

Pakistan Veterinary Journal

ISSN: 0253-8318 (PRINT), 2074-7764 (ONLINE) DOI: 10.29261/pakvetj/2022.088

RESEARCH ARTICLE

Immunohistochemical Investigation of TNF- α and IFN- γ Expressions in Sheep Fetuses with Brucellosis

Emin Karakurt^{1*}, Hilmi Nuhoğlu¹, Serpil Dağ¹, Özgür Çelebi², Fatih Büyük², Enver Beytut¹, Ayfer Yıldız¹, Mushap Kuru³ and Doğan Akça⁴

¹Department of Pathology, Faculty of Veterinary Medicine, Kafkas University, Kars, Türkiye ²Department of Microbiology, Faculty of Veterinary Medicine, Kafkas University, Kars, Türkiye ³Department of Obstetrics and Gynecology, Faculty of Veterinary Medicine, Kafkas University, Kars, Türkiye ⁴Department of Midwifery, Faculty of Health Science, Kafkas University, Kars, Türkiye *Corresponding author: mehmeteminkarakurt@hotmail.com

ARTICLE HISTORY (22-307)

Received: September 10, 2022 Revised: November 18, 2022 Accepted: November 20, 2022 Published online: December 25, 2022 Key words: Brucellosis Cytokine Fetus Sheep

ABSTRACT

The purpose of the study is to evaluate the expression of TNF- α and IFN-gamma (IFN- γ) in the lung and liver tissues of aborted sheep fetuses using immunohistochemical methods and determine, which type of cells specifically secrete TNF- α and IFN- γ . Moreover, the roles of these cytokines in the immune response and inflammatory reaction associated with the disease were evaluated. The materials used in the study consisted of abomasum contents and lung and liver tissue samples from 114 aborted sheep fetuses. Of the 114 fetuses brought to the Microbiology and Pathology Department, Faculty of Veterinary Medicine for routine histopathological and microbiological diagnoses. As a result of cultural and phenotypic analysis, Brucella spp. were isolated from 100 (87.71%) of 114 fetal tissue samples and all of them were identified as B. melitensis. These isolates identified as B. melitensis were also confirmed by the Bruce-ladder PCR in the presence of relevant amplified products representing specific gene regions. Bronchopneumonia and hepatitis were the most important pathological lesions. TNF- α and IFN- γ immunoreactivities were significantly increased in the brucellosis group compared to the control group. In conclusion, it is supported by the data obtained from this study that cytokines such as TNF- α and IFN- γ were highly effective in the cellular immune response (Th1) developed against ovine brucellosis.

To Cite This Article: Karakurt E, Nuhoğlu H, Dağ S, Çelebi Ö, Büyük F, Beytut E, Yıldız A, Kuru M and Akça D, 2023. Immunohistochemical investigation of TNF- α and IFN- γ expressions in sheep fetuses with brucellosis. Pak Vet J, 43(1): 85-90. <u>http://dx.doi.org/10.29261/pakvetj/2022.088</u>

INTRODUCTION

Brucellosis, caused by the bacteria *Brucella*, affects animals (sheep, cattle, pigs, dogs, etc.), wildlife and humans. As one of the most prevalent zoonotic diseases worldwide, it is responsible for significant economic losses due to abortion, stillbirth, infertility, and reduced milk production in livestock (Dorneles *et al.*, 2015). The Brucellosis Expert Committee of the World Health Organization divided *Brucella* into 6 species and 19 types: *Brucella melitensis* (3 subtypes), *Brucella abortus* (8 subtypes), *Brucella suis* (5 subtypes), *Brucella ovis* (1 subtype), *Brucella neotomae* (1 subtype), and *Brucella canis* (1 subtype) (Zhou *et al.*, 2020). *B. melitensis* and *B. ovis* are the primary agents of ovine brucellosis such as sheep and goats (Bayu, 2018). Isolation, molecular techniques (PCR), histopathology and immunohistochemical techniques are methods frequently used to diagnose brucellosis (Unver *et al.*, 2006; Yesilmen *et al.*, 2018).

Brucella spp. are facultative intracellular bacteria whose disease-causing capacity depends on invasion, longterm survival, and proliferation within host cells (Galindo *et al.*, 2009; Poester *et al.*, 2013; Adem and Duguma, 2020). The cellular immune response to many intracellular bacterial infections, including brucellosis, listeriosis, and tuberculosis, plays a critical role in the host defense (Salas-Téllez *et al.*, 2005; Sözmen *et al.*, 2010; Priyanka *et al.*, 2021a). The course of brucellosis is determined by the different T cell subtypes (Th1 and Th2) that results from the production of specific cytokines (Dorneles *et al.*, 2015; Priyanka *et al.*, 2021b) those play a key role in the pathogenesis of *Brucella*. The Th1/Th2 ratio can be involved in resistance or susceptibility to *Brucella* infection (Priyanka *et al.*, 2021a). Macrophages have the role of stimulating and shaping adaptive immune response through cytokine production and antigen presentation. Bactericidal activity of macrophages increases with the activation of cytokines such as tumor necrosis factor-alpha (TNF- α) and interferon (IFN), which, together with lipopolysaccharides, act as key players in brucellosis (Adem and Duguma, 2020; Priyanka *et al.*, 2021a; Priyanka *et al.*, 2021b).

The purpose of the study is to evaluate the expression of TNF- α and IFN-gamma (IFN- γ) in the lung and liver tissues of aborted sheep fetuses using immunohistochemical methods and determine which type of cells specifically secrete TNF- α and IFN- γ . Moreover, the roles of these cytokines in the immune response and inflammatory reaction associated with the disease were evaluated.

MATERIALS AND METHODS

Ethical Approval: This study was approved by the Kafkas University Animal Experiments Local Ethics Committee (KAU-HADYEK-2019/125).

Animals: The materials used in the study consisted of abomasum contents and lung and liver tissue samples from 114 aborted sheep fetuses. Of the 114 fetuses brought to the Microbiology and Pathology Department, Faculty of Veterinary Medicine for routine histopathological and microbiological diagnoses between 2013-2021, 86 (75.43%) were at 3-5 months of gestation, 18 (15.78%) were at 1-3 months of gestation, and 10 (8.77%) lived between 1 and 16 hours. Lung and liver tissues were evaluated because macroscopic and microscopic findings related to brucellosis are known to be more severe in these tissues. Placenta tissues could not be assessed as they were not provided. Metritis, high fever, weight loss, diarrhea, mastitis, and lameness in pregnant sheep were recorded according to the animal owner's information. In addition, 10 lung and liver samples obtained from fetuses aborted due to non-infectious causes (trauma, etc.) were evaluated as controls.

Isolation and identification by culture: Investigation of Brucella spp. from fetal tissue samples was performed by in vitro culture (Büyük and Sahin, 2011). Tissue samples were inoculated directly onto blood agar (Thermo Fischer Sci, CM0271B) containing 7% sheep blood (SBA) and Brucella-selective agar medium base (Oxoid CM0169) with a Brucella-selective supplement (Oxoid SR0083) and left to incubate aerobically and microaerobically at 37°C for 5–7 days. Brucella spp. identification was performed by phenotypically evaluating growth characteristics, macroscopic and microscopic morphologies, hydrogen sulfide activity, and agglutination reactions with A and M antigen monospecific sera (Alton et al., 1988).

Identification by bruce-ladder PCR: Identification of *Brucella* spp. was conducted using the Bruce-ladder PCR method, which allows differentiation of all identified classic *Brucella* spp. (López-Goñi *et al.*, 2008). Genomic DNA extraction from fresh *Brucella* cultures on SBA was conducted with single colony lysis buffer solution

supplemented with heat treatment (Marmur, 1961). Bruceladder PCR was adjusted to 25µl per sample with 3µl DNA. 5µl 5XLongAmpTM Taq (Mg-free) template Reaction Buffer, 1µl MgCl₂ (20 mM), 0.75µl dNTP mix (0.2mM), 1µl of each primer (12 pieces) (20pmol), 1µl LongAmp[®] Taq DNA Polymerase (5U), and 2.25µl nuclease-free water. The thermal cycle of the Bruce-ladder PCR was carried out by initial denaturation at 95°C for 3 min, followed by 30 cycles with denaturation at 95°C for 35 sec, primer attachment at 62°C for 45 sec, elongation at 65°C for 3 min, and finally elongation at 65°C for 10 min. The amplified products were analyzed using 1.5% agarose gel electrophoresis, and the simultaneous presence of products of 1682, 1071, 794, 587, 450, and 152bp for B. melitensis were evaluated. B. melitensis biotype 1 (16M) and *B. abortus* biotype 1 (544) were used as controls.

Macroscopy: Detailed photographs were taken of the fetuses before and after necropsies. The condition of vital organs, such as lungs (pneumonia, etc.) and liver (hepatitis, etc.), presence of any fluid in the abdominal cavity, abomasum contents, and fetal edema were evaluated. Macroscopic lesions observed were recorded for each case separately.

Histopathology: Lung and liver tissue samples from both *Brucella*-infected (pneumonic) and healthy animals were processed routinely. Fixated in 10% neutral buffered formalin, embedded using paraffin wax, 5μ m, sections were taken, stained with Hematoxylin-Eosin (H&E). Examinations were performed under a light microscope (Olympus Bx53) and detected histopathological changes were photographed.

Immunohistochemistry: The routine streptavidin-biotin peroxidase complex method was used for immunohistochemistry (Thermo Scientific Histostain-Plus IHC Kit, HRP, broad-spectrum, REF: TP-125-HL). Anti-Brucella (Becton Dickinson, Cat: 240934, polyclonal, 1/1000 dilution ratio), anti-TNF-α (MyBioSource, MBS2025729, monoclonal, 1/100 dilution ratio), and anti-IFN-γ (MyBioSource, MBS2091397, polyclonal, 1/100 dilution ratio) antibodies were used after antigen retrieval and nonspecific protein blocking. The reactions were detected with aminoethyl carbazole (AEC) chromogen (Thermo Scientific, TA-125-HA). Counterstaining was conducted using hematoxylin. Glass slides were mounted with AEC special adhesive and a coverslip. Instead of the primary antibodies, drops of PBS were applied to the control lung tissue sections. Same microscope (Olympus Bx53) was used for examining slides and Cell^P software (Olympus Soft Imaging Solutions GmbH, 3,4) was used for photographing. Images were analyzed with the Image J Program (1.51j8). Immunohistochemical analysis of TNF- α and IFN- γ was performed using a grading system for positively stained cell numbers on sites with intensive staining characteristics. A total of 5 different areas on each slide were examined at 40X magnification. The rating system was as follows: (-) no immunoreactivity; (+) low = 1%-10% positive cells; (++) moderate = 11%-59% positive cells; and (+++) intense = more than 60% positive cells.

Statistical analyses: SPSS® software (SPSS 26.0, Chicago, IL, USA) was used for statistical analysis. A Mann-Whitney U test was used for pairwise comparisons of TNF- α and IFN- γ expressions according to positive cell scoring. P<0.05 was accepted as statistically significant.

RESULTS

Microbiology: As a result of culture and phenotypic analyses, *Brucella* spp. Were isolated from 100 of 114 (87.71%) fetal tissue samples, and all were identified as *B. melitensis*. These isolates identified as *B. melitensis* were also confirmed by Bruce-ladder PCR with the presence of relevant amplified products representing specific gene regions (Fig. 1).

Macroscopy: Varying degrees of subcutaneous edema were detected in the fetuses infected with *B. melitensis*. There were hemorrhagic fluid accumulations in the abdominal and thoracic cavities. Inflammation was observed in the pleura. In the lungs, pneumonia was the most striking macroscopic finding. The color of the lungs became darker, and the tissue consistency hardened. Rib impressions were evident on the lung. The liver was enlarged, and pale, whitish foci were detected on the cross-sectional surface. In addition, the content of the abomasum was quite dense and coagulated with a lemon yellow color which was considered abnormal. There were no remarkable macroscopic findings in other organs (Fig. 2).

Histopathology: No pathologic lesions were detected in the lungs of the control animals as normal histologic structure was observed. In fetuses with brucellosis, interstitial and bronchopneumonia were dominant findings in the lungs. There was inflammatory cell infiltration, mainly in the bronchioles, where macrophages, lymphocytes, and neutrophils made up the majority of cells. In addition to these findings, edema with interalveolar septal hyperemia was detected. Similar to the bronchiolar lumens, there were varying amounts of the same type of inflammatory cell infiltration in the alveolar lumens, primarily macrophages, lymphocytes, and neutrophils. In addition to these cells, dense cellular debris and fibrin had accumulated in the alveolar lumens (Fig. 3 a-b-c). It was determined that the livers of the control animals had a normal structure and did not exhibit any pathologic changes. At the same time, severe degeneration and necrosis of hepatocytes were recorded in the livers of Brucella-positive fetuses. Areas of mild and intense inflammatory cell infiltration were found, especially around the vena centralis or portal triad. While most of these cells were mononuclear, small numbers of neutrophils were detected (Fig. 3 d-e-f).

Immunohistochemistry: Group immune positivity scores are shown in Table 1. The control group was negative for *Brucella* spp., TNF- α , and IFN- γ reactions. TNF- α and IFN- γ immunoreactivities were significantly increased in the brucellosis group compared to the control group. *Brucella* spp. Immune-positive reactions were detected in the cytoplasm of inflammatory cells (alveolar macrophages, lymphohistiocytic cells, and neutrophils), mainly in the exudates of the alveoli and bronchioles, in dark red and granular form. Inflammatory cell infiltration

Table I: Immune positivity scores of groups

Groups		TNF-α	IFN-γ
Control	Mean	0ª	0 ª
(n=10)	Median	0	0
	Minimum	0	0
	Maximum	0	0
	Percentiles25	0	0
	Percentiles75	0	0
Brucellosis	Mean	2.7 ^b	2.8 ^b
(n=100)	Median	3	3
	Minimum	2	2
	Maximum	3	3
	Percentiles25	2	3
	Percentiles75	3	3
E ab E		1.00	

Footnote: ^{a-b}: Expresses the statistical difference between groups (P<0.001). Positive cell scoring is shown in the table as negative (-) = 0, low (+) = 1, moderate (++) = 2, and severe (+++) = 3



Fig. 1: 1.5% agarose gel electrophoresis images of Bruce-ladder PCR products. BA: *B. abortus* biotype I (544), BM: *B. melitensis* biotype I (16M), S: Field sample (*B. melitensis*), M: HyperLadder[™] 100bp Plus DNA ladder (BIOLINE, 33071).

in the bronchioles and alveolar lumens, cellular debris, and dense Brucella antigens in the cytoplasm of glandular epithelial cells around the bronchi and bronchioles were observed. In particular, TNF- α and IFN- γ positive stains were detected in alveolar macrophages, neutrophils, and lymphohistiocytic cells in the alveolar and bronchiole lumens of the lung. The reactions were dark red in color and granular in the cytoplasm of the aforementioned cells. The intensity of immune-positive expressions was more pronounced, particularly in areas where inflammatory cell infiltration was intense (Fig. 4 a-b-c). In the cytoplasm of hepatocytes and Kupffer stellate cells in the liver, Brucella spp. Positive reactions were detected. Brucella spp., TNF- α , and IFN- γ immunoreactivities were primarily observed in inflammatory cell infiltration, especially mononuclear cells around the vessels and portal triad. Immune positivity was detected mainly in the cytoplasm of lymphohistiocytic cells, and plasma cells were more remarkable in regions where the inflammatory reaction was severe (Fig. 4 d-e-f).

DISCUSSION

Bacteriological isolation, PCR, histopathology, and immunohistochemistry are frequently used reliable methods to definitively diagnose *Brucella* agents (Unver *et al.*, 2006; Büyük *et al.*, 2011; Yesilmen *et al.*, 2018).



Fig. 2: Pneumonia in the lung, enlargement of the liver and the pale areas on the cross-section, hemorrhagic fluid accumulation in the abdominal and thoracic cavities.



Fig. 3: a= Lung, bronchopneumonia, b= Inflammatory cell infiltration in bronchiole lumens (arrowheads), c= Higher magnification, cell infiltration mostly composed of neutrophil leukocytes (arrow), d= Liver, hepatitis, e= Intense cell infiltration around the vena centralis and portal triad (arrow), f= Inflammatory cell proliferation (arrowhead) mostly composed of mononuclear cells and few neutrophil leukocytes.



Fig. 4: a= Brucella spp. positive reactions (arrows) on macrophages and neutrophils in the alveolar lumens and inflammatory cells in the bronchiolar lumen (arrowhead), b= Immune positive TNF- α reactions in lympho-histiocyte cells and macrophages in alveolar lumens (arrows) and inflammatory cells in bronchiole lumen (arrowhead), c= IFN- γ positive staining in alveolar macrophages, lymphocytes (arrows) and inflammatory exudate in the bronchiole (arrowhead), d= In the cytoplasm of hepatocytes (arrows) and kupffer stellate cells (arrowhead) Brucella spp. existence, e= TNF- α immune positive reactions in inflammatory cells (*) around the vessel, f= Intracytoplasmic IFN- γ expressions in lympho-histiocyte cells around the vena centralis.

The macroscopic, histopathologic, and immunohistochemical findings observed in the lungs and livers of *Brucella*-positive sheep fetuses in the current study were consistent with the literature (Salas-Téllez E *et al.*, 2005; Poester *et al.*, 2013; Bayu, 2018; Yesilmen *et al.*, 2018). Cytokines are key molecules that play significant roles in determining protective immune responses (Li *et al.*, 2021). *Brucella* spp. can stimulate the secretion of cytokines responsible for regulating immune and inflammatory responses (Eskandari-Nasab and Moghadampour, 2018). In particular, proinflammatory cytokines enable the emergence of antimicrobial responses in monocytes and macrophages, which have a significant role in defending against intracellular pathogens such as *Brucella* spp. (Ritchie *et al.*, 2012).

TNF is a proinflammatory cytokine that regulates host responses to microbial challenges and initiates the expression of chemokines and adhesion molecules required for the recruitment of neutrophils to the site of infection, which is particularly important for the restriction of initial infection (Hop et al., 2017). TNF-α increases the elimination of Brucella spp. by activating bactericidal activities in macrophages, thus regulating the protective cellular immune response against this infection (Antunes et al., 2013; Zhu et al., 2016; Adem and Duguma, 2020). TNF-a also induces CD8+ cytotoxic T lymphocytemediated cytotoxicity against macrophages infected with Brucella spp. (Priyanka et al., 2021a). TNF-α, produced from many cells such as neutrophils, natural killer cells, macrophages, lymphocytes, and fibroblasts, is a vital mediator for clearance of brucellosis infection from a host (Eskandari-Nasab and Moghadampour, 2018). This study detected TNF-a positive reactions mostly in alveolar macrophages, neutrophils, and lymphohistiocytic cells in lung tissue. In the liver, TNF- α positive reactions were primarily observed in mononuclear cells around vessels and Kupffer stellate cells. Inhibition of the TNF- α response in human and mouse macrophages in the initial stages of brucellosis is associated with greater tolerance of these cells to bacterial proliferation and thus the ability of B. abortus to overcome the host's innate immune response and establish infection (Dorneles et al., 2015). It is known that serum levels of proinflammatory cytokines such as TNF increase significantly in brucellosis cases (Li et al., 2021). Hop et al., 2017 reported that TNF expression and secretion were significantly induced due to B. abortus infection. Eskandari-Nasab and Moghadampour, 2018 demonstrated a link between polymorphism in the TNF-a gene and an increased risk of brucellosis. Privanka et al., 2021b revealed rhythmic induction of the cytokine profile by enhanced expression of genes encoding IFN- γ , IL-1 β , IL-6, and iNOS, and reduced expression of TNF- α , IL-4, and IL-12p40, showing the transformation from a predominantly Th1-like model to a Th2-like model, which contributes to the development of chronic brucellosis of cattle. Consistent with the literature data (Li et al., 2021), it was determined that TNF-α expression was significantly increased in cases with brucellosis compared to the control group. Although many studies evaluated TNF- α levels in association with human, mouse, or bovine brucellosis, there is no literature detailing the evaluation of brucellosis in sheep. Cells that showed positive staining for TNF- α expression were mostly alveolar macrophages, neutrophil leukocytes, Kupffer stellate cells and mononuclear cells. In the light of these findings, it was concluded that $TNF-\alpha$ triggered the infiltration of immune system cells into the inflammatory region in ovine brucellosis and played a role in the elimination of bacterial agents. In this study, the remarkable increase in TNF- α expression in sheep fetal tissues in parallel with the severity of the disease suggests that this proinflammatory cytokine is also active in the cellular immune defense associated with ovine brucellosis.

IFN- γ is an important proinflammatory cytokine critical to the host's protective cellular immune response after B. abortus infection (Zhu et al., 2016; Feng et al., 2017; Zhou et al., 2020). IFN-y is produced mainly by CD4⁺, CD8⁺, and CD5⁺ T lymphocytes (Pérez-Sancho et al., 2014; Agnone et al., 2019). IFN-y functions to increase the antimicrobial capacity of macrophages (He, 2012; Eskandari-Nasab and Moghadampour, 2018). In vivo and in vitro experiments revealed that IFN- γ is the most potent inducer of anti-Brucella activity in monocytes and macrophages. Agnone et al., 2019 reported that IFN-y positive T lymphocytes increased in cattle samples infected with *B. abortus* compared to a control group. In a similar study, Feng et al., 2017 found that IFN-y levels in Brucellainfected samples were much higher than in vaccinated and negative control samples. Eskandari-Nasab and Moghadampour, 2018 suggested that polymorphism in the IFN- γ gene, similar to TNF- α , is an important parameter that increases the risk of brucellosis. Zhu et al., 2016 found that IFN- γ and TNF- α levels increased remarkably in their Brucella vaccine study in mice. In another vaccine study in mice, Sancho *et al.*, 2014 observed that IFN- γ and TNF- α were at the highest level. Suraud et al., 2008 revealed that IFN-γ is mainly produced by CD4⁺, CD8⁺, and CD4⁻, CD8⁻ γδ cells in sheep acutely infected with B. melitensis. Durán-Ferrer et al., 2004 reported nonvaccinated diseased ewes dispersing the pathogen had antibody levels and antigenspecific IFN-y profiles higher and notably different from those of vaccinated ewes that neither contracted B. melitensis nor excreted the pathogen. In this study, in parallel with the literature data, (Durán-Ferrer et al., 2004; Feng et al., 2017; Agnone et al., 2019) it was determined that IFN- γ expression in the lung and liver tissues of fetuses naturally infected with Brucella spp. were increased statistically compared to the control group. In addition, IFN-y was primarily produced from lymphocytes and macrophages, as previously reported (Durán-Ferrer et al., 2004; Pérez-Sancho et al., 2014; Agnone et al., 2019). According to current study data, IFN- γ is also expressed by neutrophil leukocytes. This shows that this cytokine activates neutrophils as well as macrophages and lymphocytes. The similarity of TNF- α and IFN- γ results indicates that the two cytokines exert a synergistic effect especially in the cellular immunity acquired against this disease. Notably, IFN-y expression increased especially in areas where inflammatory reactions were severe. These study data indicate that IFN- γ is a crucial cytokine involved in the cellular immune response of ovine brucellosis.

Conclusions: Cytokines such as TNF- α and IFN- γ are highly effective in the cellular immune response (Th1) developed against ovine brucellosis. No other study was found in the literature in which the levels of these cytokines and interleukins were evaluated in sheep fetal tissues. In addition, these proinflammatory cytokines increased in parallel with the severity of the inflammatory reaction. To better understand the cytokine profile associated with ovine brucellosis, different pro- and anti-inflammatory cytokines should be evaluated comparatively and in detail in future studies.

Authors contribution: EK designed and wrote the manuscript; EK, EB and SD performed immunohisto-

chemical and histopathological analysis; HN and AY performed immunohistochemical and H&E stainings. MK performed statistical analysis. ÖÇ, FB and DA performed the diagnosis of Brucella agents.

Acknowledgments: This study was funded by the Scientific Research Projects Coordinatorship of Kafkas University (2019-TS-56).

Conflict of Interest: The authors declare that they have no conflicts of interest associated with this research.

REFERENCES

- Adem A and Duguma A, 2020. Characteristics and intracellular life of Brucella organism: a review. J Microb Biochem Technol 12:431.
- Agnone A, La Manna MP, Vesco G, et al., 2019. Analysis of interferongamma producing cells during infections by Yersinia enterocolitica O:9 and Brucella abortus in cattle. Vet Ital 55:149-155.
- Alton GG, Jones LM, Angus RD, et al., 1988. Techniques for the brucellosis laboratory. 17-62, Institut National de la Recherche Agronomique, Paris.
- Antunes JM, Allendorf SD, Appolinário CM, et al., 2013. Rough virulent strain of *Brucella ovis* induces pro- and anti-inflammatory cytokines in reproductive tissues in experimentally infected rams. Vet Microbiol 161:339-343.
- Bayu MD, 2018. Overview on common pathological changes and diagnostic methods of caprine and ovine Brucellosis. J Veter Sci Med 6:1-12.
- Büyük F, Çelebi Ö, Şahin M, et al., 2011. İki farklı koyun ve keçi sürüsünde Brucella ve Campylobacter ortak enfeksiyonu. Kafkas Univ Vet Fak Derg 17:177-180.
- Büyük F and Şahin M, 2011. Kars yöresinde atık yapan ineklerin çeşitli örneklerinden Brucella etkenlerinin kültürel ve moleküler yöntemlerle araştırılması ve olguların epidemiyolojik analizi. Kafkas Univ Vet Fak Derg 17:809-816.
- Dorneles EM, Teixeira-Carvalho A, Araújo MS, et al., 2015. Immune response triggered by *Brucella abortus* following infection or vaccination. Vaccine 33:3659-3666.
- Durán-Ferrer M, Léon L, Nielsen K, et al., 2004. Antibody response and antigen-specific gamma-interferon profiles of vaccinated and unvaccinated pregnant sheep experimentally infected with Brucella melitensis. Vet Microbiol 100:219-231.
- Eskandari-Nasab E and Moghadampour M, 2018. The relationship between IFN- γ and TNF- α gene polymorphisms and brucellosis: A meta-analysis. Adv Clin Exp Med 27:1701-1709.
- Feng Y, Zhu L, Peng X et al., 2017. Development of an interferon-γ release assay (IGRA) for detection of Brucella abortus and clinical diagnosis of brucellosis. | Infect Dev Ctries 11:847-853.
- Galindo RC, Muñoz PM, de Miguel MJ, et al., 2009. Differential expression of inflammatory and immune response genes in rams experimentally infected with a rough virulent strain of *Brucella ovis*. Vet Immunol Immunopathol 127:295-303.

- He Y, 2012. Analyses of Brucella pathogenesis, host immunity, and vaccine targets using systems biology and bioinformatics. Front Cell Infect Microbiol 2:2.
- Hop HT, Reyes AWB, Huy TXN, et al., 2017. Activation of NF-kBmediated TNF-induced antimicrobial immunity is required for the efficient Brucella abortus clearance in RAW 264.7 cells. Front Cell Infect Microbiol 7:437.
- Li G, Lv D, Yao Y, et al., 2021. Overexpression of ASMT likely enhances the resistance of transgenic sheep to brucellosis by influencing immune-related signaling pathways and gut microbiota. FASEB J 35:e21783.
- López-Goñi I, García-Yoldi D, Marín CM, et al., 2008. Evaluation of a multiplex PCR assay (Bruce-ladder) for molecular typing of all Brucella species, including the vaccine strains. J Clin Microbiol 46:3484-3487.
- Marmur J, 1961. A procedure for the isolation of deoxyribonucleic acid from micro-organisms. J Mol Biol 3:208-218.
- Poester FP, Samartino LE and Santos RL, 2013. Pathogenesis and pathobiology of brucellosis in livestock. Rev Sci Tech 32:105-115.
- Priyanka C, Shringi BN, Choudhary OP, et al., 2021a. Cytokines in Brucellosis: biological rhythm at the interface of innate and adaptive immunity. Biol Rhythm Res 52:1031-1043.
- Priyanka C, Shringi BN, Choudhary OP, et al., 2021b. Expression profiling of cytokine-related genes in *Brucella abortus* infected cattle. Biol Rhythm Res 52:654-665.
- Pérez-Sancho M, Durán-Ferrer M, García-Seco T, et al., 2014. Interferongamma responses in sheep exposed to virulent and attenuated Brucella melitensis strains. Vet Immunol Immunopathol 160:123-128.
- Ritchie JA, Rupper A, Cardelli JA, et *al.*, 2012. Host interferon-γ inducible protein contributes to Brucella survival. Front Cell Infect Microbiol 2:55.
- Salas-Téllez E, Núñez del Arco A, Tenorio V, et al., 2005. Subcellular fractions of *Brucella ovis* distinctively induce the production of interleukin-2, interleukin-4, and interferon-gamma in mice. Can J Vet Res 69:53-57.
- Sancho P, Tejedor C, Sidhu-Muñoz RS, et al., 2014. Evaluation in mice of Brucella ovis attenuated mutants for use as live vaccines against B. ovis infection. Vet Res 45:61.
- Sözmen M, Tunca R, Beytut E, et al., 2010. Brucella melitensis ile doğal enfekte koyun abortuslarında CD3 ve lambda hafif zincir immunoglobulin ekspresyonu. Kafkas Univ Vet Fak Derg 16:353-363.
- Suraud V, Jacques I, Olivier M, et al., 2008. Acute infection by conjunctival route with Brucella melitensis induces IgG+ cells and IFN-gamma producing cells in peripheral and mucosal lymph nodes in sheep. Microbes Infect 10:1370-1378.
- Unver A, Erdogan HM, Atabay HI, et al., 2006. Isolation, identification, and molecular characterization of *Brucella melitensis* from aborted sheep fetuses in Kars, Turkey. Rev Méd Vét 157:42-46.
- Yesilmen S, Yaman T, Sağsöz H, et al., 2018. Diagnosis of Q Fever and Brucellosis in aborted ovine fetuses by microbiological, pathological and immunohistochemical methods. Acta Vet-Beograd 68:168-177.
- Zhou Z, Gu G, Luo Y, et al., 2020. Immunological pathways of macrophage response to Brucella ovis infection. Innate Immun 26:635-48.
- Zhu L, Feng Y, Zhang G, et al., 2016. Brucella suis strain 2 vaccine is safe and protective against heterologous Brucella spp. infections. Vaccine 34:395-400