Part 4. Brief communications

UDC 619:616.98:578.821.2(560)

LUMPY SKIN DISEASE: CURRENT EPIDEMIOLOGICAL SITUATION AND PREVENTION IN TURKEY AND NEIGHBORING COUNTRIES

Yilmaz H. [1], Turan N. [1], Yilmaz A. [1], Richt J. A. [2]

[1] Department of Virology, Veterinary Faculty, University of Istanbul-Cerrahpasa, Avcilar, Istanbul, Turkey, e-mail: hyilmaz@istanbul.edu.tr, nturan@istanbul.edu.tr, yilmazaysun@istanbul.edu.tr
[2] Department of Diagnostic Medicine and Pathobiology, College of Veterinary Medicine, Kansas State University, Manhattan, KS, USA jricht@vet.k-state.edu

Lumpy skin disease (LSD) is an economically important disease affecting cattle health and export of cattle products in endemic countries. It is caused by a *Capripoxvirus* and shows characteristic skin lesions in infected cattle. The disease was first reported in 1929 in Zambia. It then spread throughout Africa, the Middle East, Southeast Europe, the Balkans, Caucasus, Russia and Kazakhstan. The first Turkish outbreak of LSD was reported in 2013 in Kahramanmaras, Turkey. Many cattle in Turkey were affected and the disease has spread to farms located in various parts of the country. After the first outbreak in 2013, rapid diagnostic methods have been developed and used in order to identify infected animals. Prevention, control and eradication programs have been conducted by the Ministry of Agriculture and Forestry of Republic of Turkey including contingency plan, culling and compulsory vaccination. In this presentation, the current situation of LSD epidemiology and prevention in Turkey and neighboring countries will be discussed.

Keywords: lumpy skin diseases, cattle, Turkey, epidemiology, prevention

UDC 619:616.98-036.22:578.832.1A:578.831.11:598.2(560.1)

FREQUENCY AND GENOTYPES OF AVIAN INFLUENZA VIRUS (AIV) AND NEWCASTLE DISEASE VIRUS (NDV) IN MIGRATORY PASSERIFORM AND NONPASSERIFORM BIRDS, AND DUCKS IN ISTANBUL, TURKEY

Turan N. [1], Ozsemir C. [1], Yilmaz A. [1], Cizmecigil U. Y. [1], Aydin O. [1], Ozsemir K. [2], Ozsoy S. [2], Iqbal M. [3], Tali H. E. [1], Tekelioglu B. K. [4], Kutukcu A. [1], Richt J. A. [5], Yilmaz H. [1]

[1] Department of Virology, Veterinary Faculty, University of Istanbul-Cerrahpasa, Avcilar, Istanbul, Turkey, e-mail: nturan@istanbul.edu.tr, yilmazaysun@istanbul.edu.tr, hyilmaz@istanbul.edu.tr
[2] Wild Life Clinic, Veterinary Faculty, University of Istanbul-Cerrahpasa, Avcilar, Istanbul, Turkey
[3] The Pirbright Institute, Pirbright, Surrey, UK
[4] Department of Virology, Veterinary Faculty, University of Cukurova, Ceyhan, Istanbul, Turkey
[5] Department of Diagnostic Medicine and Pathobiology, College of Veterinary Medicine, Kansas State University, Manhattan, KS, USA jricht@vet.k-state.edu

Avian influenza (AI) and Newcastle disease (ND) are economically important viral diseases of birds, endemic in many countries. Both viruses can infect humans, but the H5 and H7 subtypes of AI viruses (AIVs) have caused devastating public and animal health problems worldwide. Both viruses are among the most important infectious disease problems in the poultry industry and new preventive and control strategies are urgently needed. ND virus (NDV) and particularly AIV spread *via* migratory birds, especially waterfowl, among birds within a country, between countries and even between continents. Importantly, the Republic of Turkey is geographically situated in one of the world's most important migratory bird flyways.

In the present study, passeriform and nonpasseriform birds, and ducks were investigated for the presence and genotypes of AIVs and NDVs. For this purpose, field studies were performed with birds migrating on the South East European flyway, in the Marmara region of Turkey which borders the European Union. Traps were placed around the Kucukcekmece lake Avcilar, Istanbul, in the spring season of 2016 and 2017 to catch passeriform and nonpasseriform

birds. The trapped birds were categorized according to species and sex, ringed and oropharyngeal and cloacal swabs were taken. In total, 200 oropharyngeal and 200 cloacal swabs were collected. In addition, in 2017, swabs from 80 green headed ducks (*Anas platyrhynchos*) were sampled by hunters in the Edirne area in Turkey, which is close to the Greek border. Also, swab samples from birds (n = 150) treated at the Wild life clinic at the Veterinary Faculty of Istanbul were analyzed. Laboratory investigations consisted of RNA extraction and real-time RT-PCR analyses for the presence of AIV and NDV genetic signatures. Positive samples were further subjected to sequencing. Phylogenetic analyses were performed to determine genotypes of AIV and NDV in the targeted bird population. AIV-RNA was detected in 12 duck samples and two birds of prey and they all belonged to the H9N2 subtype of avian influenza viruses. NDV-specific RNA was found in two waterfowl samples and the viruses belong to the NDV lineage VII. Results of this study indicate that migratory birds present a threat for Turkey to spread both AIVs and NDVs.

Keywords: avian influenza virus, Newcastle disease virus, migratory birds, genotypes, Turkey

UDC 619:616.98-07:579.841.93:577.2.08(479.22)

MOLECULAR TECHNIQUES FOR DIAGNOSIS AND CONTROL OF HUMAN AND ANIMAL *BRUCELLA* ISOLATES FROM GEORGIA

Sidamonidze K. [1], Ramishvili M. [1], Malania L. [1], Zhgenti E. [1], Donduashvili M. [2], Nikolaishvili M. [2], Vepkhvadze N. [2], Kokhreidze M. [2], Avaliani L. [3], Imnadze P. [1]

[1] National Center for Disease Control and Public Health, Tbilisi, Georgia,
e-mail: m.ramishvili@ncdc.ge, pimnadze@ncdc.ge
[2] Laboratory of the Ministry of Agriculture, Tbilisi, Georgia
[3] National Food Agency, Tbilisi, Georgia

Brucellosis is an ancient and highly contagious zoonotic disease caused by the genus *Brucella* that remains to be a major public and animal health problem in Georgia and is considered one of the most important health disorders spread worldwide. The leading institutions conducting surveillance on brucellosis in Georgia are the National Center for Disease Control and Public Health under the Ministry of Health. the Laboratory of the Ministry of Agriculture, and the National Food Agency under the Ministry of Agriculture.

The aim of this study was evaluation of implemented molecular diagnostic tests for the assessment of animal and human cases of brucellosis in Georgia.

Isolates from human blood and ruminant milk or blood suspected as *Brucella* by microbiological, biochemical and serological testing were confirmed by real-time PCR (*Brucella* T1, Biofire Technology). Species identity of *Brucella* cultures were confirmed and typed by conventional AMOS PCR, Single Nucleotide Polymorphism (SNP) assays and later 'Bruce-ladder' assay. A multi-locus variable number tandem repeat analysis (MLVA) approach was applied for providing valuable information for epidemiological investigations.

AMOS PCR supported biochemical test results for 72 *Brucella melitensis* and four *Brucella abortus* strains, but not for 39 suspected *B. abortus* human and animal isolates. SNP typing of all 115 isolates supported the AMOS PCR results, but also confirmed suspected *B. abortus* species of the 39 strains not amplified by AMOS PCR. Above-mentioned *Brucella* strains were confirmed later also by 'Bruce-ladder' assay. In the present study, for the first time we have studied the genetic variability of 115 strains obtained in Georgia. Genotypes were revealed by a MLVA-15 approach with good subspecies discriminatory capabilities providing valuable information for epidemiological investigations and obtained data were utilized for construction of the phylogenic tree using Bionumerics Software version 6.1.

Evidences of the molecular-genetic research first have confirmed the existence of *B. melitensis* and *B. abortus* strains circulating in humans and animals in Georgia. Basing on our results of molecular-genetic researches, we can suppose, that *B. abortus* 3, 5, 6 and/or 9 biovars are more frequently spread, than *B. abortus* 1, 2 and 4 in Georgia. Thus, we can say, that application of AMOS PCR method is limited in our country. Species-specific SNP typing and 'Bruce-ladder' assays resolved the difficulties caused by limitations of AMOS PCR to recognize all biovars of *B. abortus*. Obtained results suggest that diversity of *Brucella* strains in Georgia is greater than captured in this study and it needs continuation of a large-scale molecular-biological researches in this direction. Establishment and application of MLVA genotyping will serve invaluably to track the source of infection in case of bioterrorism or outbreak in Georgia or in surrounding areas. Thus, implementation of sustainable set of assays and a 'One Health' approach resulted in a more effective monitoring system for both human and animal brucellosis in Georgia.

Keywords: animal brucellosis, *B. melitensis, B. abortus*.