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Dear Scientist,

The 9th International Congress on Advances in Veterinary Sciences & Technics (icavst) was hybrid organized in Sarajevo, Bosnia and Herzegovina. We are very happy for organizing this congress in such a beautiful city and country that we have strong historical ties.

We wanted to make this conference little bit special by bringing scientist together from different disciplines of veterinary area and to open new research and cooperation fields for them. In this sense, we desired to bring the distinguished scientist together to get know each other and to develop and implement new joint projects.

The scientist joined the congress was from different country and mostly from Turkey. Total over the one hundred scientists were registered in the congress. The total number of submissions were 39 and after a careful evaluation 35 submissions were accepted by our scientific committee and 6 of them were accepted as poster presentation and 29 of them were accepted as oral presentation and all those presentations was taken place in the conference booklet.

We would like to send our special thanks to **Prof Dr. Hesham El Enshasy**, also the International University of Sarajevo, Universiti Teknologi Malaysia, for their contributions. Also, we would like to express our special thanks to the organization team especially **Mr. Musa Köse** and Mr. **İsmet Uzun,** ZENITH Group workers, and the scientific committee. And finally, most importantly we thank all the participants individually to join this conference.

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ANTIBIOTIC RESISTANT MICROBES (THE NEW GENERATION OF SMART KILLERS): ARE WE PREPARED FOR?

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Abstract:

Antibiotics have been used for decades as the most potent therapy for the treatment of many infectious diseases based on their high antimicrobial properties. By definition antibiotics are chemical substances produced by living organisms and inhibit the growth of other microorganisms when used at low concentration. Since the discovery of antibiotics in the mid of 1930s, these group of compounds saved live of hundred of millions. It was also assumed that the victims of the second world war could be tripled if there were no antibiotics discovered and used in the treatment. Nowadays, antibiotics are widely used not only for human health sector but also in agriculture, aquaculture, and animal feed industries. This widespread of application of antibiotics for non-medical uses in addition of misuse and mis-dose of antibiotics create big problem related to antibiotics resistance. This will lead to that antibiotics resistant pathogens will be the main human killers by 2050. Therefore, new approaches need to be carried out to minimize this risk. At first, the control of antibiotic applications in non-medical fields to minimize the creation of antibiotic resistance by continued exposure to sub-therapeutic doses of antibiotics. Second, the integration of new strategies on controlling human and animal pathogens such as natural (plant based and animal based) anti-infective, probiotics, immunomodulators can be applied as first line in the treatment before using antibiotics. This presentation, highlights the potential new trends for utilization of new anti-infective classes in human and animal health care industries.

Keywords: Antibiotic resistance, human health, food security

MICROBIOLOGICAL FOOD SAFETY CHALLENGES ASSOCIATED WITH NOVEL PLANT-BASED FOOD PRODUCTS

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Abstract:

Contamination of foods with pathogenic microorganisms, chemicals, allergens, or physical hazards can pose health risks for consumers and economic loss to the industry. Several known food safety hazards are associated with animal-based food products. Plant-based food products have emerged as a major group of novel foods in the global food supply. Similar to animal-based or other foods, plant-based foods could naturally contain certain biological or chemical contaminants. Food safety hazards including bacteria, viruses, parasites, mycotoxin, heavy metals, and pesticide residues could be introduced in new plant-based food products through external factors or cross-contamination. Furthermore, the processing of plant-based ingredients can also create their unique type of food safety risks. For example, applying extreme temperatures and mechanical energy to manufacture extruded products may generate unwanted chemical residues. Undoubtedly, plant-based food products offer promising substitutions for animal-based food choices to meet the future protein demand. The major challenge is the availability of limited information on the microbiological risk assessment of new plant-based food products entering the market. This presentation will discuss microbiological food safety issues, challenges, and uncertainties in manufacturing plant-based food products.

Keywords: Alternative proteins, Plant-based foods, Food safety, Microbiological hazards, Food processing, Health risks

INVESTIGATION OF *CRYPTOSPORIDIUM* SPECIES IN CALVES IN BITLIS PROVINCE

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Abstract:

Cryptosporidium species are protozoan parasites that mainly affect intestinal epithelial cells in various animal species and humans and are characterized by diarrhea and other gastrointestinal symptoms. Infection usually occurs in calves within the first few weeks of life and causes severe watery diarrhea in the animals. In addition to diarrhea, animals also suffer from dehydration, weight loss and growth retardation. The risk of parasite transmission is particularly high on farms with poor hygiene conditions. This study was conducted to determine the prevalence of *Cryptosporidium* species in calves in Bitlis province. Stool samples were obtained from 100 calves aged 0-3 months on various farms. Samples from the rectum of each animal were placed in pre-labeled stool containers. The samples brought to the laboratory were stained with Kinyoun Acid-Fast staining method and examined under a microscope at X1000 magnification for oocysts of *Cryptosporidium* species. Subsequently, DNA extraction and nested PCR analyses were performed. DNA extraction and Nested PCR analysis were then performed. Samples were then run on a 1.5% agarose gel and images were obtained using a gel imager. After bidirectional sequencing analyses of positive PCR samples, comparisons were made with relevant reference genes in GenBank through BLAST and alignment. *Cryptosporidium* spp. were detected in 11 (11%) of 100 samples by microscopic examination and in 14 (14%) samples by nested PCR. *Cryptosporidium parvum* in 12 were detected by sequence analysis and *Cryptosporidium ryanae* in two samples. In this study, the prevalence of *Cryptosporidium* spp. in calves in Bitlis province was determined and the species were identified. The detection of *C. parvum* in this study suggests that calves with diarrhea may be a source of transmission to other animals and humans. Therefore, animal owners and people in close contact with animals need to be informed about cryptosporidiosis. It is also necessary to examine the water resources in the region.

Keywords: *Cryptosporidium parvum, Cryptosporidium ryanae*, calves, Bitlis

** This study was supported by Van Yüzüncü Yıl University Scientific Research Projects Coordination Unit as a Research Project with Undergraduate Student Participation with Project Code TLO-2024-10969.*

DOPPLER ECHOCARDIOGRAPHIC VALUES OF THE AORTA AND MAIN PULMONARY ARTERY İN CONSCIOUS HEALTHY RABBITS AND THE EFFECT OF PROPOFOL

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Abstract:

Objective: The aim of study is to determine the reference intervals of Doppler echocardiographic parameters obtained from the aorta (Ao) and main pulmonary artery (MPA) flows in unsedated healthy rabbits and to evaluate the effect of propofol on these echocardiographic parameters in sedated rabbits.

Material-Method: Forty healthy male New Zealand white rabbits were used in the study. After obtaining the aortic and pulmonary artery flow parameters from conscious rabbits(Group C), the same parameters were remeasured under sedation (Group P) following the administration of propofol(15 mg/kg).Propofol caused significant changes in aortic and pulmonary flow parameters in both groups but did not significantly affect the mitral flow parameters.Reference interval mean values were determined as follows: for aortic(Ao) acceleration time(AT), 0.028±0.006 seconds(s) (0.018-0.035s); Ao ejection time(ET), 0.116±0.017s (0.096-0.154s); and Ao AT/ET, 0.24±0.036 (0.18-0.3). For MPA AT, 0.05±0.01s (0.03-0.07s); MPA ET, 0.137±0.018s (0.099-0.174s); and MPA AT/ET, 0.38±0.037 (0.33-0.49). After the administration of propofol, the reductions in left ventricular ejection fraction (EF), fractional shortening (FS), Ao peak velocity, and peak pressure gradient were statistically significant ($p< 0.0001$). AT was longer in both Ao and MPA ($P<0.05$), and AT/ET was increased ($P<0.001$). The changes were statistically significant for mitral flow E wave deceleration time (Edec) and A wave peak velocity (Avel)($P<0.05$). Propofol caused significant changes in aortic and pulmonary flow parameters in both groups but did not significantly affect the mitral flow parameters.

Conclusion: The use of a sedative protocol to reduce stress and facilitate echocardiography in rabbits is common, especially in experimental studies. This study is the first to present reference intervals for AT, ET, and AT/ET ratios of aortic and pulmonary artery flows in rabbits. Propofol slightly affected left ventricular systolic function parameters but did not change its pattern on mitral flow. The changes in aortic and pulmonary AT/ET ratios should be taken into account in future studies.

Keywords: acceleration and ejection time, aorta, echocardiography, main pulmonary artery, propofol, rabbit.

INVESTIGATION OF THE PROGNOSTIC SIGNIFICANCE OF SERUM PENTRAXIN-3 CONCENTRATIONS IN CANINE PARVOVIRUS INFECTION: A PRELIMINARY REPORT

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Abstract:

Parvovirus infection (CPV) is a rapidly progressing fatal viral disease with high virulence and affinity for cells with high mitotic activity such as gastrointestinal epithelium, bone marrow, lymph tissue, cardiac myocytes in dogs. Studies involving many biomarkers are being carried out to determine the severity and diagnosis of the disease in infected animals. This study aims to evaluate Pentraxin-3, which is produced by damaged tissues in the first hours following inflammation and increases in direct proportion to the severity of the disease, for the first time in CPV infection. Haemogram and PTX-3 concentrations were compared between the three groups by taking blood samples from 0-6 month old healthy control group (n=7) and gastroenteritis group (n=7) on day 0 and from parvoviral enteritis patients (n=14) on days 0, 1, 3, and 7. The mean values of serum PTX-3 concentrations were 196.929pg/mL in the gastroenteritis group and 212.643pg/mL in the control group, while they were 298.9pg/mL, 316.69pg/mL, 333.653pg/mL, 254.07pg/mL in the parvovirus group on days 0, 1, 3, and 7, respectively. PTX-3 concentration values were also measured from necropsy samples taken from some deceased animals: 938.25 pg/mL in the heart and 602.875 pg/mL in the intestine. Preliminary findings indicate that there is a relationship between PTX-3 concentrations and disease severity.

Keywords: Parvovirus, canine, viral

* *This study was supported by Aksaray University Scientific Research Projects Coordination Office (Project no: 2023-002).*

INVESTIGATION OF THIOL/DISULFIDE BALANCE IN DOGS WITH MONOCYTIC EHRLICHIOSIS

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Abstract:

Ehrlichiosis is a zoonotic disease commonly seen in dogs and transmitted through ticks, characterized by a decrease in blood cells. Canine Monocytic Ehrlichiosis (CME) is primarily caused by Ehrlichia canis. The most common vector for transmission is the Rhipicephalus sanguineus tick. CME progresses through three stages: subclinical, acute, and chronic, with symptoms such as hyperthermia, anemia, splenomegaly, myalgia, lethargy, and thrombocytopenia appearing during these stages.

During the presence of the disease, the production of oxygen radicals increases, and the balance with antioxidants is disrupted, a condition known as oxidative stress. Thiol groups, which are abundantly present in plasma, play a crucial role in reducing oxidative damage. The oxidation of thiol groups leads to the formation of reversible disulfide bonds. The thiol-disulfide homeostasis acts as an important defense mechanism against oxidative stress at the cellular level.

In this study, 10 dogs with Canine Monocytic Ehrlichiosis formed the test group, while 10 healthy dogs served as the control group. The serum samples were analyzed using the method developed by Erel and Neşelioğlu (2014). The control group's Total Thiol Level (TTL) was measured at 371.13 µmol/L, Native Thiol Level (NTL) at 254.0 µmol/L, and the NT/TTL ratio at 68.32 µmol/L. For the Ehrlichiosis group, the Total Thiol Level (TTL) was measured at 271.3636 µmol/L, Native Thiol Level (NTL) at 193.9090 µmol/L, and the NT/TTL ratio at 72.18489 µmol/L. The control group's disulfide level was 58.56 µmol/L, DsTT 16.72 µmol/L, and DsNT 23.75 µmol/L. The Ehrlichiosis group's disulfide level was 38.7272 µmol/L, DsTT 13.90755 µmol/L, and DsNT 21.85309 µmol/L.

The results of the study revealed that the thiol-disulfide balance parameters (NT, TT, Ds) were significantly ($p<0.005$) lower in dogs with Ehrlichiosis. These findings indicate that the thiol-disulfide balance is significantly reduced in dogs with Ehrlichiosis and that oxidative stress is present. As the first study in the literature to examine this balance in canine monocytic ehrlichiosis, it has demonstrated the presence of oxidative stress in the pathophysiology of Ehrlichiosis.

Keywords: Canine Monocytic Ehrlichiosis, Thiol/Disulfide Balance, Oxidative Stress

**TÜBİTAK 2209-A*

INVESTIGATION OF THIOL/DIOXULPHIDE BALANCE IN CORANAVIRUS INFECTION OF CATS

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Abstract:

Coronavirus is a disease with a variable prognosis that progresses from a mild clinical case to a more severe clinical case in humans and animals. It is known to cause mostly respiratory, gastrointestinal and various systemic infections. Feline coronavirus (FCoV) is a virus that is transmitted by the faecal-oral route and infects intestinal cells. FCoV is divided into two main biotypes: Feline enteric coronavirus (FECV) and feline infectious peritonitis virus (FIPV). FECV remains a mild and spontaneous infection with symptoms that are usually confined to the intestines, whereas FIPV is a more aggressive form that occurs when FECV mutates and is often fatal. Oxidative stress is caused by an imbalance of free radicals and antioxidant defence mechanisms and can damage cell membranes, proteins and DNA. Thiol is a new and important antioxidant mechanism used to eliminate reactive oxygen against oxidative stress by non-enzymatic means. Oxidative stress has been found to play a role in the pathogenesis of many diseases. In this study, it was aimed to determine oxidative damage by determining thiol/disulphide balance.

Eleven cats showing symptoms of FIP diagnosed with coronavirus constituted the patient group. Seven cats with no health problems in general health screening and negative coronavirus test in rapid diagnostic test kit constituted the control group. The samples obtained from the groups were analysed using a new commercially available automated and spectrophotometric method developed by Erel and Neselioğlu (2014) (Rel Assay Diagnostics, Turkey).

Serum total thiol, native thiol and NT/TT ratio were found to be lower in FCoV patients compared to the control group ($P<0.05$), while DsTT and DsNT were found to be higher ($P<0.05$).

In the study, thiol-disulphide balance parameters (NT, TT) were significantly ($P<0.05$) lower, indicating that oxidative stress develops and the antioxidant system is activated in cats with coronavirus."

Keywords: Cat, oxidative stress, thiol/disulphide balance, coronavirus

**TÜBİTAK 2209-A*

ANIMAL HEALTH RESEARCH TENDENCIES IN TÜRKİYE: GDARP SUPPORTED PROJECTS

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Abstract:

The General Directorate of Agricultural Research and Policies (GDARP) is the primary public institution in Türkiye that supports agricultural research projects in line with the Agricultural Research Master Plan. The "Animal Health" research opportunity area (ROA) in this plan is the strongest area and directs animal health research in Türkiye with the projects carried out by the institutes. This study examines 351 finalized research projects within the scope of the animal health ROA, supports by GDARP since its establishment (between 1992-2024).The distribution of projects across programs and institutes, the number of resulting articles, and the keyword frequencies in final reports are analyzed. On average, between 3 and 22 projects are finalized annually during the years under review. The institutes with the highest project finalizations are respectively Etlik (62), Pendik (52), Bornova (45), and Şap (45). In terms of program rankings, bovine and ovine animal health 47.9% (168/351), veterinary health products 21.4% (75/351), aquaculture health 14% (49/351), and poultry health 9.4% (33/351) occupy the top positions. Analysis of keyword density reveals sheep as the most frequently mentioned term with (54) repetitions, followed by vaccine (53), bovine (48), ELISA (46), foot and mouth (45), PCR (43), and virus (42). The correlation between research programs and keywords indicates a focus on sheep, bovine, foot-and-mouth disease for bovine and ovine health, as well as vaccine, ELISA, and PCR for veterinary health products. Furthermore, viral diseases, specifically foot and mouth and virus, emerge prominently. This underscores the current emphasis on researching animal health related to food value and the development of vaccines and diagnostic methods for their improvement. Future trends in animal health research are expected to incorporate new technologies, modeling, artificial intelligence, and data analysis methods.

Keywords: Animal health, GDARP, project, research tendency, Türkiye

EFFECTS OF LACTATION PERIOD ON SOME BLOOD PARAMETERS AND ANAE/ACP-ASE ENZYME ACTIVITIES IN DOMESTIC DONKEYS

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Abstract:

It was aimed to research the influences of the lactation period on some hematological (RBC, WBC and its subtypes, HCT, HGB, MCH, MCHC, MCV, and PLT) and biochemical parameters (ALT, AST, GGT, BUN, and CREAT) as well as ANAE and AcP-ase positive lymphocytes percentages in domestic donkeys. For this purpose, 20 female donkeys were selected and divided into two equal groups as control (non-lactating, n = 10) and lactating (n = 10). They were in the middle of lactation (three to six months old), ranging in age from five to fourteen. Following the routine clinical examination, blood samples were taken from the animals in order to measure the activities of the ANAE/AcP-ase enzyme as well as several blood parameters. As a result, RBC, HCT, and HGB values were higher in lactating donkeys than non-lactating donkeys ($p < 0,05$). Serum AST and GGT values were found to be statistically higher in lactating animals ($p < 0,05$). Although enzyme activities were high in lactating donkeys, ANAE and AcP-ase positive lymphocyte percentages were found to be similar between the groups ($p > 0,05$). In conclusion, the middle-lactation phase in female donkeys was found to have an impact on several blood parameters, but not on the activity of enzymes (AcP and ANAE).

Keywords: AcP-ase, ANAE, Biochemistry, Donkey, Hematology, Lactation

**Balıkesir Üniversitesi BAP birimi tarafından Desteklenmiştir.*

THE ASSESSMENT OF NEUTROPHILIC, BASOPHILIC AND EOSINOPHILIC LEUKOCYTES BY GEOMETRIC-MORPHOMETRIC ANALYSIS AFTER THE APPLICATION SOME DENTAL CEMENTS IN RODENTS

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Abstract:

The aim of the research was to determine possible changes in the morphology of cells of the granular leukocyte order of peripheral blood, using geometric morphometric tests, after the application of calcium-aluminate and calcium-silicate cements to the dental pulp in adult rats.

The study included 27 Wistar rats, divided into an experimental group (n=18) and a control group (n=9). In all animals, cavity preparation was performed on the occlusal surface of the maxillary first and second molars, using a technical micromotor and a sterile round diamond drill. Trepanation of the tip of the pulp cavity was performed, and placement of calcium-aluminate and calcium-silicate dental cements directly on the pulp. Peripheral blood samples were collected by v. caudalis puncture, with the aim of making blood smears. In the tpsUtil program, two-dimensional models of the examined leukocytes were created and they were converted into tps files, on which sixteen specific points were marked in the tpsDig program. Eight points were marked on the outside, and the remaining eight points were marked on the nucleus of the leukocytes examined. We analyzed their shape in the MorphoJ program.

No morphological differences between the neutrophilic and eosinophilic leukocytes from the experimental group and those from the control group were proven. Basophils was not represented in a sufficient percentage and did not meet the statistical criteria for inclusion in the study. Further research is necessary.

Keywords: granular leukocytes, rat, calcium-aluminate and calcium-silicate cements, dentin

A COMBINATION OF MULTIPLEX PCR AND QUANTITATED CAPILLARY ELECTROPHORESIS (QCE) FOR THE DETECTION OF NINE RESPIRATORY PATHOGENS SIMULTANEOUSLY IN CATS AND THE CLINICAL RELEVANCE

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Abstract:

Studies of Mycoplasma felis (My), Bordetella bronchiseptica (B), Chlamydophila felis (Cf), Feline Herpesvirus-1 (FHV), and Feline Calicivirus (FCV) have shown to be pathogenic in Feline Upper Respiratory Tract Disease (FURTD). Moreover, severe acute respiratory syndrome coronavirus 2 (SA2), Streptococcus equi subsp. zooepidemicus (SE), Streptococcus canis (SC), and influenza virus (INF) have been proven to be significant in FURTD in recent years and may complicate the management of FURTD. Although coinfection of some pathogens seems often in FURTD, there is still a lack of studies on the roles of these 9 pathogens in FURTD synchronously and the correlation of the pathogen loads to their clinical importance. This study aimed to screen these pathogens simultaneously and quantitate the pathogens in one test. The former could reveal the relationship among these pathogens, and the latter could implicate the clinical severity. A platform using multiplex PCR/RT-PCR with quantitated capillary electrophoresis (qCE) was developed. One hundred and ten upper respiratory swab samples of symptomatic cats were collected from March 2021 to February 2024 for quantitated detection of 9 respiratory pathogens at the same time, including My, B, Cf, FHV, FCV, SA2, SE, SC, and INF. The prevalence of the pathogens was My (18.2% (20/110)), B (19.1% (21/110), Cf (5.5%(6/110)), FHV (25.5%(28/110)), FCV (6.4%(7/110)), SA2 (4.5% (5/110)), SE (17.3%(19/110)), SC (0.9%(1/110)), and INF (0.9%(1/110)). Coinfection with other pathogens was common in My, B, FHV, SA2, and SE. A higher FHV load showed significantly more severe clinical signs. This study not only developed a more efficient detection system but also provided a more comprehensive diagnosis of FURTD. The role of SA2 in cats in Taiwan was revealed as well.

Keywords: coinfection, Feline Upper Respiratory Tract Disease, quantitated capillary electrophoresis, SARS-CoV-2

FELINE HYPERTROPHIC CARDIOMYOPATHY: AN ECHOCARDIOGRAPHIC OVERVIEW

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Abstract:

First described in veterinary medicine in 1977, Hypertrophic Cardiomyopathy (HCM) is now the most common heart disease in cats, with an estimated prevalence of 15% in the general feline population and up to 29% in older cats. By definition, HCM is concentric left ventricular hypertrophy in the absence of other haemodynamic or metabolic causes. Although a genetic cause has been identified in some breeds, the aetiology of HCM is still unknown in many affected individuals. It is worth noting that feline HCM is known for its heterogeneity. With different morphological and haemodynamic patterns and variable clinical presentations and outcomes. From benign subclinical forms to fatal cardiovascular complications and even sudden cardiac death. Accordingly, and similar to its human counterpart, feline HCM often goes unrecognised and represents a real diagnostic challenge in practice.

In fact, it seems absurd to try to visualise an intricately shaped organ with a complex 3D structure such as the heart, on a 2D orthographic plan. Fortunately, however, this challenging task has become achievable thanks to the ultrasound modality and its different application modes (2D, Motion and Doppler). Cardiac ultrasound, or echocardiography, is the gold standard for diagnosing HCM in cats. This real-time imaging technique allows assessment of myocardial hypertrophy and its distribution within both ventricles, assessment of left atrial size and mitral valve apparatus morphology, identification of outflow tract obstruction and evaluation of systolic and diastolic function. In addition, echocardiography plays a key role in the staging of HCM patients, in guiding therapeutic decisions and in prognostication.

This review aims to provide updated information on the main echocardiographic features of feline HCM and related ultrasound prognostic indicators.

Keywords: Feline hypertrophic cardiomyopathy, cat, echocardiography

EVALUATION OF SIRS AND QSOFA SCORE IN DOGS WITH PYOMETRA

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Abstract:

The aim of the presented thesis is to evaluate the utility of Systemic Inflammatory Response Syndrome (SIRS) and quick Sequential Organ Failure Assessment (qSOFA) scores for the rapid, reliable, and accurate detection of organ damage caused by sepsis resulting from endotoxemia in dogs with pyometra. For this purpose, the study utilized a group of dogs brought to the Ankara University Faculty of Veterinary Medicine Animal Hospital Obstetrics and Gynecology Clinic, exhibiting clinical symptoms of pyometra such as depression, vaginal discharge, lethargy, fever, polyuria, polydipsia, and anorexia. The dogs were diagnosed with pyometra following gynecological, clinical, and laboratory examinations and underwent surgical treatment (experimental group, n:20). A control group consisting of healthy dogs aged 1-8 years undergoing routine ovariohysterectomy (OHE) surgery was also included (control group, n:20). Prior to surgery, complete blood count and serum biochemistry analysis (blood urea nitrogen, creatinine, alkaline phosphatase, alanine aminotransferase, aspartate aminotransferase, albumin, creatine kinase) were performed for both groups for preoperative control and diagnostic assessment. SIRS and qSOFA scores were measured in both groups before surgery. According to the study results, the sensitivity of qSOFA score in diagnosing sepsis in dogs with pyometra was determined as 65%, with a specificity of 100%. The sensitivity of the SIRS score was found to be 95%, with a specificity of 100%. The AUC value of the SIRS score was 0.985, indicating a high accuracy of the SIRS score in the diagnosis of sepsis. The AUC value for the qSOFA score was found to be 0.896, suggesting good performance in diagnosing sepsis but with lower accuracy compared to the SIRS score. Evaluations concluded that the SIRS score is a more effective screening tool than the qSOFA score and that the combined use of both scores provides more accurate results in the diagnosis of sepsis in dogs with pyometra.

Keywords: Pyometra, qSOFA, Sepsis, SIRS

RESEARCH OF THE SEROPREVALENCE OF TOXOPLASMA GONDII, BRUCELLA ABORTUS, COXIELLA BURNETII AND CHLAMYDOPHILA ABORTUS FACTORS IN THE SHEEP POPULATION IN THE TURKISH REPUBLIC OF NORTHERN CYPRUS

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Abstract:

There is no detailed and comprehensive research previously conducted in the TRNC on the infectious factors that cause abortion in sheep and goats. It is seen that the districts with the highest sheep breeding in TRNC are Nicosia with the presence of 61.613 sheep, Vadili with the presence of 44.795 sheep, and Ziyamet district with the presence of 42.632 sheep. In this study, it is aimed to serologically determine the presence of antibodies to Brucellosis, Chlamydiosis, Toxoplasmosis and Q Fever, which are important abortion factors in sheep, and to investigate the prevalence rate in these 3 regions. 10 sheep samples were collected from each 45 establishments located in Nicosia, Vadili and Ziyamet districts, where sheep breeding is most intense in TRNC. 150 ewes from 15 farms have been sampled in each district as of 10 samples from each farm. Brucellosis, Chlamydiosis, Toxoplasmosis and Q Fever were examined in blood samples. With the complement fixation test, all samples were determined negative for Brucellosis. Antibody presence was searched with an ELISA kit for the other diseases. During the tests 14 positive Chlamydophila abortus, 96 positive Toxoplasma gondii in and 175 positive Coxiella burnetii samples were detected. Which gave us 3,11%, 21,33 % and 38,88 % prevalences respectively. It has been determined that the pathogens C. abortus, T. gondii and C. burnetii have been identified in TRNC and the abortion problem can be reduced in these regions by eradication programs and taking biosecurity measures, also as a result of eradication in progress, Brucellosis is no more a serious problem in these regions.

Keywords: Abortion, Northern Cyprus, Seroprevalance, Sheep

MICROSCOBIC AND MOLECULAR INVESTIGATION OF THE PREVALENCE OF *CRYPTOSPORIDIUM* SPP. IN CALVES IN AĞRI PROVINCE, TÜRKIYE

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Abstract:

Cryptosporidium species are obligate intracellular protozoa that occur in many animal species and humans worldwide and cause significant intestinal disorders. The aim of this study was to investigate the prevalence of *Cryptosporidium* spp. in calves in Ağrı province. In this study, stool samples were taken from a total of 150 calves aged 0-3 months from different farms in Ağrı province. The stool samples taken from the rectum of the calves were placed in stool containers, labeled and delivered to the Research Laboratory of the Department of Parasitology, Faculty of Medicine, Van Yüzüncü Yıl University. The samples were examined microscopically (Kinyoun's acid-fast staining method) for *Cryptosporidium* spp. oocysts. DNA was then extracted from the samples and Nested PCR was performed. It was then run on a 1.5% agarose gel and visualized on a gel imaging device. *Cryptosporidium* spp. were detected in 16% of the samples by microscopic examination and in 20% of the samples by Nested PCR. Similar to previous studies, the molecular method was detected to be more sensitive than the microscopic method.

Keywords: *Cryptosporidium* spp., Ağrı province, calves, Nested PCR

** This study was supported by Van Yüzüncü Yıl University Scientific Research Projects Coordination Unit as a Research Project with Undergraduate Student Participation with Project Code TLO-2022-10140.*

INVESTIGATION OF *EHRLICHIA CANIS, EHRLICHIA CHAFFEENSIS* AND *EHRLICHIA EWINGII* IN TICKS OBTAINED FROM SHEEP IN IĞDIR PROVINCE BY MOLECULAR METHODS

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Abstract

Ehrlichia species are obligate intracellular rickettsial pathogens carried by ticks and affect sheep. Ehrlichiosis can cause fever, loss of appetite, respiratory disorders, neurological symptoms and even death in sheep. The aim of this study was to investigate the presence of *Ehrlichia canis*, *Ehrlichia chaffeensis* and *Ehrlichia ewingii* in ticks obtained from sheep in Iğdır province. A total of 648 ticks were obtained from 150 sheep in different farms in Iğdır province and transported to Research Laboratory of Department of Parasitology, Medical Faculty, Van Yüzüncü Yıl University under cold chain conditions. Tick species identification was performed under a stereo microscope. A total of 100 tick pools were created based on the tick species. Six or seven ticks were placed in each tick pool. DNA extraction was performed from tick samples taken from tick pools using a commercial tissue kit. *Erlichia canis*, *E. chaffeensis* and *E. ewingii* were analyzed by Nested PCR using specific primers to determine their distribution. PCR products were run on 1.5% agarose gel electrophoresis and images were obtained using a gel imager. Sequence analysis was applied to positive samples and sequencing results were compared with the corresponding reference genes in GenBank using BLAST and alignment. Microscopic examination revealed that all tick specimens were *Rhipicephalus bursa*. By Nested PCR, *E. canis* was detected in 10 out of 100 tick pools, while *E. chaffeensis* and *E. ewingii* were not detected in any pool sample. In this study, *E. canis* was detected in *R. bursa* samples obtained from sheep in Iğdır province and it was concluded that people residing in the province should be careful against this tick species which is the carrier of this zoonotic agent. In addition, initiating tick control activities is of great importance in preventing the transmission of the disease.

Keywords: *Ehrlichia canis*, *Ehrlichia chaffeensis*, *Ehrlichia ewingii*, sheep, tick

** This study was supported by Van Yüzüncü Yıl University Scientific Research Projects Coordination Unit as a Research Project with Undergraduate Student Participation with Project Code TLO-2024-11293.*

INVESTIGATION OF *GIARDIA INTESTINALIS* IN WATER BUFFALOES IN IĞDIR PROVINCE BY MICROSCOPIC AND MOLECULAR METHODS

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Abstract

Giardia intestinalis is a common intestinal protozoan that infects a variety of domestic and wild mammals, birds and humans, and is particularly common in farm animals. The aim of this study was to determine the prevalence and assemblages of *Giardia duodenalis* in water buffaloes in the Iğdır province. Stool samples were taken from 100 water buffaloes in various farms in Iğdır province. The samples were placed in fecal containers and transported to Research Laboratory of Department of Parasitology, Medical Faculty, Van Yüzüncü Yıl University under cold chain conditions. The samples were examined for G. intestinalis cysts by native-Lugol method under light microscope at X400 magnification. DNA extraction and Nested PCR analysis were then performed. The samples were then run on a 1.5% agarose gel and images were obtained using a gel imager. After pairwise sequencing analysis of positive PCR samples, comparisons were made with the corresponding reference genes in GenBank by BLAST and alignment. *Giardia intestinalis* was found in 7% of the samples by microscopic examination and in 10% by nested PCR. By comparison with the corresponding reference genes in GenBank, three samples were determined to belong to Assemblage A, two samples to Assemblage B, and five samples to Assemblage E. As a result of this study, Assemblage E was most frequently encountered in farm animals, and in addition, zoonotic Assemblage A and B were also detected. Zoonotic assemblages are important in the infection of farmers. More comprehensive studies need to be carried out in the province.

Keywords: *Giardia intestinalis*, water buffalo, Nested PCR, Iğdır

**This study was supported by Van Yüzüncü Yıl University Scientific Research Projects Coordination Unit as a Research Project with Undergraduate Student Participation with Project Code TLO-2024-11292.*

INVESTIGATION OF THE PREVALENCE OF TOXOPLASMA GONDII IN OWNED CATS IN DIYARBAKIR REGION

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Abstract:

Toxoplasmosis is a zoonotic disease caused by Toxoplasma gondii, an obligate intracellular protozoan in the Apicomplexa phylum. The agent has a wide host range and infects cats and other warm-blooded vertebrates. Toxoplasmosis is generally subclinical in cats, but various clinical findings may be encountered depending on the affected system. Although there are many studies on Toxoplasma gondii in Türkiye, no data has been found to investigate the prevalence of Toxoplasma gondii in cats in our region. This study aimed to reveal the prevalence of Toxoplasma gondii in owned cats in the Diyarbakır region. The research material consisted of 59 cats of different breeds, ages and genders showing clinical findings related to toxoplasmosis. As a result of the examination of blood samples taken for diagnostic purposes from the cats included in the study by ELISA, %S/P≥50 was detected and positivity was detected in 7 of the 59 cats, and it was determined that all of these positive results were female cats. As a result, it was determined that the prevalence of toxoplasmosis in owned cats in the Diyarbakır region was 11.86%, and it was concluded that toxoplasmosis is an important problem that needs to be addressed.

Keywords: Cat, prevalance, toxoplasmosis

DETERMINATION OF BLOOD SERUM MAGNESSIUM LEVELS IN DOGS WITH DEGENERATIVE MITRAL VALVE DISEASE

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Abstract:

Degenerative mitral valve disease has been identified as the most common acquired heart disease of dogs characterized by accumulation of glycosamonoglycans on atrioventricular valves. Hypomagnesemia is a common finding in people with mitral valve disease. There are also few studies considering this possible association in veterinary literature were defined. The aim of this study was to evaluate the association between magnessium levels and severity of the mitral valve diasease. Fifteen Stage A (clinically healthy) and 15 Stage C mitral valve dogs classified according to ACVIM consensus were enrolled into the study. All dogs were evaluated by physical examination, routine blood analyses (complete blood count, urea, creatinine, ALT, ALP, AST, CK, glucose, sodium, potassium and serum magnessium levels) and diagnostic imaging (radiography and echocardiography). Dogs with secondary disease affecting cardiac health were excluded. Although magnessium levels were vary among groups, no statistical differences were defined (p=0.882). In conclusion: Although few studies reported hypomagnesemia in veterinary literature in dogs with mitral valve diseas were present, the study here could not clearly reflects this possible association. Further studies with larger dog population with standadises feedig regimes are requied.

Keywords: Degenerative Mitral Valve Disease, Dog, Magnessium

DYSBIOSIS AND HEMORRHAGIC SHOCK: CARDIOVASCULAR EFFECTS

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Abstract:

Gut dysbiosis refers to the imbalance or maladaptation of the gut microbial community. Hemorrhagic shock is a state of hypoperfusion caused by an inadequate circulatory system, leading to an imbalance between the oxygen supply to tissues and their metabolic demands. Several compensatory mechanisms are activated in the body to prevent or reverse the changes in cardiovascular parameters after hemorrhagic shock. Although studies have shown that gut dysbiosis affects the cardiovascular system through direct or indirect mechanisms, there is no evidence regarding its role in reversing hypotension. Therefore, this study aimed to investigate the effects of hemorrhagic shock on the cardiovascular system in rats with gut dysbiosis. Six pregnant Sprague Dawley rats were divided into two groups: the dysbiosis group, treated with oral antibiotics (amoxicillin+vancomycin;n=3), and the control group, treated with oral saline (n=3) during the last week of pregnancy. Treatments continued until the offspring were weaned at 4 weeks of age. Dysbiosis was induced in the dysbiosis group offspring (n=7) by administering antibiotics for an additional 4 weeks, while control group offspring (n=7) received saline. At 12 weeks of age, baseline MAP and HR were recorded using femoral artery catheterization. Hemorrhagic shock was induced, and cardiovascular parameters were continuously monitored. Statistical analyses were performed using two-way RM-ANOVA followed by post hoc Bonferroni tests ($p<0.05$). The study revealed significant differences in cardiovascular recovery between the dysbiosis and control groups. In the control group, MAP dropped from 120 mmHg to 45 mmHg during hemorrhagic shock but recovered to 60 mmHg within one hour. In contrast, the dysbiosis group only achieved a maximum MAP of 50 mmHg during recovery. Similarly, HR increased from 240 bpm to 300 bpm in the control group following hemorrhagic shock, whereas the dysbiosis group exhibited a more modest increase to 260 bpm. The findings of our study demonstrate that intestinal dysbiosis negatively impacts the cardiovascular system's recovery process following hemorrhagic shock. These results suggest that dysbiosis hinders the reversal of hypotension by weakening the cardiovascular system's compensatory mechanisms.

Keywords: Dysbiosis, Hemorrhagic shock, MAP, HR

**This research was funded by Bursa Uludag University Scientific Research Project Foundation, grant number TGA-2022-1216*

INVESTIGATION OF COMPLETE BLOOD COUNT INDICES (NLR, LMR, PLR, MPV/PLT, SIRI, and SII) LEVELS IN DOGS WITH PARVOVIRAL ENTERITIS COMPLICATED BY SYSTEMIC INFLAMMATORY RESPONSE SYNDROME

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Abstract:

It is believed that canine parvovirus type 2 evolved either as a result of the differentiation of the feline panleukopenia virus or from a mutation of another wildlife virus type. Complete blood count is an inexpensive and straightforward method used in both human and veterinary medicine for disease confirmation and for determining the number and relationships of blood cells such as neutrophils, lymphocytes, and platelets. While the neutrophil-to-lymphocyte ratio (NLR), lymphocyte-to-monocyte ratio (LMR), platelet-to-lymphocyte ratio (PLR), mean platelet volume-to-platelet ratio (MPV/PLT), systemic immune-inflammation index (SII), and systemic inflammatory response index (SIRI) are frequently used for confirming inflammatory diseases in human medicine, these markers have only recently begun to be utilized in veterinary medicine. This study focuses on investigating these markers in dogs with parvoviral enteritis that are showing symptoms of systemic inflammatory response syndrome (SIRS). The study consists of two groups: a control group (22 healthy dogs of different breeds) and a patient group (60 dogs of different breeds). It was found that the values of WBC, NEU, NLR, SIRI, and SII were higher in the patient group compared to the control group. There was no significant difference between the groups in other haematological parameters. In conclusion, it was determined that hematologic indices yield significant results in dogs with parvoviral enteritis complicated by SIRS, and that these indices are valuable for validating inflammatory conditions associated with parvoviral enteritis.

Keywords: Neutrophil to lymphocyte ratio, parvoviral enteritis, systemic immune inflammation index, systemic inflammatory response index.

POLYCYSTIC KIDNEY DISEASE IN A BRITISH SHORTHAIR CAT

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Abstarct:

The animal material of this case report was a three-year-old British Shorthair cat with a history of pulmonary embolism. Despite the absence of pathological findings in the hematological and biochemical analyses of the renomegaly observed during the routine abdominal palpation, advanced imaging techniques revealed the presence of polycystic kidney disease (PKD). This case report illustrates that hematological and biochemical alterations are inadequate for a definitive diagnosis of PKD in cats. It is therefore recommended that imaging techniques be employed, even in cats that exhibit no clinical symptoms.

Keywords: Cat, Polycystic kidney disease, Ultrasound, Radiography

LITHOPHAGIA: RECURRENT DIARRHEA AS A REFLECTION OF BEHAVIORAL DISORDER IN A GERMAN SHEPHERD DOG

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Abstract:

Licking, chewing or ingesting non-nutritive substances is defined as pica. Here, we report the clinical reflections of lithophagia associated with behavioral disorder in a German shepherd dog and the haematobiochemical and some radiographic findings. The research material consisted of a 1.5-year-old female German shepherd mine detection dog brought to the Animal Hospital of Dicle University Faculty of Veterinary Medicine with complaints of vomiting and diarrhea. Hence it is known that pica is generally caused by trace element deficiencies, blood samples were taken to perform hematological and serum biochemical analyses. As a result of the hematobiochemical analysis, it was determined that there was no significant change that could lead to pica, but clinical and radiographic examination revealed that there were many pebbles in the rectum. It is thought that behavioral disorders in dogs showing pica symptoms is an important issue that needs to be addressed.

Keywords: behavioral disturbances, dog, lithophagia, pica

THE EFFECTS OF OSTEOCALCIN, OSTEONECTIN AND OSTEOPONTIN ON THE GENITAL SYSTEM

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Abstract:

Bone tissue, which has the property of supporting tissue, has mechanical functions such as providing protection of blood cells in the bone marrow along with the internal organs of the body, head and chest cavity organs, forming the internal skeleton in vertebrates. In addition, thanks to the cells and matrix parts that make up the bone tissue, the bone tissue also functions as an endocrine organ. The matrix part consists of organic and inorganic compounds such as glycosaminoglycans, small glycoproteins such as osteocalcin, osteonectin, osteopontin, and sialoproteins. All three proteins have been shown to affect the development and proliferation of Leydig and testicular germ cells, as well as stimulating sperm count, testosterone secretion and synthesis. In addition to these, osteocalcin; affects the epididymis and seminal vesicles, while osteonectin and osteopontin affect Sertoli cells, playing a role in physiological processes. Osteopontin and osteonectin have been observed in the epithelium and secretions of many tissues including the fallopian tube, uterus, trophoblast and placenta, in theca and granulosa cells of the ovary and in the corpus luteum in females, and have critical roles in the physiological processes of these organs. However, it has been shown that osteocalcin is generally limited to the ovary in females and can undertake physiological roles by affecting the FSH and LH hormones secreted by the female genital system. In light of this information, it has been determined that osteopontin, osteocalcin and osteonectin proteins act as an endocrine organ for the male and female genital system, in addition to their functions in bone tissue. Thus, it has been seen that these proteins may have critical roles in many physiological processes, especially in the realization of healthy reproduction, the detection and treatment of genital system diseases.

Keywords: Osteocalcin, Osteonectin, Osteopontin, Genital system

INVESTIGATION OF DISEASE CLUSTERING IN VETERINARY MEDICINE USING EXPLORATORY SPATIAL DATA ANALYSIS (ESDA): WHAT CAN BE LEARNED FROM RECORDED CASES?

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Abstract:

Exploratory Spatial Data Analysis (ESDA) is the set of methods used to characterize and visualize spatial distributions, spot anomalous locations (also known as spatial outliers), identify spatially associated patterns (also known as spatial clusters), and propose alternative spatial regimes as well as other types of spatial instability or non-stationarity. The aim of this study is to examine the spatial patterns of bovine tuberculosis (bTB) in Türkiye using disease cases registered in the World Animal Health Information System (WAHIS) database between 2005 and 2022. With an average of 7013.06 cases each year in Türkiye, there were a total of 126 235 bTB cases recorded. The average number of cases per provincial was 86.58 per province year. Local Indicator of Spatial Association (LISA) was used to determine the location of spatial clusters and outliers. The analysis was used 95% confidence interval and 999 permutations. The calculated Moran's I was 0.1856 (Z-score = 2.9225, p = 0.007). In comparison to local spatial outliers (High-Low or Low-High 6.17%), there are more local clusters (High-High or Low-Low, 16.05%). According to the results, it has been shown that bTB cases in Türkiye tends to be partially clustered. High-high clusters were detected especially in the Aegean Region. Producing thematic maps of outbreaks, investigating whether they form any clusters, and examining their relationship with various factors are important for better understanding the epidemiology of the disease and for it to be brought under control.

Keywords: Autocorrelation, Clustering, Disease, Exploratory Spatial Data Analysis, Mycobacterium Bovis.

**This study is supported by Selçuk University Scientific Research Projects Coordination Unit (Project Number:23401143).*

HIGHER PREVALENCE OF BOVINE HERPESVIRUS 4 IN NASAL SWABS: A STUDY ON SUBCLINICAL INFECTIONS IN CATTLE POPULATIONS

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Abstract:

Bovine Herpesvirus 4 (BoHV-4) is a common viral agent causing mainly subclinical reproductive and respiratory disease in cattle all around the world. BoHV-4 is a Rhadinovirus belonging to Gammaherpesvirinae subfamily and Herpesviridae family. It is known that infection of the virus leads to important economical loses in cattle farms such as decreased milk yield and infertility. In addition to that, latency and persistent infection features of the virus make itself an unignorable pathogen for herd management. So, routine surveillance of this virus in herds is important.

In this study, it was aimed to investigate the presence of BoHV-4 in cattle that are not showing any clinical sign and not having any disease history in a cattle farm located near Ankara province. For this purpose, 34 nasal swabs and 34 vaginal swabs of a total of 34 asymptomatic and healthy looking in clinical observation cattle from various breeds were investigated. Total viral genetic material was extracted by a modified Phenol:Chlorofrom:Isoamylalcohol (25:24:1) method. Partial region of the viral gB gene was amplified using PCR. 19 animals (55,8%) were detected as positive in terms of BoHV-4 DNA. The virus was detected in 11 nasal (32,35% of nasal samples) and 8 vaginal (23,52% of vaginal samples) swab samples. The virus was detected only in either nasal or vaginal swab sample in positive animals. According to the literature about the epidemiology of the virus in world and Türkiye, it is surprising that the obtained data shows a higher prevalence of the virus in nasal mucosa rather than the genital mucosa. Findings also show the presence of the virus in the animals that are appearing healthy in the herd. Management measurements such as routine surveillance of the virus presence should be taken to prevent subclinical disease and unaware yield losses caused by persistent and latent infection.

Keywords: Bovine herpesvirus 4, cattle, epidemiology, PCR

IDENTIFICATION AND MOLECULAR ANALYSIS OF BOVINE ADENOVIRUS SEROTYPE-1 IN CALVES WITH RESPIRATORY TRACT INFECTION

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Abstract:

Bovine adenoviruses (BAdV) are a group of viruses associated with various diseases affecting cattle, including respiratory and enteric infections, and some of them have oncogenic potential. BAdV are classified into two genera: Mastadenovirus (BAdV-1, -2, -3, -9 and -10) and Atadenovirus (BAdV-4, -5, -6, -7, and -8). BAdV-1 and -3 are recognized as important respiratory pathogens in cattle, leading to acute or subacute viral diseases characterized by symptoms such as fever, naso-ocular discharge, and pneumonia. In this study, a total of 24 swab samples from calves aged 0 to 6 months with respiratory symptoms were tested for the presence of bovine mastadenoviruses. After the viral DNA extraction, samples were subjected to PCR using primers targeting the hexon gene region of mastadenoviruses. As a result of PCR, six samples demonstrated the anticipated amplicon size (with a 25% positivity rate). Subsequently, five samples underwent sequencing, and phylogenetic analyses were conducted. Phylogenetic analysis revealed that all sequenced samples were grouped within the BAdV-1 serotype. Additionally, BAdV-1 was identified as the sole causative agent in five of the positive samples. Although investigations have shown the existence of BAdVs in Türkiye, there is limited data on the molecular characterization of the bovine adenoviruses in our country. This study, which was conducted on samples obtained from calves with respiratory system disease in Kastamonu, is the first report on the molecular characterization of BAdV-1 in Türkiye. In conclusion, this investigation has shown that BAdVs have played as an important agent in respiratory system infections. Further studies on the molecular characterization and epidemiology of these viruses would contribute to a better understanding of the role of bovine adenoviruses in respiratory disease.

Keywords: Bovine adenovirus, BAdV serotype-1, molecular characterization, respiratory system viruses.

INVESTIGATION OF HISTOLOGICAL AND HISTOCHEMICAL STRUCTURE OF THE SPLEEN OF THE PARTRIDGE (ALECTORIS CHUKAR)

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Abstract:

The spleen is an organ located just near the stomach, above the right lobe of the liver. It is usually dark blue-brown in color. Although the spleen is spherical or egg-shaped in poultry, it is triangular in waterfowl. Structurally and functionally, the spleen is a blood-producing organ, but it is also an effective element of the immune system. The aim of this study was to investigate the histological and histochemical characteristics of the spleen in partridges (Alectoris chukar). In this study, 8 partridges (Alectoris chukar) were used. Spleen tissues dissected from the partridges were fixed in 10% formaldehyde solution for 36 hours. These fixed tissues were subjected to dehydration and transparency procedures for histological examinations. Then, they were embedded in paraffin blocks and 5µm thick sections were taken. The sections were stained with Hematoxylin Eosin (H&E) to determine the general structure and with Periodic Acid Schiff (PAS), Periodic Acid Schiff/Alcian Blue pH:2,5 (PAS/AB pH:2,5) to determine the histochemical structure, and their histological structure was examined. Histologically, it was observed that the partridge spleen is surrounded by a thick capsule and there are small trabeculae inside. It was seen that red pulp and white pulp are scattered in the parenchyma and white pulp is composed of reticular cells, reticular fibers and lymphocytes. It was determined that the red pulp is composed of numerous blood vessels, lymphocytes, macrophages, venous sinuses, and anastomoses of reticular cells. Histochemically, PAS staining revealed intense neutral mucins concentrated around the blood vessels and in the capsule. In PAS/AB pH:2,5 staining method, a positive reaction was observed for neutral mucins and negative reaction was observed for acidic mucins. In conclusion, the histologic structure of partridge spleen is similar to chicken, ostrich and quail spleens.

Keywords: Alectoris chukar, Spleen, Histology, Histochemical

POSTER PRESANTATION

INVESTIGATION OF THE PREVALENCE OF *TOXOPLASMA GONDII* AND *NEOSPORA CANINUM* IN ABORTED SHEEP FETUSES IN BATMAN PROVINCE

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Abstract:

Toxoplasma gondii causes diseases in both domestic and wild animals and causes significant economic losses. Both parasites are important causes of abortions in ruminants. The aim of this study was to investigate the prevalence of *T. gondii* and *N. caninum* in brain tissues of aborted sheep fetuses in Batman province by molecular methods. In the study, tissue samples were taken from the brains of 150 aborted sheep fetuses. DNA extraction was performed using commercial kits, followed by PCR analyses using primers specific to the parasites. DNA extraction and PCR analysis were then performed. Samples were then run on a 1.5% agarose gel and images were obtained using a gel imager. After bidirectional sequencing analyses of positive PCR samples, comparisons were made with relevant reference genes in GenBank through BLAST and alignment. *T. gondii* was detected in 23 of 150 samples (15.33%) by PCR method, and N. caninum was not found in any sample. Positive *T. gondii* samples showed 99.76-100% similarity with isolates KX963353.1, OL871238.1, OL871239.1, MH884735.1 and MH884737.1 in GenBank. In the present study, *T. gondii* was detected in aborted sheep fetuses, but *N. caninum* was not found. More extensive research is needed to detect *N. caninum*. To protect sheep from *T. gondii* infections, they should be kept away from cat feces and the feces-contaminated feed.

Keywords: *Toxoplasma gondii, Neospora caninum*, sheep fetuses, abortion

** This study was supported by Van Yüzüncü Yıl University Scientific Research Projects Coordination Unit as a Research Project with Undergraduate Student Participation with Project Code TLO-2024-11122.*

DRUG RESISTANCE PATTERNS OF SOME ENTEROBACTERIACEAE ISOLATED FROM CHICKEN IN THE WEST OF ALGERIA

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Abstract:

Antibiotic-resistant bacteria may arise and proliferate as a result of the overuse of antibiotics in the chicken business. Antibiotics may be less effective in treating human illnesses if humans eat chicken products that include antibiotic-resistant bacteria or their genes.

Objectives: Determining the antimicrobial resistance (AMR) patterns of some Enterobacteriaceae obtained from poultry in different regions of the west of Algeria.

Research methods; In order to isolate E. coli, samples from chicken were gathered and prepared for culture using conventional microbiological techniques. While isolated E,coli was typed for O1, O2, and O78 antigens using slide agglutination. Isolates were identified biochemically using API 20E. In accordance with CLSI guidelines, all isolates were identified and analyzed using the Kirby Bauer disk diffusion technique against 26 antibiotic disks, conjugative plasmid transfer, plasmid incompatibility, and colicin assays were employed.

Results: A total of 150 distinct species of E. coli were isolated. Fifty-two agglutinable E. coli isolates with O78:K80 (n28), O1:K1 (15), and O2:K1 (9) were found. E. Coli resistance to nalidixic acid (95.6%), tetracyclin (79.2%), nitrofurantoin (71.4%), ampicillin (53.6%) and chloramphenicol (21.3%).

Salmonella present a resistance of 59.62% to nalidixic acid, ofloxacin, 29.54% to streptomycin. The Klebsiella species shows no resistance for gentamicin and amikacin, but 73% of resistance to ciprofloxacin 48% ofloxacin, and a total resistance to ampicillin.

All the Enterobacter isolated were resistant to ampicillin, however no resistance was observed for gentamicin, and amikacin.

Multidrug resistance, was present in 81.8%. of the isolates. The predominant plasmid-mediated resistance markers in E. coli isolates, as determined by conjugative transfer, are ASTeSuTmp (25.8%).

Regarding the clustring of plasmids only 9 plasmids were not grouped out of the 67 tested (Com1 and F1). The colicin test shows that 5 transconjugants were colicin positive, these results let us suppose that colicin production and antibiotic resistance are two characters carried by the same plasmid structures.

Conclusion: This work demonstrates that these antibiotic resistance characteristics may be easily transferred by plasmids, it also confirms that meat chicken has multidrug resistance E. coli.

Keywords: Chicken, Enterobacteriaceae, multidrug resistance, plasmid, colicin.

INVESTIGATION OF *GIARDIA INTESTINALIS* PREVALENCE AND ASSEMBLAGES IN CALVES IN BITLIS PROVINCE

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Abstract:

Giardia intestinalis is a flagellated protozoan parasite that parasitizes in the intestines of various animal species and humans, causing diarrhea and digestive disorders. The infection caused by the parasite is called giardiosis. The most common clinical sign of giardiosis is diarrhea, which may be watery or slightly mucous. In chronic cases, weight loss and growth disturbances may also be seen. This infection also causes significant economic losses. This present study was conducted to determine the prevalence and assemblage of *G. intestinalis* in calves in the Bitlis province. Stool samples were obtained from 100 calves aged 0-3 months on various farms. Samples from the rectum of each animal were placed in pre-labeled stool containers. The samples were placed in fecal containers and transported to Research Laboratory of Department of Parasitology, Medical Faculty, Van Yüzüncü Yıl University under cold chain conditions. The specimens were examined for *G. intestinalis* cysts by native-Lugol method under light microscope at X400 magnification. DNA extraction and Nested PCR analysis were then performed. Samples were then run on a 1.5% agarose gel and images were obtained using a gel imager. After bidirectional sequencing analyses of positive PCR samples, comparisons were made with relevant reference genes in GenBank through BLAST and alignment. *Giardia intestinalis* was detected in 12 (12%) of 100 samples by microscopic examination and in 16 (16%) samples by nested PCR analysis. When compared with relevant reference genes in GenBank, it was determined that 12 of the positive samples belonged to zoonotic Assemblage A, while 4 belonged to zoonotic Assemblage B. Giardiosis causes significant economic losses by causing low productivity and even death in young animals. Since only Assemblages A and B are observed in humans, these assemblages are considered potentially zoonotic. Further extensive studies are needed to better understand the distribution of *G. intestinalis* assemblages in calves in the Bitlis region.

Keywords: *Giardia intestinalis*, Assemblage A, Assemblage B, calves, Bitlis

** This study was supported by Van Yüzüncü Yıl University Scientific Research Projects Coordination Unit as a Research Project with Undergraduate Student Participation with Project Code TLO-2024-10967*

FELINE HYPERTROPHIC CARDIOMYOPATHY: A DEEP DIVE INTO PATHOPHYSIOLOGY

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Abstract:

Cardiomyopathies are a group of myocardial disorders that cause impairment of heart structure and function. They are the most common form of cardiac diseases in cats, with the hypertrophic phenotype being the most prevalent.

Hypertrophic Cardiomyopathy (HCM) is characterized by hypertrophy of left ventricular (LV) walls with non-dilated cavity, in the absence of other causes capable of producing myocardial thickening (such as systemic hypertension or aortic stenosis). HCM is characterized by histopathologic features of myocyte disorganization or disarray, interstitial and replacement fibrosis as well as intramural arteriosclerosis.

On the pathophysiological level, HCM leads to diastolic dysfunction and failure. In fact, LV hypertrophy increases myocardial stiffness and impairs the heart's ability to relax, thus increasing LV filling pressure. The elevated pressure is then transmitted back into the left atrium and the pulmonary veins, leading to left-sided congestive heart failure. Additional pathophysiological features include myocardial ischemia, cardiac rhythm disturbances and arterial thromboembolism. In obstructive forms of HCM, the anterior mitral valve leaflet moves towards the interventricular septum, causing an obstruction to systolic blood flow, thus increasing pressure over the LV outflow tract, further exacerbating hypertrophy and diastolic dysfunction.

In practice, HCM represents a diagnostic dilemma. With its diverse morphological patterns and various clinical manifestations, it often goes underdiagnosed. However, recognizing and discerning its complex pathophysiology would help practitioners perceive its clinical manifestations and progression.

This review aims to provide updated information on the main pathophysiological mechanisms of feline HCM.

Keywords: Feline hypertrophic cardiomyopathy, pathophysiology, diastolic dysfunction, heart failure

THE CASE OF UTERINE HYPERPLASIA AND PYOMETRA COMPLEX IN A GUINEA PIG

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Abstract:

Ovarian and uterine diseases are highly prevalent in female guinea pigs, with an incidence exceeding 75%. Cystic endometrial hyperplasia (CEH) is a known precursor to pyometra, and this condition has been reported in various small animals, including guinea pigs. This case report describes a 6-year-old female guinea pig diagnosed with CEH-pyometra based on clinical and histopathological findings. After presenting with abdominal swelling, vaginal discharge, and appetite loss, the guinea pig underwent surgery, and the removed uterine mass was found to contain numerous uterine glands with eosinophilic fluid, confirming the diagnosis.

Keywords: Guinea pig, ceh, pyometra

FULL TEXTS

IDENTIFICATION AND MOLECULAR ANALYSIS OF BOVINE ADENOVIRUS SEROTYPE-1 IN CALVES WITH RESPIRATORY TRACT INFECTION

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Abstract

Bovine adenoviruses (BAdVs) are a group of viruses associated with various diseases affecting cattle, including respiratory and enteric infections, and some of them have oncogenic potential. BAdVs are classified into two genera: *Mastadenovirus* (BAdV-1, -2, -3, and -10) and *Barthadenovirus* (BAdV-4, -5, -6, -7, and -8). BAdV-1 and -3 are recognized as important respiratory pathogens in cattle, leading to acute or subacute viral diseases characterized by symptoms such as fever, naso-ocular discharge, and pneumonia. In this study, a total of 24 swab samples from calves aged 0 to 6 months with respiratory symptoms were tested for the presence of bovine mastadenoviruses. After the viral DNA extraction, samples were subjected to PCR using primers targeting the hexon gene region of mastadenoviruses. As a result of PCR, six samples demonstrated the anticipated amplicon size (with a 25% positivity rate). Subsequently, five samples underwent sequencing, and phylogenetic analyses were conducted. Phylogenetic analysis revealed that all sequenced samples were grouped within the BAdV-1 serotype. Additionally, BAdV-1 was identified as the sole causative agent in five of the positive samples. Although investigations have shown the existence of BAdVs in Türkiye, there is limited data on the molecular characterization of the bovine adenoviruses in our country. This study, which was conducted on samples obtained from calves with respiratory system disease in Kastamonu, is the first report on the molecular characterization of BAdV-1 in Türkiye. In conclusion, this investigation has shown that BAdVs have played as an important agent in respiratory system infections. Further studies on the molecular characterization and epidemiology of these viruses would contribute to a better understanding of the role of bovine adenoviruses in respiratory disease.

Keywords: Bovine adenovirus, BAdV serotype-1, molecular characterization, respiratory system viruses.

INTRODUCTION

One of the most significant problems in animal production on a global scale is bovine respiratory system disease (BRD). Especially herd management, environment, and infectious agents (both bacterial and viral) all interact to cause BRD. The disease causes significant economic losses in cattle herds (Shi et al., 2014; Zhang et al., 2019).

Bovine adenoviruses (BAdVs), are a group of viruses that belong to the family *Adenoviridae*. To date, there are six genera (*Aviadenovirus, Barthadenovirus, Ichtadenovirus, Mastadenovirus, Siadenovirus, and Testadenovirus*) in the *Adenoviridae* family (ICTV, 2022). BAdVs are classified into two genera: *Mastadenovirus* and *Barthadenovirus* (earlier: *Atadenovirus*) and include ten types of viruses; BAdV-1 to -10. BAdVs in genus *Mastadenovirus* are currently BAdV-1, BAdV-2, BAdV-3, and BAdV-10 (ICTV, 2022; Zhu et al., 2011). Vidovszky et al. (2022) reported finding a new type and suggested that it was proposed to be BAdV-11. The epidemiology of BAdVs indicates that these viruses are widely distributed across cattle populations globally, with BAdV-3 being frequently isolated from calves suffering from respiratory illnesses (Zhang et al., 2019). These viruses are significant infectious agents in cattle, especially those that are connected with respiratory disorders and other health problems (Hartel et al., 2004). The complex interaction between agents in the development of respiratory disorders in cattle is demonstrated by metagenomic investigations. These investigations have revealed that Bovine Adenoviruses (BAdVs) often occur together with other viral infections such as bovine rhinitis A virus and influenza D virus (Ng et al., 2015).The BAdVs has the double-stranded DNA genome that contains inverted terminal repeats (ITRs) at the ends and encodes a number of proteins that are important in the viral replication process (Gaba et al., 2018). In the past, the identification of adenovirus serotypes relied on neutralization testing. A serotype is defined by either no cross-reactivity with other serotypes or a homologous:heterologous titer ratio over 16. Surface antigens on the virion are mostly type-specific. Neutralization and hemagglutination inhibition are processes in which hexons and fibers participate (Adám et al., 1998; Mennechet et al., 2019). Nowadays, like many other microbial agents, determination of phylogenetic relationships by comparison of sequence data plays an important role in classifying adenoviruses.

Many different clinical indications may be caused by BAdVs, such as fever, conjunctivitis, pneumonia, diarrhea, and polyarthritis, but they are usually associated with mild respiratory diseases and sometimes gastrointestinal infections (Jesse et al., 2022; Shi et al., 2014). The detection of BAdVs in respiratory specimens from cattle suffering from BRD necessitates the thorough diagnostic procedures that take into account a variety of infections in order to precisely determine the health condition of cattle populations (Ng et al., 2015; Zhang et al., 2019).

Bovine adenovirus serotype 1 (BAdV-1) is one of several serotypes within the genus *Mastadenovirus*, primarily infecting cattle. The significance of this virus particularly is due to its possible involvement in respiratory disorders and its consequences for the health and management of cattle. The epidemiological analysis of BAdV-1 reveals its extensive distribution among cattle herds, while its detection is less common in comparison to other serotypes like BAdV-2 and BAdV-3 (Karayel Hacioglu et al., 2022; Tuncer & Yeşilbağ, 2015). Although infections with BAdV-1 may affect both young and adult cattle, calves are more vulnerable due to their growing immune systems.

In Türkiye, the presence of different adenovirus serotypes based on several serological studies with various seropositivity rates (8.1%-87.87%) and the detection of BAdVs as a causative agent for BRD were reported (Alkan, 1998; Alpay et al., 2014; Avci et al., 2014; Duman, et al., 2009; Erol et al., 2007; Kale et al., 2013; Koc & Oguzoglu, 2018; Ozgunluk & Gur, 2012; Ozturk et al., 1992; Yazici et al., 2007). Recently, a study was presented that defines the molecular characterization of BAdV-2 and -3 from cattle with BRD (Karayel Hacioglu et al., 2022).

The aims of this study were i) to investigate BAdVs in the *Mastadenovirus* genus in the samples from cattle with BRD in Kastamonu province and ii) to perform a phylogenetic analysis of the detected BAdVs.

MATERIALS AND METHODS

Samples and Extraction of viral DNA

In this study, 24 swab samples from cattle with respiratory symptoms such as fever, cough, and nasal discharge were analyzed in farms in Kastamonu province. There were a total of five farms from which swab samples were collected. Two of these farms were large-scale ($X \geq 20$ cattle), while the other three were small-scale ($X \leq 10$ cattle) (Table 1). The samples were obtained from cattle aged 0-6 months between December 2022 and January 2024. After collection, the samples were transported to the laboratory in a cold chain and stored at -20 ^{o}C until extraction. The extraction of viral DNA was performed using the procedure described by Sambrook et al. (1989).

PCR and Phylogenetic analysis

After the extraction, samples were subjected to semi-nested PCR using primer sets that target the hexon gene of mastadenoviruses as reported earlier with minor modifications (Sibley et al., 2011). PCRs were conducted using Taq DNA Polymerase from Thermo Fisher Scientific, USA. The reaction mixture included 18.35 µl of nuclease-free water, 2.4 µl of MgCl2 (25 mM), 3 µl of 10×Taq buffer, 1.25 µl of each primer, 1 µl of dNTP (10 mM each), 0.25 µl of Taq polymerase (500 U/µl), and 3 µl of DNA. The PCR procedure used for both rounds of semi-nested amplification were as follows: Following an initial denaturation step at 94°C for 5 minutes, followed by 35

cycles of 94°C for 30 seconds, 55°C for 30 seconds, and 72°C for 1 minute, culminating in a final extension at 72°C for 7 minutes. A 1% agarose gel electrophoresis was used to examine the amplification results, which were subsequently observed using ultraviolet light.

Table 1. Information about the nasal swab samples in this study.

Enterprise No/Code	District	Farm scale	Number of tested samples	Number of positive samples	Sequenced samples/Acc numbers
1/M1	Merkez	Small	1	-	
2/M2	Merkez	Small	1	1	BAdV1/M2/TUR/2024/ PQ363008
3/M3	Merkez	Small	1	-	
4/G	Devrekani	Large	6	3	BAdV1/G2/TUR/2024/ PQ363009 BAdV1/G6/TUR/2024 PQ363010
5/S	Devrekani	Large	15	2	BAdV1/S4/TUR/2024 PQ363011 BAdV1/S12/TUR/2024 PQ363012

The GenBank database was accessed to get sequences of BAdV strains that represent AdV serotypes. Alignment of the nucleotide sequences in the present study and those from the Genbank was performed using the Aliview Software (Larsson, 2014). Phylogenetic analyses were performed using MEGA X software, using the Kimura2+G+I method and bootstrap testing with 1000 repetitions (Kumar et al., 2018). Using online resources (SIAS, http://imed. med.ucm.es/Tools/sias.html), the identities of nucleotide (nt) and amino acid (aa) sequences between sequences were examined.

RESULTS

In this study, after PCR analysis of 24 samples, a total of six nasal swab samples from three different farms were found to be positive by PCR (with a 25% positivity rate) (Table). When the positive samples were also tested for some other viral pathogens (Bovine Herpes Virus-1 (BHV-1), Bovine Respiratory Syncytial Virus, Bovine Coronavirus, Bovine Paraınfluenza-3 virus), BHV-1 was detected in one sample (BAdV-1/G6/TUR/2024). BAdV-1 was identified as the sole causative agent in the remaining five of the positive samples. From the six amplicons with the anticipated size of 588–714 base pairs, five were successfully sequenced and the sequences were submitted to GenBank (PQ363008- PQ363012). According to the results of the phylogenetic analysis, the BAdVs were grouped together in the BAdV-1 serotype (Figure 1).

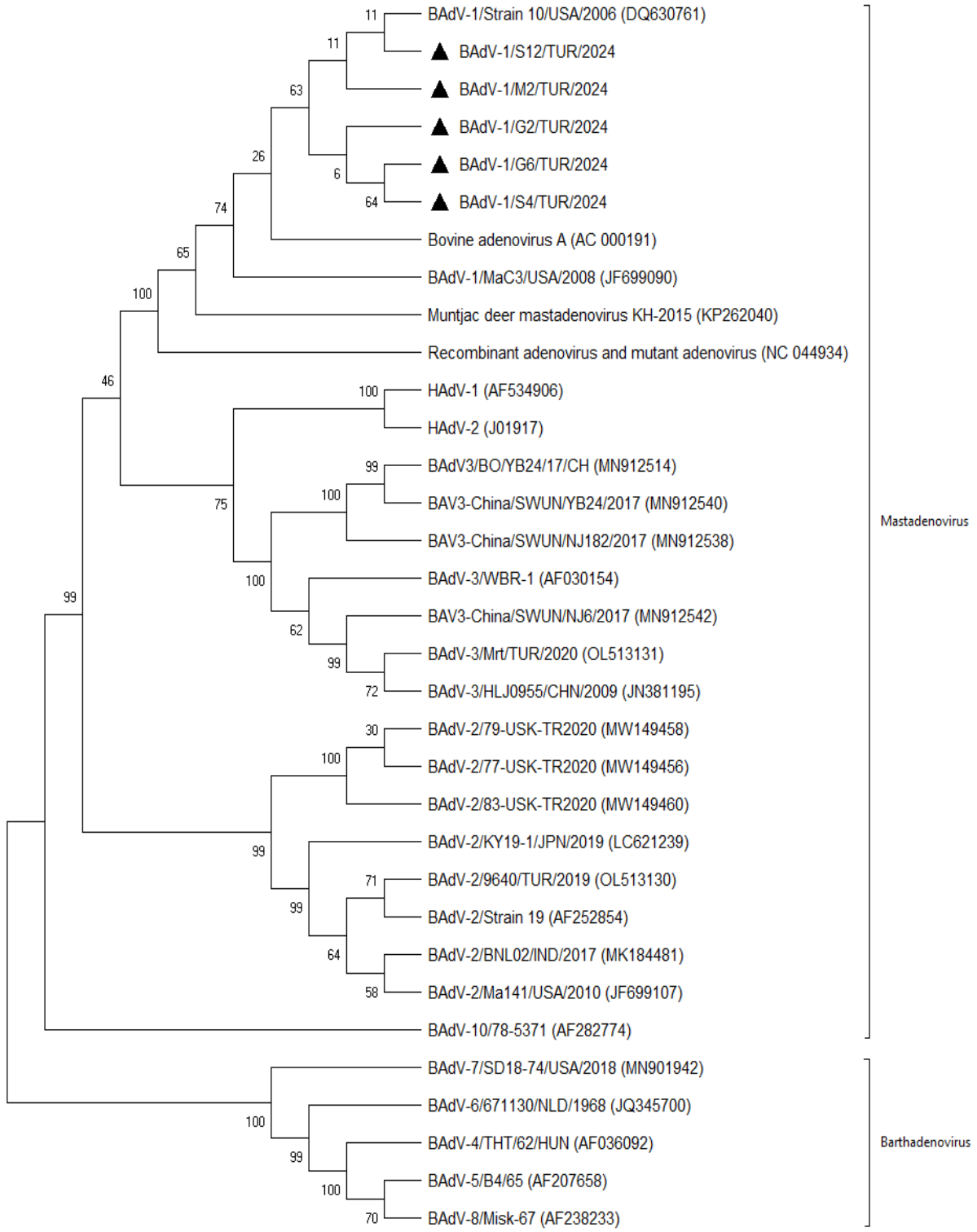

Figure 1. Phylogenetic tree based on the partial nucleotide sequences of the adenovirus hexon gene. Black triangles indicate the samples in this study.

The nt and aa identities of the partial hexon gene of the identified viruses with those of other BAdV-1 sequences that are accessible in GenBank are presented in the Figure 2a,b.

a

KP262040 Muntjac deer KH-2015	100%									
DQ630761 BAdV-1/Strain 10	99.41%	100%								
AC_000191 Bovine adenovirus A	99.6%	99.8%	100%							
JF699090 BAdV-1/MaC3/USA/2008	99.6%	99.8%	100%	100%						
NC_044934 Recombinant AdV	99.6%	99.8%	100%	100%	100%					
BAdV-1/S12/TUR/2024	99.41%	100%	99.8%	99.8%	99.8%	100%				
BAdV-1/M2/TUR/2024	99.41%	100%	99.8%	99.8%	99.8%	100%	100%			
BAdV-1/G2/TUR/2024	99.41%	100%	99.8%	99.8%	99.8%	100%	100%	100%		
BAdV-1/G6/TUR/2024	99.21%	99.8%	99.6%	99.6%	99.6%	99.8%	99.8%	99.8%	100%	
BAdV-1/S4/TUR/2024	99.21%	99.8%	99.6%	99.6%	99.6%	99.8%	99.8%	99.8%	100%	100%
	KP262040 Muntjac deer KH-2015	DQ630761 BAdV-1/Strain 10	AC_000191 Bovine adenovirus A	JF699090 BAdV-1/MaC3/USA/2008	NC_044934 Recombinant AdV	BAdV-1/S12/TUR/2024	BAdV-1/M2/TUR/2024	BAdV-1/G2/TUR/2024	BAdV-1/G6/TUR/2024	BAdV-1/S4/TUR/2024

b

KP262040 Muntjac deer KH-2015	100%									
DQ630761 BAdV-1/Strain 10	99.4%	100%								
AC_000191 Bovine adenovirus A	100%	99.4%	100%							
JF699090 BAdV-1/MaC3/USA/2008	100%	99.4%	100%	100%						
NC_044934 Recombinant AdV	100%	99.4%	100%	100%	100%					
BAdV-1/S12/TUR/2024	99.4%	100%	99.4%	99.4%	99.4%	100%				
BAdV-1/M2/TUR/2024	99.4%	100%	99.4%	99.4%	99.4%	100%	100%			
BAdV-1/G2/TUR/2024	99.4%	100%	99.4%	99.4%	99.4%	100%	100%	100%		
BAdV-1/G6/TUR/2024	99.4%	100%	99.4%	99.4%	99.4%	100%	100%	100%	100%	
BAdV-1/S4/TUR/2024	99.4%	100%	99.4%	99.4%	99.4%	100%	100%	100%	100%	100%
	KP262040 Muntjac deer KH-2015	DQ630761 BAdV-1/Strain 10	AC_000191 Bovine adenovirus A	JF699090 BAdV-1/MaC3/USA/2008	NC_044934 Recombinant AdV	BAdV-1/S12/TUR/2024	BAdV-1/M2/TUR/2024	BAdV-1/G2/TUR/2024	BAdV-1/G6/TUR/2024	BAdV-1/S4/TUR/2024

Figure 2. Nucleotide (a) and amino acid (b) sequence identity ratios of the adenovirus strains in this study and closely related references in GenBank.

DISCUSSION

Bovine adenoviruses are significant viral pathogens affecting cattle, with implications for both animal health and agricultural productivity. In Türkiye, detection and characterization of BAdVs remain important in herd health, especially in the context of respiratory diseases. The presence of respiratory infections caused by BAdVs might result in substantial economic losses as a consequence of reduced production, escalated veterinary expenses, and elevated death rates in the afflicted herds (Ince et al., 2021). The prevalence and impact of BAdVs in Türkiye have been the subject of

various studies, highlighting the need for comprehensive epidemiological surveillance and molecular characterization. To date, in the data from serological studies conducted in Türkiye, where varying seroprevalence rates were reported for different serotypes, BAdV-1 positivity was reported between 23.82% and 89.5% (Alpay et al. 2014; Erol et al., 2007; Kale et al., 2013; Koc & Oguzoglu, 2018; Ozgunluk & Gur, 2012; Yavru et al., 2001; Yesilbag & Gungor, 2008). Additionally, the detection of BAdVs from cattle with BRD has been reported in several studies (Alkan, 1998; Karayel Hacioglu et al., 2022). Unfortunately, the studies on the molecular characterization of bovine adenoviruses in our country are not at acomparable level to these studies. In the first study (Alkan, 1998) to investigate BAdVs in nasal swab samples from cattle with BRD, a direct immunofluorescence method using the specific conjugate for subgroup I BAdVs (BAdV-1, -2, -3, -9, and -10) was used. However, it was naturally not possible to determine the serotype of adenoviruses belonging to the BAdV subgroup I in the mentioned study. In another study (Karayel Hacioglu et al., 2022) reporting a positivity rate of 4.6% in swab samples taken from cattle with symptoms of BRD, detected adenoviruses were classified as BAdV-2 and BAdV-3.

In this study, out of the 24 nasal swab samples, six were found positive by PCR thus the positivity rate was detected as 25% (6/24) in samples and 60% (3/5) for sampled farms. These rates are much higher than those reported in previous studies (Alkan, 1998; Karayel Hacioglu et al., 2022) in Türkiye. Additionally, investigations for other viral pathogens in positive samples revealed that only one sample (BAdV-1/G6/TUR/2024) was also positive for BHV-1, while the others contained only BAdVs. It is known that effective farm management plays a crucial role in controlling and preventing infections within the farms. In this context, it is natural that both serological and virological studies may present different rates. However, considering the previously reported data, especially from serological studies (Alpay et al., 2014; Duman et al., 2009; Erol et al., 2007; Kale et al., 2013; Koc & Oguzoglu, 2018; Ozgunluk & Gur, 2012; Ozturk et al., 1992; Yazici et al., 2007) our results indicates that adenoviruses are a significant pathogen in BRD cases in some farms.

We also evaluated the nt and aa identities of the partial hexon gene of the identified viruses with those of other sequences that are accessible in GenBank. It was determined that the BAdVs in this study shared 99.8%-100% nt and 100% aa identity among themselves, and 99.6%-100% nt and 99.4%-100% aa identity with other BAdV-1 sequences in GenBank (Figure 2a,b). Because presence of limited sequence data of BAdV-1 in GenBank, and no sequences have been reported in our country before, it was not possible to assess on the origin and evolution of our BAdV-1. It is known that virus evolution, especially in DNA viruses, involves a range of genetic changes and adaptations driven by various factors. This evolution is influenced by several factors and can lead to significant changes in the virus' characteristics, including its

pathogenicity, transmissibility, and resistance to treatments. Naturally, the genetic characterization of BAdV isolates from different regions can also provide insights into the virus's evolution and potential for adaptation (Vidovszky et al., 2022). While research into the role of bovine adenoviruses in cattle health and their potential use as vaccine vectors continues, no standard vaccinations for BAdVs are presently available. Therefore, studies should focus on examining the molecular epidemiology of these viruses and their interactions with other diseases.

CONCLUSION

The conclusion is that bovine adenoviruses are one of the major cause for be concerned in the field of cattle health, especially in connection to respiratory illnesses. Because of their prevalence, the fact that they may co-infect with other infections, they are an important subject for continuing research and veterinary treatment. When it comes to creating effective strategies for controlling BRDC and improving the general health of cattle herds, it will be vital to have a solid understanding of the epidemiology and molecular characterization of BAdVs.

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Conflict of Interest

The authors have fully disclosed no cases of conflict of interest or financial support.

Ethical Statement

Retrospective materials (nasal swab samples) were used in the study. In accordance with the Regulation on the Working Procedures and Principles of Animal Experimentation Ethics Committees (HADMEK) (Article 8, Subparagraph k), an ethics committee decision is not required for studies involving swab samples. The study was carried out in accordance with ethical principles and rules.

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INVESTIGATION OF COMPLETE BLOOD COUNT INDICES (NLR, LMR, PLR, MPV/PLT, SIRI, AND SII) LEVELS IN DOGS WITH PARVOVIRAL ENTERITIS COMPLICATED BY SYSTEMIC INFLAMMATORY RESPONSE SYNDROME

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Abstract

It is believed that canine parvovirus type 2 evolved either as a result of the differentiation of the feline panleukopenia virus or from a mutation of another wildlife virus type. Complete blood count is an inexpensive and straightforward method used in both human and veterinary medicine for disease confirmation and for determining the number and relationships of blood cells such as neutrophils, lymphocytes, and platelets. While the neutrophil-to-lymphocyte ratio (NLR), lymphocyte-to-monocyte ratio (LMR), platelet-to-lymphocyte ratio (PLR), mean platelet volume-to-platelet ratio (MPV/PLT), systemic immune-inflammation index (SII), and systemic inflammatory response index (SIRI) are frequently used for confirming inflammatory diseases in human medicine, these markers have only recently begun to be utilized in veterinary medicine. This study focuses on investigating these markers in dogs with parvoviral enteritis that are showing symptoms of systemic inflammatory response syndrome (SIRS). The study consists of two groups: a control group (22 healthy dogs of different breeds) and a patient group (60 dogs of different breeds). It was found that the values of WBC, NEU, NLR, SIRI, and SII were higher in the patient group compared to the control group. There was no significant difference between the groups in other haematological parameters. In conclusion, it was determined that hematologic indices yield significant results in dogs with parvoviral enteritis complicated by SIRS, and that these indices are valuable for validating inflammatory conditions associated with parvoviral enteritis.

Keywords: Neutrophil to lymphocyte ratio, parvoviral enteritis, systemic immune inflammation index, systemic inflammatory response index.

INTRODUCTION

Parvoviruses are small, non-enveloped DNA viruses that predominantly replicate within rapidly dividing cells (Smith-Carr et al., 1997). Canine parvovirus type 2 (CPV-2) is believed to have originated from the differentiation of feline panleukopenia virus or the mutation of another wildlife parvovirus species (Prittie, 2004). Parvoviral enteritis begins with the ingestion of parvoviruses due to fecal-oral contamination. Two days following the ingestion of canine parvovirus (CPV), viral replication occurs in the oropharynx and local lymphoid tissues. Five days after the onset of infection, the viremia phase begins and the virus spreads into the bloodstream, targeting rapidly dividing tissues such as the intestinal epithelium, bone marrow, lymphoid tissues, and myocardium (Smith-Carr et al., 1997).

A complete blood count (CBC) is a cost-effective and straightforward diagnostic tool employed in both human and veterinary medicine to confirm diseases and assess the quantity and relationship between various blood cells, including neutrophils, lymphocytes, and platelets. In addition, using these haemogram data, markers of systemic inflammatory response such as the neutrophil-lymphocyte ratio (NLR), lymphocyte-monocyte ratio (LMR), platelet-lymphocyte ratio (PLR), and mean platelet volume to platelet ratio (MPV/PLT) can be easily determined. The systemic immune-inflammation index (SII), calculated as platelet count × neutrophil count / lymphocyte count, and the systemic inflammatory response index (SIRI), calculated as neutrophil count × monocyte count / lymphocyte count, can also be readily assessed (Li et al., 2022; Liu et al., 2023; Rejec et al., 2017). Neutrophils are a key component of the initial immune response, leading the defense against pathogens. In addition to their primary role in pathogen elimination, they are involved in the activation of T lymphocytes and the release of inflammatory mediators (Lewis et al., 2012). Lymphocytes primarily play a key role in the adaptive immune system and the cell-mediated immune response (Ayala et al., 1996). Platelets are blood cells that, in addition to their role in hemostasis, are involved in regulating antimicrobial cellular defense, triggering the release of proinflammatory cytokines, and promoting tissue repair (Rondina et al., 2013). Monocytes are reported to have a regulatory role in the increased inflammatory response (Lee et al., 2018). Mean platelet volume (MPV) and mean platelet component concentration are markers of platelet activation (Goddard et al., 2015). White blood cell (WBC) count is less sensitive in assessing systemic inflammatory status, whereas the NLR, PLR, and LMR provide more relevant indicators for determining systemic inflammation (Kriplani et al., 2022). The aim of this study was to determine the values of NLR, PLR, LMR, MPV/PLT, SIRI, and SII in dogs with parvoviral enteritis presenting with systemic inflammatory response syndrome (SIRS).

MATERIALS AND METHODS

Animals

The experimental group for the animals subject to the study consisted of dogs (60 dogs) of different breeds and sexes with parvoviral enteritis showing SIRS symptoms in 1-6 months of clinical and haematological examinations. The healthy control group consisted of dogs (22 dogs) of different breeds and sexes, aged 1-6 months, which did not show any pathological condition in clinical and haematological examinations.

Determination of clinical and haematological findings

SIRS criteria for the experimental group; Animals with at least 2 of the clinical and haematological picture in which body temperature < 37.8 °C or > 39.4 °C, heart rate > 140 bpm, respiration rate > 30 respirations/min, WBC < 6000 or > 16,000 cells/µL or > 3% band neutrophil count were accepted as the experimental group (parvoviral enteritis group with SIRS (Alves et al., 2020). The control group was selected from animals with no abnormalities detected in clinical and haematological examinations (using Abacus Junior Vet 5®, Hungary) and were brought to the clinic for routine vaccinations and health check-ups.

Identification of the etiological pathogen

The etiology of the disease was determined using a rapid diagnostic kit on fecal samples collected from animals presenting with symptoms of parvoviral enteritis, including vomiting, bloody diarrhea, hyperthermia or hypothermia, anorexia, and weakness (GenBody Inc., Korea). Animals diagnosed with coronavirus or a mixed infection using this test kit, as well as those with any parasites detected in the fecal samples, were excluded from the study.

Statistical analysis

The statistical analysis of the data was performed using the SPSS software version 27.0.1.0. Shapiro-Wilk normality test was applied for normality test and Levene's test was applied to determine the homogeneity of the data. Mean ± standard deviation and Quartile (Q1-Q3) descriptive units were used for descriptive statistics. An independent samples t-test was used for normally distributed data, while the Mann-Whitney U test was applied for non-normally distributed data.

RESULTS

The clinical parameters between groups are presented in Table 1. Compared to the control group, temperature data were significantly lower in the SIRS group ($p < 0.001$), whereas heart rate and respiration rate were significantly higher in the SIRS group ($p < 0.001$ for both). The data of haematological indices between groups are presented in Table 2. The WBC, NEU, NLR, SIRI, and SII values were higher in the SIRS group compared to the control group (p values < 0.05 for WBC, NEU, NLR, and SII; $p \leq 0.05$

for SIRI). No significant differences were observed for the other hematological parameters ($p > 0.05$).

Table 1. Comparing clinical values between control and SIRS groups

Groups			
Parameters	**Control group** Median (Q1-Q3) (n=22)	**SIRS group** Median (Q1-Q3) (n=60)	***P***
Temperature (°C)	38.5 (38.1-38.8)	35.9 (34.7-37.7)	<0.001
Parameters	**Control group** (n=22) $\bar{x}$±sd	**SIRS group** (n=60) $\bar{x}$±sd	***P***
Heart rate	129.36±8.15	171.96±17.06	<0.001
Respiration rate	16.04±2.73	34.93±8.17	<0.001

$P \leq 0.05$ is statistically important

Table 2. Comparison of hematological indices values between control and SIRS groups

Groups			
Parameters	**Control group** Median (Q1-Q3) (n=22)	**SIRS group** Median (Q1-Q3) (n=60)	***P***
WBC	8.25 (7.07-10.69)	19.22 (3.71-23.77)	<0.05
LYM	1.42 (0.84-1.73)	1.35 (0.86-1.87)	>0.05
MON	0.50 (0.35-0.64)	0.78 (0.19-1.15)	>0.05
NEU	5.75 (4.98-8.64)	16.97 (2.46-20.97)	<0.05
PLT	340.50 (271.75-474.25)	384.00 (310.00-565.00)	>0.05
MPV	7.70 (7.17-8.15)	8.10 (7.10-9.97)	>0.05
NLR	5.79 (2.90-8.78)	10.18 (4.46-13.95)	<0.05
LMR	2.74 (1.37-4.40)	2.08 (1.01-4.10)	>0.05
PLR	224.85 (179.24-512.39)	345.34 (193.51-558.23)	>0.05
MPV/PLT	0.02 (0.01-0.02)	0.02 (0.01-0.02)	>0.05
SIRI	2.40 (1.15-5.00)	7.95 (0.49-18.93)	≤0.05
SII	1789.74 (953.45-2798.70)	3444.30 (1648.37-6322.41)	<0.05

WBC: White blood cell; LYM: Lymphocyte; MON: Monocyte; NEU: Neutrophil; PLT: Platelet; NLR: Neutrophil-to-lymphocyte ratio; LMR: Lymphocyte-to-monocyte ratio; PLR: Platelet-to-lymphocyte ratio; MPV: Mean platelet volume; SIRI: Systemic inflammation response index; SII: Systemic inflammatory index. $P \leq 0.05$ is statistically important

DISCUSSION

Although parvoviral enteritis can affect dogs of any breed, sex, or age, it is more commonly seen in puppies younger than 6 months. One of the most significant complications of parvoviral enteritis is sepsis. Endotoxemia occurs in 82% of dogs with parvoviral enteritis. SIRS develops as a result of endotoxemia, and clinical and hematological findings are observed in affected animals (Muñoz et al., 2022). Clinical symptoms of parvoviral enteritis include nonspecific anorexia, depression, fever,

vomiting within 24-48 hours, and diarrhea that may be bloody. Due to excessive fluid loss, many dogs develop severe dehydration and hypovolemic shock. Weak pulse, hypothermia, and tachycardia have been reported as compensatory responses to the shock state (Prittie, 2004). Similarly, in this study, dogs with parvoviral enteritis complicated by SIRS exhibited lower body temperatures and higher pulsation and respiration rates compared to the control group. This may be attributed to a mechanism that compensates for shock induced by hypovolemia or facilitates the removal of harmful metabolites produced by SIRS/sepsis.

Hematological indices are frequently utilized in human medicine to assess the prognosis and severity of diseases. However, in veterinary medicine, the use of these markers has been relatively recent. The aim of this study was to evaluate the levels of these hematological indices in dogs with parvoviral enteritis complicated by SIRS. NLR is a cost-effective and easily measurable biomarker that effectively reflects the balance between innate and acquired immunity (Buonacera et al., 2022). NLR, PLR, and SII have recently been employed to assess inflammatory status and prognosis in conditions such as oncological and cardiovascular diseases, sepsis, and COVID-19 (Acar et al., 2021; Wang et al., 2022; Yang et al., 2020). One study reported that NLR could not distinguish between septic and non-septic dogs; however, another study found that increased NLR levels could be used to identify septicaemia in dogs (Hodgson et al., 2018; Pierini et al., 2019). Another study reported that lower NLR levels were observed in dogs with septic SIRS compared to those with non-septic SIRS (Pierini et al., 2020). It has been reported that the low level of NLR may be attributed to a distinct inflammatory response in leukocyte counts in dogs or, in later stages, to an advanced state of sepsis (Conway et al., 2021). In a recent study conducted by us, calves with SIRS were found to have higher NLR values compared to the control group (Aydın and Apaydın Yıldırım, 2024). In this study, consistent with the findings of Kalli et al. (2010), leucocytosis was observed rather than leucopenia in dogs with parvoviral enteritis complicated by SIRS, leading to an increase in the NLR ratio in the hematological profile. The observed situation may be attributed to the fact that most blood samples from dogs with parvoviral enteritis in the study were collected during the early stages of viremia, rather than during leukocytosis associated with secondary bacterial infections (Dash et al., 2017). Another potential cause may be the continuous release of functionally impaired neutrophils from the bone marrow due to prolonged sepsis (Lewis et al., 2012). Similar to the NLR, the LMR is recognized as a simple and easily measurable marker. It has been reported that high MLR (monocyte to lymphocyte ratio) was obtained in dogs with SIRS symptoms with pyometra compared to the control group and that this was due to the fact that monocytes are a more sensitive and active haematological marker in an inflammatory condition (Yazlık et al., 2022). In our study, the absence of significant differences in monocyte and lymphocyte counts between dogs with parvoviral enteritis showing signs of SIRS and

the control group resulted in no substantial variation in LMR values between the groups.

It has been reported that in dogs that died from non-septic critical illness, the PLR levels were higher compared to the surviving dogs, while no significant difference in NLR levels was observed between the two groups. This finding is potentially attributed to an insufficient sample size (Dourmashkin et al., 2023). MPV is a marker that indicates the level of platelet activation and the rate of platelet production (Bancroft et al., 2000). A study has reported that there was no significant difference in MPV values between dogs with parvoviral enteritis and healthy control dogs. However, this situation has been suggested to be a result of insufficient sample size (Koenhemsi, 2019). However, different results have been obtained in other studies involving dog models with parvoviral enteritis and endotoxemia, as follows:

It has been reported that MPV levels are statistically significantly higher in dogs with parvoviral enteritis compared to healthy control dogs (Engelbrecht et al., 2021). A study involving dogs with endotoxemia similarly reported that elevated MPV levels provided significant results in the diagnosis and prognosis of endotoxemia (Yilmaz et al., 2008). In our study, no significant differences were observed between dogs with parvoviral enteritis showing signs of SIRS and the control group in terms of PLR, MPV, and MPV/PLT levels. This situation is attributed to the lack of development of lymphocytosis, lymphopenia, or changes in lymphocyte levels in some cases due to SIRS, as well as the inconsistent changes in platelet counts observed in dogs with parvoviral enteritis complicated by SIRS.

SII values have been reported to initially determine the severity of inflammatory conditions and prognosis in patients with hepatocellular carcinoma (Hu et al., 2014). Another study on prognosis in cancer patients reported that an SII value greater than 750 is an indicator of poor prognosis (Tian et al., 2022). A study on dogs with leishmaniasis reported that SII values increased in parallel with elevated neutrophil counts (Durán-Galea et al., 2024). In cancer patients, an increase in SIRI values, similar to SII, has been associated with a lower survival rate (Zhou et al., 2021). A study on patients with sepsis indicated that elevated SIRI values positively correlate with increased mortality rates and are an important marker in determining the prognosis of sepsis (Ru and Luo, 2023). A recent study we conducted on calves with SIRS determined that SIRI and SII values were significantly higher compared to the healthy control group (Aydın and Apaydın Yıldırım, 2024). In this study, higher SII values were observed in the SIRS group compared to the control group. Although the SIRI value was higher in the SIRS group compared to the control group, no significant difference was found between the groups at the expected level. This situation may be due to the fact that, in some cases of SIRS, elevated neutrophil counts and, in some instances, the development of neutropenia, along with a lack of a significant decrease

in lymphocyte counts, could have contributed to the observed results, particularly regarding SIRI values.

CONCLUSION

The results of this study suggest that markers such as NLR, SII, and SIRI may be useful in determining the inflammatory status of the disease in dogs with parvoviral enteritis complicated by SIRS. Additionally, these markers could provide insights into the prognosis of the disease, especially when assessed through repeated measurements. However, to gain a better understanding of the issue, it is suggested that repeated measurements should be conducted. Additionally, larger-scale studies investigating the relationships between these hematologic indices and acute phase proteins or pro-inflammatory cytokines are anticipated to yield more diverse and specific data.

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Ethical statement or informed consent: The study received approval from the Local Ethics Committee for Animal Experiments at Atatürk University (Approval number: 2024/07; Approval date: 23.07.2024).

Author Contributions: The design of the study, sample collection, statistical analysis, manuscript writing, and editing were all conducted by ÖA.

Availability of data and materials: All data and materials related to the study are available upon request from the corresponding author.

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POLYCYSTIC KIDNEY DISEASE IN A BRITISH SHORTHAIR CAT

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Abstract

The animal material of this case report was a three-year-old British Shorthair cat with a history of pulmonary embolism. Despite the absence of pathological findings in the haematological and biochemical analyses of the renomegaly observed during the routine abdominal palpation, advanced imaging techniques revealed the presence of polycystic kidney disease (PKD). This case report illustrates that haematological and biochemical alterations are inadequate for a definitive diagnosis of PKD in cats. It is therefore recommended that imaging techniques be employed, even in cats that exhibit no clinical symptoms.

Keywords: Cat, Polycystic kidney disease, Ultrasound, Radiography

INTRODUCTION

Polycystic kidney disease (PKD) constitutes an autosomal dominant genetic disorder characterized by the progressive development of multiple fluid-filled cysts within the bilateral renal parenchyma. The disease process may also extend to involve other vital organs, including liver and pancreas (Bosje et al., 1998). Over time, renal cysts undergo progressive proliferation and enlargement, a consequence of the aging process. This phenomenon leads to the gradual deterioration of kidney tissue via pressure necrosis, ultimately culminating in chronic kidney failure and feline mortality (Wills et al., 2009). In the majority of patients, CKD development is insidious, with a clinically normal presentation persisting for extended periods (often exceeding seven years) (Bosje et al., 1998). The precise mechanisms underlying PKD pathogenesis remain elusive, with numerous potential causes currently under investigation. One hypothesis posits that cyst formation arises from tubular epithelial hyperplasia, leading to partial tubule obstruction and subsequent impairment of urine flow (Eaton et al., 1997).

Clinical presentation alone is insufficient for definitive PKD diagnosis. While palpation might reveal renomegaly, this finding is non-specific and can indicate other underlying pathologies. A comprehensive diagnostic approach integrates clinical signs, laboratory findings suggestive of renal dysfunction, breed predisposition, and potentially, epidemiological data (Barthez et al., 2003). However, advanced imaging techniques, particularly ultrasound examination, and recently developed genetic testing methods have emerged as the preferred diagnostic modalities.

MATERIALS AND METHODS

Animal

The study material consisted of 3 old female British Shorthair cats. The history of the cat began with an ovariohysterectomy. After surgery she was readmitted to hospital with tachypnea and pale mucous membranes and was diagnosed with pulmonary embolism. After the diagnosis, treatment was started and she was asked to return to the hospital at 6-month intervals for follow-up. No clinical signs of pulmonary embolism were observed at the 6-month routine examination, but irregular enlargement of the kidneys was noted on abdominal palpation. Haematological and biochemical tests were performed to evaluate this finding. An Abacus Junior Vet 5 haematology analyser was used for haematological analysis and a Randox chemistry analyser for biochemical analysis. Radiographic and ultrasonographic examinations were then performed for renal imaging. A Mex-100 unit was used for radiography, and a Mindray Vetus 8 ultrasound unit was used for ultrasonography.

RESULTS

The results of the haematological and biochemical analyses are presented in Tables 1 and 2, respectively. While lymphocytosis was identified in the haematological analysis, hypercalcemia was observed in the biochemical analysis. The remaining results fell within the reference ranges.

Table 1. Haematological analysis findings in a car with polycystic kidney disease

Parameters	Patient	Reference ranges
WBC	19.02	5.5-19.5
LYM	**14.45**	1.5-7.0
MON	0.07	0-0.9
NEU	4.49	2.5-12.5
EOS	0.01	0-0.8
BAS	0	0-0.2
RBC	7.84	5-10
HGB	15.8	9.8-15.4
HCT	38.49	24-45.0
MCV	49	39-55
MCH	16.1	13-17
PLT	382	300-800
MPV	12.7	12-18.0

WBC: White blood cell; LYM: Lymphocyte; MON: Monocyte; NEU: Neutrophil; EOS: Eosinophil, BAS: Basophil; RBC: Red blood cell; HGB: Haemoglobin; HCT: Haematocrit; MCV: Mean corpuscular volume; MCH: Mean corpuscular haemoglobin; PLT: Platelet; MPV: Mean platelet volume

Table 2. Biochemical analysis results in a cat with polycystic kidney disease

Parameters	Patient	Reference ranges
Glucose	89.9	60-120 mg/dl
Total Protein	7.08	6.0-7.9
Globulin	3.29	2.6-5.1 g/dl
Albumin	3.79	2.8-3.9 g/dl
BUN	23.13	19-34 mg/dl
Creatinine	1.94	0.9-2.2 mg/dl
Phosphor	4.26	3.0-6.1 mg/dl
Potassium	4.7	3.7-6.1 mg/dl
Sodium	155	146-156 mEq/L
Chlorine	114.06	115-130 mg/dl
Magnesium	1.97	1.7-2.6 mg/dl
Calcium	**13.82**	8.7-11.7 mg/dl
Creatinine kinase	660	69-214 mg/dl
AST	28.2	7-38 U/L
ALT	53.7	25-97 U/L
ALP	20.2	0-45 U/L
LDH	109.3	58-120 U/L
GGT	0.5	0-25 U/L
Total Bilirubin	0.17	0-0.8 mg/dl
Direct Bilirubin	0.03	0-0.3 mg/dl
Cholesterol	217.9	71-156 mg/dl

The radiographic and ultrasonographic examination findings are presented in Figures 1 and 2, respectively. The radiographic examination revealed a length of 58.41 mm along the longitudinal axis and a width of 44.38 mm of the renal structure. The ultrasonographic examination revealed the presence of an extra-renal cystic structure.

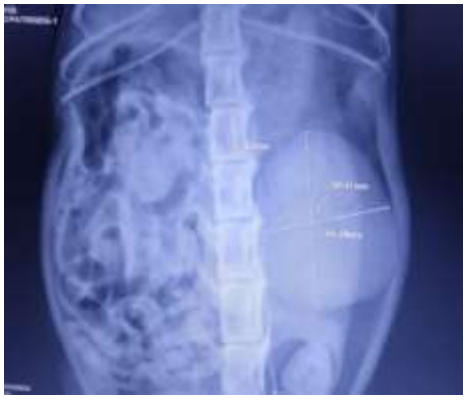

Figure 1. Radiographic examination result of a cat with polycystic kidney disease.

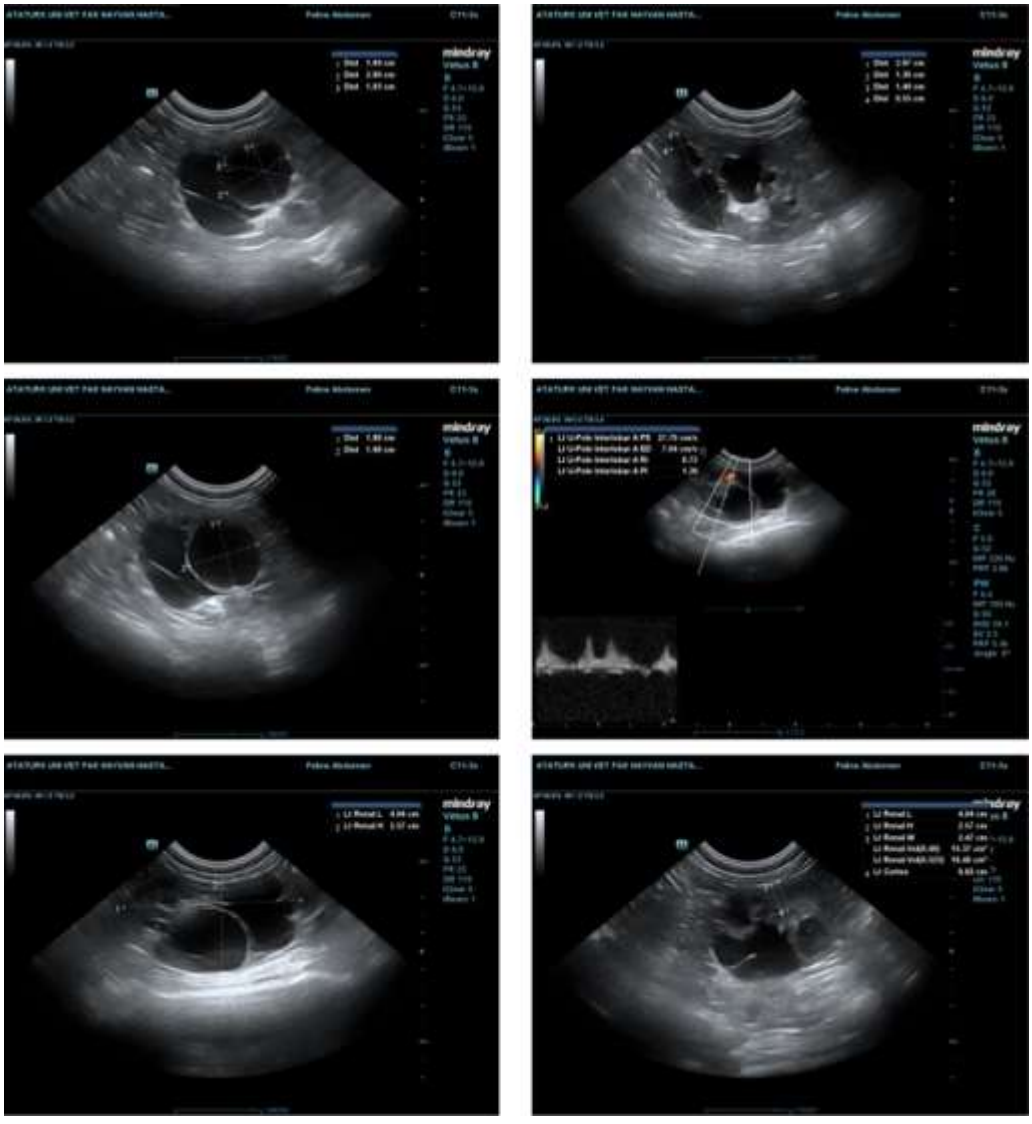

Figure 2. The ultrasonographic findings in a cat with polycystic kidney disease.

DISCUSSION

This case report describes a feline patient diagnosed with PKD in the absence of overt clinical manifestations. This atypical presentation contrasts with the commonly reported clinical signs associated with PKD in this species (Schirrer et al., 2021; Beck and Lavelle 2001). Given the patient's age relative to the typical age of PKD onset, it is plausible that the disease was detected in its early stages. Hematological and biochemical findings corroborate this hypothesis.

Abnormalities were identified in the results of the hematological and biochemical analyses. The initial abnormality identified is lymphocytosis. A number of potential causes for lymphocytosis have been put forth, including acute and chronic infections, stress and the release of adrenaline, and lymphoproliferative diseases (Raskin et al., 2004; Boone 2008). It is noteworthy, however, that the patient has a history of pulmonary embolism. The patient's history of pulmonary embolism serves to reduce the number of potential causes of lymphocytosis and to highlight the role of the pulmonary embolism-related stress response. Previous studies have documented changes in various immune system cells as a result of the stress caused by pulmonary embolism (Ateş et al., 2017; Rezania et al., 2017). In light of these findings, it is reasonable to propose that an impaired immune system may be the underlying cause of lymphocytosis.

The results of the biochemical analyses demonstrated a notable elevation in calcium levels. There are numerous potential causes of elevated calcium levels in cats, including parathyroid gland disorders, lymphoma, renal disease, and fungal infections (Savary et al., 2000; Coady et al., 2019). Nevertheless, the most notable of these causes is kidney disease. A review of the literature reveals a growing body of research examining the association between calcium metabolism disorders and chronic kidney disease (Van den Broek et al., 2017; Geddes et al., 2021). It is therefore reasonable to make this interpretation in the context of our patient. However, it is noteworthy that the biochemical analysis results, which indicated renal failure, did not support this finding. In light of the aforementioned evidence, the exclusion of other potential causes for the elevated calcium levels underscores the necessity for a comprehensive examination of calcium homeostasis in cats with PKD. The radiographic and ultrasonographic examination findings were consistent with a diagnosis of PCD, which corroborates previous studies that emphasize the pivotal role of imaging modalities in detecting PKD in cats.

CONCLUSION

This case report demonstrates that haematological and biochemical changes are insufficient for a definitive diagnosis of PKD in cats. It is therefore recommended that imaging techniques be employed, even in cats that exhibit no clinical symptoms.

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Conflict of Interest: The author declares that there is no competing interest.

Ethical statement or informed consent: Since the study was a case report, an informed consent form was obtained from the patient owner.

Author Contributions: The design of the study, sample collection, statistical analysis, manuscript writing, and editing were all conducted by KEY.

Availability of data and materials: All data and materials related to the study are available upon request from the corresponding author.

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INVESTIGATION OF HISTOLOGICAL AND HISTOCHEMICAL STRUCTURE OF THE SPLEEN OF THE PARTRIDGE (*ALECTORIS CHUKAR*)

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ABSTRACT

The spleen, located near the stomach and above the right lobe of the liver, typically appears dark blue-brown. In poultry, it is spherical or egg-shaped, while in waterfowl, it takes on a triangular shape. The spleen serves as a blood-producing organ and plays a vital role in the immune system.This study aimed to explore the histological and histochemical features of the spleen in partridges (*Alectoris chukar*). In the study, eight partridges were used, and their spleen tissues were fixed in 10% formaldehyde for 36 hours. After undergoing dehydration and transparency processes for histological analysis, the tissues were embedded in paraffin and sliced into 5µm sections. These sections were stained with Hematoxylin Eosin (H&E) for structural evaluation and with Periodic Acid Schiff (PAS) and PAS/Alcian Blue pH:2.5 for histochemical evaluation. The partridge spleen was found to be surrounded by a thick capsule with small trabeculae. Red pulp and white pulp were observed to be scattered in the parenchyma. The white pulp contains reticular cells, fibers, and lymphocytes, while the red pulp contains numerous blood vessels, lymphocytes, macrophages, venous sinuses, and reticular cell anastomoses. Histochemical analysis using PAS staining showed a high concentration of neutral mucins around the blood vessels and within the capsule. In the PAS/AB pH:2.5 staining method, a positive reaction for neutral mucins and a negative reaction for acidic mucins were noted. In conclusion, the histological structure of the partridge spleen is similar to that of chicken, ostrich, and quail spleens.

Keywords: Partridge, histological, histochemical, spleen

INTRODUCTION

The Red-legged Partridge (*Alectoris chukar*) has a wide natural habitat in Turkey. However, the number of partridges in the natural area has decreased in recent years due to overhunting, habitat destruction and unnecessary use of pesticides (Yamak, 2015; Karabag et al., 2010). Although the economic and ecological importance of these birds is known, we know less about the morphology of the bird.

The immune system consists of central and peripheral lymphoid organs. These immune system organs can produce and develop lymphocytes. The thymus and cloacal bursa are the central lymphoid organs of birds that produce differentiate and mature T and B lymphocytes, respectively. These lymphoid organs can provide normal immunological defense and resistance against diseases (Nasu et al., 1992; Rautenfeld et al., 1982). The spleen is the primary organ of systemic immunity and its importance in disease resistance is probably emphasized by the paucity of avian lymph nodes (Kozlu et al., 2019). The avian spleen tissue is one of the lymphoid organs, consisting of white and red pulp. The white pulp contains small lymph nodes, and the red pulp contains scattered lymphoid cells and blood-filled sinusoids (Powers, 2000).

The spleen is located near the right side of the junction between the proventriculus and the gizzard. It is pinkish brown in color in fresh specimens (Islam et al., 2017). The spleen is the largest peripheral lymphoid organ and the site of immune response generation in most organisms. It also has functions in hematogenesis, blood filtration, blood storage, and immune system response. Immunocompetent cells proliferate and differentiate in the spleen following antigenic stimulation, and there are interspecies differences in the morphology of the spleen. There are differences in size, morphology, and structure among animal immune organs (Liman and Bayram, 2011; Song et al., 2012).

This study aims to determine the histological and histochemical structure of the spleen of the partridge (*Alectoris chukar*).

MATERIAL and METHOD

Before starting the study, the approval was obtained from the Ethics Committee of Selcuk University, Faculty of Veterinary Medicine (SUVFEK, Ref No: 2014-11, Date: 03/2014). The spleens of 12 (6 male+6 female) partridges purchased from a private farm in Antalya were used in the study. The spleen samples were fixed in 10% formal saline for 36 hours. After fixation, histological tissue follow-up was performed, and they were embedded in paraffin. Then, 5-µm thick sections were taken from the paraffin blocks. The sections were stained with Hematoxylin and Eosin (H&E) to determine the general structure and with Periodic Acid Schiff (PAS), Periodic Acid Schiff/Alcian Blue pH:2.5 (PAS/AB pH:2.5) to determine the histochemical structure, and their histological structure was examined.

RESULTS

Histological examination revealed that the partridge spleen is surrounded by a thick capsule with small trabeculae present within (Figure 1). The red and white pulps are dispersed throughout the parenchyma, with the white pulp consisting of reticular cells, reticular fibers, and lymphocytes. The red pulp contains numerous blood vessels, lymphocytes, macrophages, venous sinuses, and anastomoses of reticular cells (Figure 2). Histochemical analysis using PAS staining showed a high concentration of neutral mucins around the blood vessels and within the capsule (Figures 3, 4). In the PAS/AB staining method at pH 2.5, a positive reaction for neutral mucins and a negative reaction for acidic mucins were observed (Figure 5).

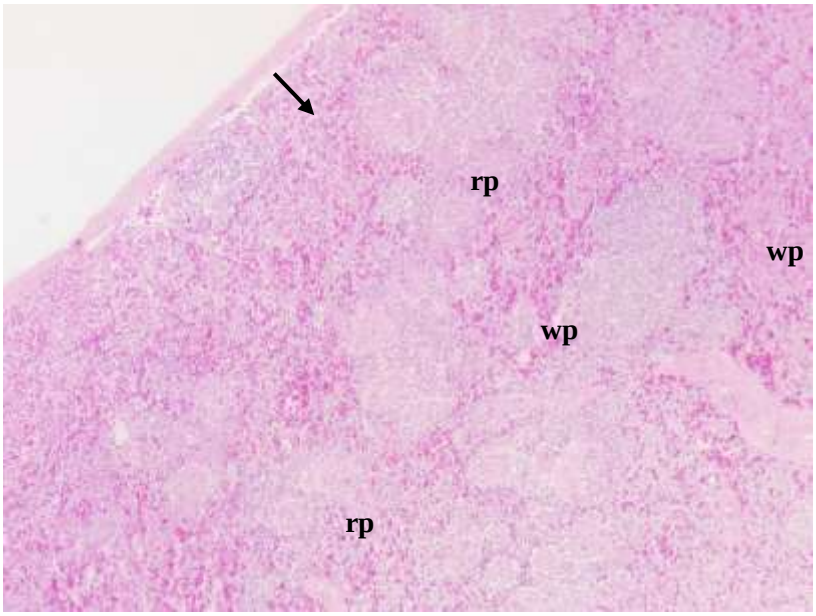

Figure 1: Partridge (*Alectoris chukar)* spleen. Externally surrounding capsule (arrow), red pulp (rp), white pulp (wp). Hematoxylin Eosin, X4.

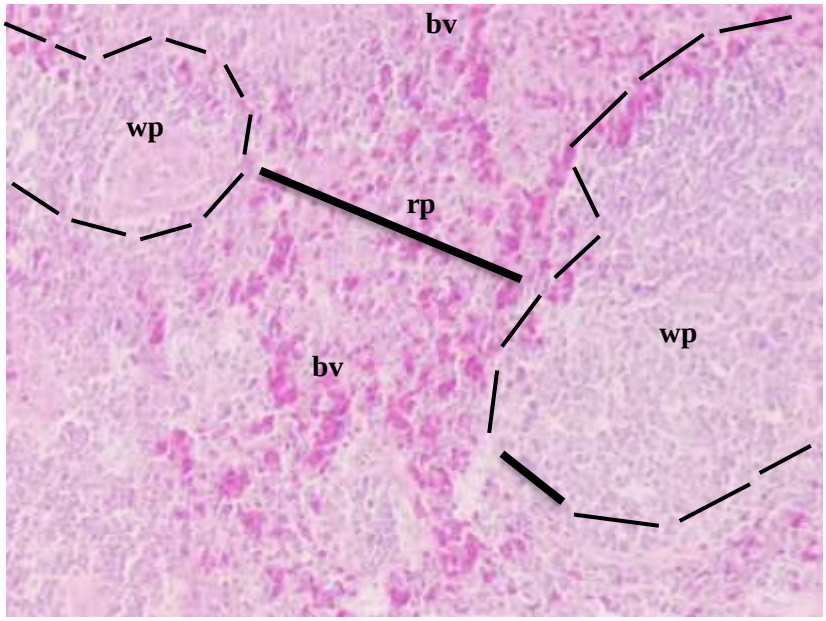

Figure 2: Partridge (*Alectoris chukar*) spleen. Blood vessel in red pulp (bd), red pulp (rp), white pulp (wp). Hematoxylin Eosin, X40.

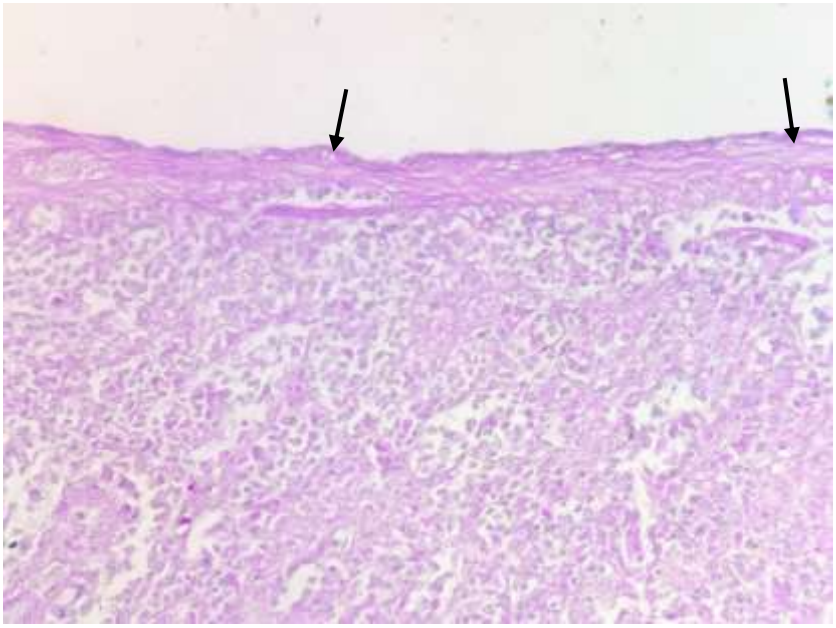

Figure 3: Partridge (*Alectoris chukar*) spleen. Externally surrounding connective tissue capsule (arrows). PAS staining method, X40.

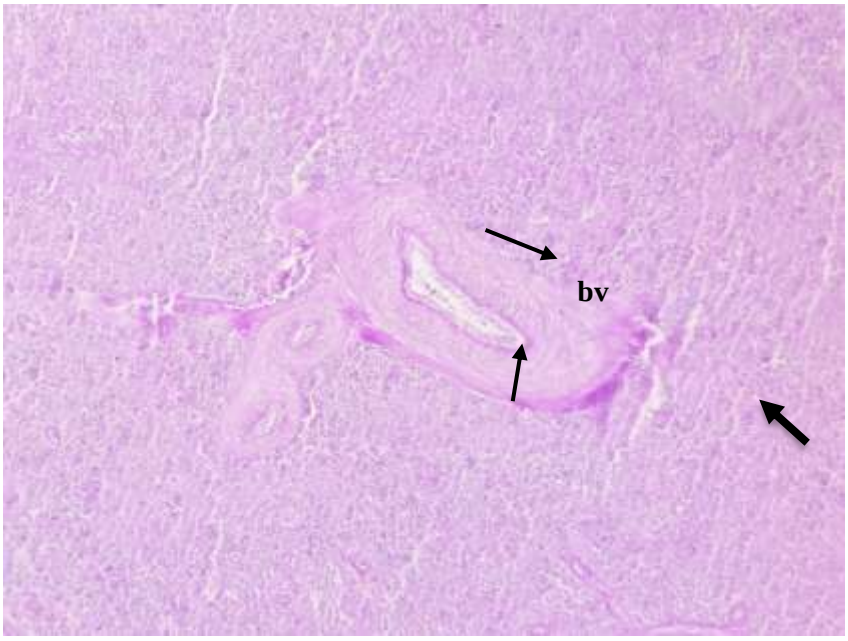

Figure 4: Partridge (*Alectoris chukar*) spleen. Blood vessel (bv). PAS positive areas (arrows). PAS staining method, X10.

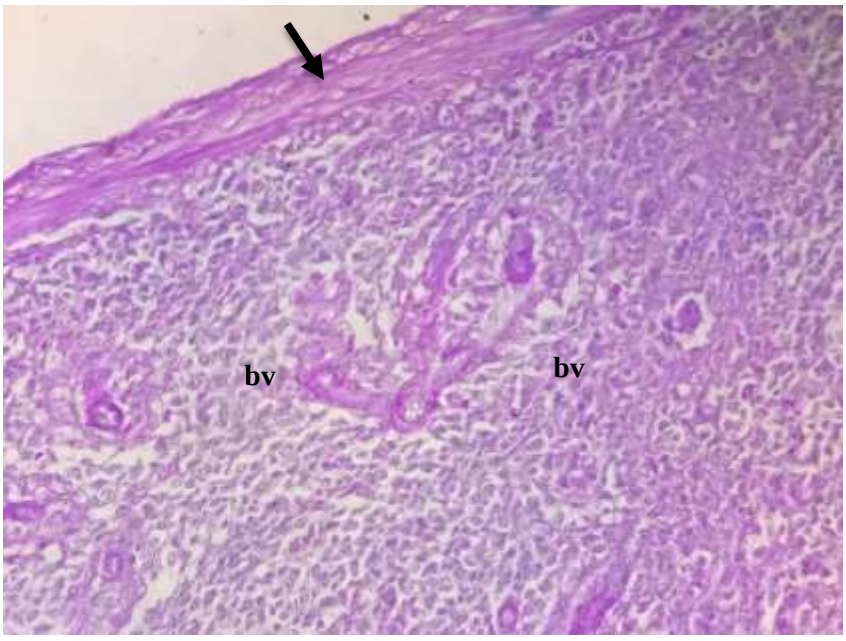

Figure 5: Partridge (*Alectoris chukar*) spleen. Externally surrounding connective tissue capsule (arrow), blood vessel (bv). PAS staining method, X40.

DISCUSSION

The spleen is the major secondary lymphatic organ that filters blood and provides immune responses against diseases and has an important role in the immune system of the organism. In addition, the spleen performs erythropoiesis during the fetal period of life (Liman and Bayram, 2011; Song et al., 2012).

The results of the study revealed that the red pulps of the spleen were less regional and the white pulps of the spleen contained reticular fibers and reticular cells and were covered with sheathed arteries and lymph nodes in red-legged partridges. Similar to our study, the same similar histological structure has been reported in Bangladeshi native duckling (Sultana et al., 2012), ostrich (Kozlu et al., 2019), hatched quail (Rautenfeld at al., 1982) and chicken (Khan et al., 2014).

The mesenchymal cell around the penicilliform capillary, known as the Schweigger-Seidel sheath, is well-developed ellipsoids in avian species. In the present study, ellipsoids were observed around the penicilliform capillary in the spleen of red-legged partridge. Similar to chicken and guinea fowl, a Schweigger-Seidel sheath covered with two similar cell layers has been reported (Mast and Goddeeris, 1997; Olah et al., 1993).

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Conflict of interest:

The authors have no conflicts of interest in reporting.

Authors' Contributions

The research ideas, obtaining materials, various processes in the laboratory and evaluation of the results were carried out by HYK.

Ethical approval

The approval was obtained from the Ethics Committee of Selcuk University, Faculty of Veterinary Medicine (SUVFEK, Ref No: 2014-11, Date: 03/2014).

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