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13.5%), *Paridae* (1; 11.1%), *Sylviidae* (5; 8.6%), *Ardeidae* (6; 6.6%), *Fringillidae* (1; 3.8%), *Muscicapidae* (1; 2.1%), and *Columbidae* (5; 50%) families. All evaluated samples were negative for H5 and H7 AIV subtypes by rRT-PCR.

Conclusion: AIV was identified in wild bird samples, including synanthropic species. Terrestrial birds and shorebirds, especially from *Meropidae*, *Sturnidae*, *Rallidae*, *Corvidae* and *Anatidae* families are carriers of AIV. AIV subtypes H5 and H7 were not detected in any evaluated samples.

23.105 Molecular characterization of ovine herpesvirus type 2 (ovhv-2) in Turkey

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Purpose: Malignant catarrhal fever (MCF) has been known for many years as a dramatic, often lethal, systemic viral infection of cattle and many species of wild ruminants. Based on the reservoir ruminant species, from which the causative virus arises, two major epizootiological entities of the disease have been described: wildebeest-associated (WA) and sheep-associated (SA) MCF, between which there are no significant differences in clinicopathological features. There is little evidence about this disease in city of Kars. We intended to gain some data about the disease.

Methods & Materials: In this study, the physical examination of 22 cattle revealed clinical signs of malignant catarrhal fever (MCF). Peripheral blood leukocyte (PBL) samples of the 22 cattle, and nasal (n = 7) and conjunctival (n = 9) swab samples from 16 sheep from two different farms, were tested for ovine herpesvirus 2 (OvHV-2) using by nested PCR. Furthermore, sequence analysis of ovine herpesvirus-2 DNA was conducted.

Results: The clinical diagnosis of MCF in cows was confirmed by the detection of ovine herpesvirus type 2 (OvHV-2) DNA by polymerase chain reaction (PCR). OvHV-2 DNA was detected by nested-PCR in PBL of one cow with clinical signs and nasal (1/7)-conjunctival (1/9) swab samples of two sheep housed in the same barn. According to the sequence analysis, three slightly divergent viruses were detected.

Conclusion: In this study, the presence of OvHV-2 in cattle and sheep was determined by PCR in Turkey. The sequence analysis of these DNA products revealed high degree of identity (69–84.1) among the isolates. The results of this study support the need for additional research in different regions of Turkey to gain a better understanding of the incidence of this disease and implications for the livestock industry.

23.106 Detection and full-length genome characterization of feline kobuviruses identified from diarrheic cats

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Purpose: Kobuviruses are non-enveloped, single stranded, positive-sense RNA viruses and represent a distinct genus in the family *Picornaviridae*. Based on their genomic organization and sequence similarities, kobuviruses are classified into 3 species, *Aichivirus A* (*Aichi virus*), *Aichivirus B* (*Bovine kobuvirus*) and *Aichivirus C* (porcine kobuvirus). Human aichi virus (AiV) is currently involved in 0.9-4.1% of sporadic cases of pediatric gastroenteritis. Viruses genetically and antigenically close related to human AiVs have been recently found in domestic and wild carnivores. Canine kobuviruses (CaKVs) were discovered in diarrhoeic and asymptomatic dogs in US. Subsequently, viral RNA genetically similar to that of CaKVs (82.0-86.0%) was detected in diarrhoeic cats in South Korea. However, to date, there is no additional information on the circulation of these novel viruses in cats.

Methods & Materials: In this study we screened 83 faecal specimens obtained from asymptomatic (n= 46) and diarrhoeic (n= 37) cats, using different sets of primers. The samples were also tested by PCR or RT-PCR for feline parvovirus (FPV) and feline enteric coronavirus (FECV).

Results: Out of 83 samples, 5 (6.0%) contained FeKoVs RNA, alone (n= 2) or in mixed infections (FPV + FeKoV, n= 3). All the positive samples were identified from diarrhoeic cats.

The complete genome of the FeKoV strain TE/52/13/IT was determined. The genome was 8,219-nt long and enconded a 2,436 aa polyprotein flanked on each side by untranslated regions. The positions of clivage sites on the polyprotein were predicted by sequence alignments and NetPicoRNA analysis. Likewise in other kobuviruses, the predicted cleavage map identified the L/VP0, VP3/VP1, VP1/2A, 2A/2B, 2B/2C, 2C/3A, 3B/3C and 3C/3D cleavage sites, all which contained Q/G residues, but the VP0/VP3 and 3A/3B sites, which contained E/G and Q/A residues. In the full-length genome, strain TE/52/13/IT displayed the highest nt identity (96.0%) to the strain FeK-13 recently identified in Korea, while identity to CaKoVs and AiVs was 80.0-83.0% and 75.0-77.0 %, respectively.

Conclusion: These findings demonstrate that FeKoVs circulate outside the Asian continent, where they were first described. It will be important to understand whether these viruses can be associated with enteritis or other diseases in cats.

23.107 Horses naturally infected with Strongylidae and Ascaridae: Evaluation of hematological and some biochemical parameters

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Background: Infectious larvae of equine parasites: *Strongylidae* and *Ascaridae* may induce direct as well as indirect damage, during their migration within the host.

Objectives: The aim of this study was to evaluate changes in hematological and biochemical parameters in naturally infected horses, with the above mentioned parasites.

Methods & Materials: Research was performed in 48 horses of *Nonius* breed, divided in four groups according to their age: I group (1 to 12 months of age); II group (12 to 24 months); III group (2 to 5 years of age) and IV group (above 10 years of age). Every group has a control group, negative to the presence of parasitic infection. Presence of parasites was determined using the methods of coprologial examination. Hematological parameters were determined on CELL DYN 1700 device. Total activity of LDH in blood serum was determined spectrophotometrically, while the relative distribution of LDH isoenzyme was analyzed by native PAGE according to Laemmli's method.

Results: Two parasitic infections were determined, with *Strongylidae* and *Ascaridae*, what was in correlation with the age of horse. In horses infected with *Strongylus spp* we found significant decreasing of erythrocyte number ($p<0.05$), concentration of hemoglobin and hematocryte values ($p<0.001$). Number of granulocytes and eosinophyles were significantly increased ($p<0.001$), while the number of basophiles, monocytes and lymphocytes were decreased ($p<0.05$).

In infected horses, we estimated increased total activity of LDH ($p<0.05$). In foals infected with *Ascaridae* there was increasing in LDH3 isoenzyme form, while in older horses there was increasing of LDH5 ($p<0.05$), compared with the control group.

Conclusion: By these analyses we demonstrated that hemathological and biochemical parameters can be very useful diagnostic tools in evaluation of the parasitic infection of horses with *Strongylidae* and *Ascaridae*, especially in pre-patent period of infection, when coprological techniques are always negative.