bactrian and hybrids). The farm in the France, had camels since several years for touristic attraction, but since June 22, milk production is started (pasteurised milk, kefir and cheese). The farm is a partner of the European project "CAMELMILK" aiming to boost the camel milk production and processing around the Mediterranean Basin. The country partners are Algeria, Turkey, France, Germany, and Croatia under the coordination of Spain and with the scientific support of Dr Bernard Faye. In Europe, dairy camel farms are already working in Netherland and in Germany. In France, camel milk production is also expected in two other farms, contributing to the diversification of milk sector in a country where camel rearing is developing recently. Due to this emergence of new camel farming out of the traditional "camel countries", Dr Bernard Faye has edited a book (in French) for all the camel farmers and vets in French-speaking countries.



The camel herd of " La Camelerie" in the North of France



Pasteurised and camel cheese making at "La Camelerie" dairy plant

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PROTEOMIC CHARACTERISATION OF SERUM DURING THE BREEDING CYCLE IN MALE BACTRIAN CAMELS

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Commercial booklets: Anonymous/Name. Conray-Contrast Media. IIIrd Edn., 1967; pp 12-15, May and Baker Ltd., Dagenham, Essex, England.

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News paper articles: Christina Adams. Camel milk: a miracle cure for children with autism?. Gulf News, Published: April 09. 2014.

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