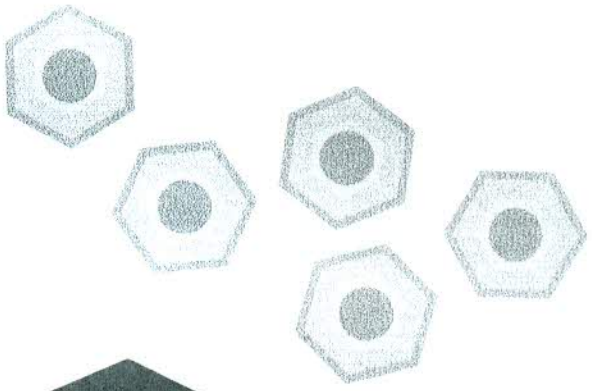
"ONE WORLD, ONE HEALTH, ONE VIROLOGY"

FINAL PROGRAM & ABSTRACT BOOK

IX INTERNATIONAL CONGRESS OF VETERINARY VIROLOGY

and joint meeting with the European Society of Clinical Virology



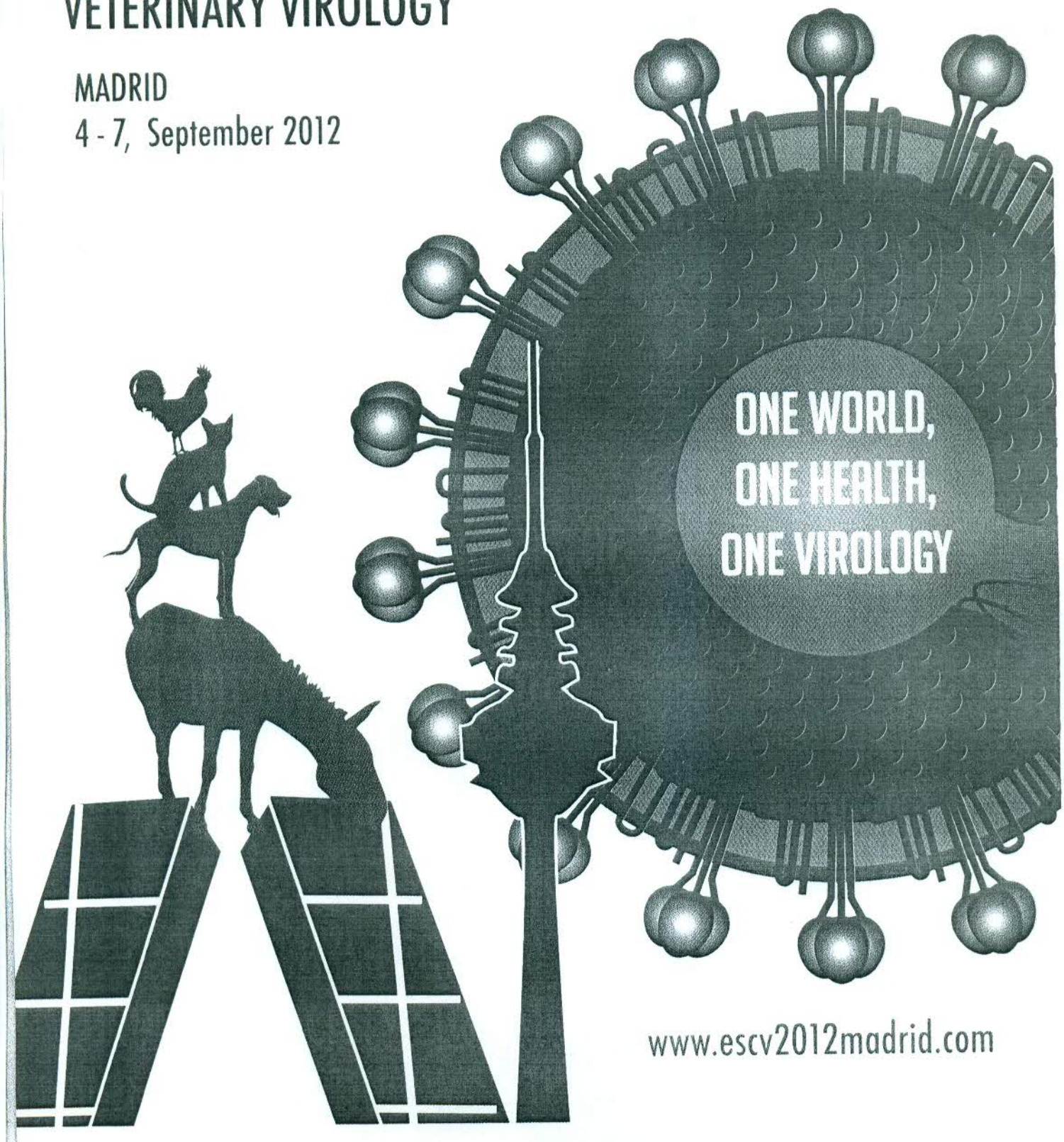
ESVV 2012

Veterinary Faculty - Complutense University of Madrid

4th - 7th September 2012

15TH ANNUAL MEETING OF THE EUROPEAN SOCIETY FOR CLINICAL VIROLOGY AND JOINT MEETING WITH THE EUROPEAN SOCIETY FOR VETERINARY VIROLOGY

MADRID
4 - 7, September 2012



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Results

Phylogenetic analysis revealed that the HA genes of the H7N3 isolates clustered within Eurasian lineage highlighted the close relationship between the wild bird and human isolates. They showed 98.9-99.5% nucleotide (nt) identity. Phylogenetic analysis demonstrated that the HA genes of the AIV isolates characterized in this study share the same lineage as highly pathogenic avian influenza (HPAI) H7 isolates from chickens in Pakistan from 1995-2004. The H7N3 isolates from Egypt and Iraq lack multi-basic amino acids (AA) at the cleavage site (PEIPX/XGR*G) and are therefore classified as low pathogenicity AIV (LPAI). Phylogenetic analysis of the NA gene showed that the three isolates were closely related with 95.9-99.8% nt identity and grouped in a single distinct lineage. The three NA genes had a full-length stalk with the exception of a single amino acid deletion at AA position 60. Based on the phylogenetic analysis of the H10 HA genes, the six H10N7 isolates were found to also lack the multi-basic AAs at the cleavage site and were classified as LPAI. The six HA genes clustered with the Eurasian lineage as reported for all previous Egyptian viruses. All HA genes showed 95-100% nt identity with other Egyptian strains. Phylogenetic analysis of NA genes revealed that the six isolates from Egypt clustered with viruses isolated from migratory birds in Egypt and South Africa.

Conclusions

This is the first report on the evolution of H7N3 viruses in Egypt. The HA genes of H7N3 viruses isolated in this study, including the 2006 Iraqi human sample were classified as LPAI and clustered with other HPAI and LPAI Eurasian strains but remain distinct from Australian and North American lineages. Even the Iraqi human isolate clustered with strains isolated from shovelers in Egypt in 2007, suggesting the possible risk for human infection in Egypt. The six H10N7 strains isolated from shovelers and teals from 2004-2007 were closely related to viruses isolated earlier from Egypt, indicating stability of this influenza subtype in the avian gene pool reservoir in the region. Sustained surveillance for avian influenza viruses is important to detect any mutations that may have impact on human and animal health.

PRESENCE OF HEPATITIS E VIRUS INFECTION IN WILD BOAR POPULATION (SUS SCROFA) IN SERBIA

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Objectives:

Hepatitis E virus (HEV) causes acute hepatitis in humans in many developing countries, where sanitary conditions and hygiene are poor. HEV was discovered in pigs in 1997. Since then many investigations have proved that hepatitis E is spread worldwide among domestic and wild pigs, which are infected with HEV genotype 3 and 4; however, the disease in them is mostly sub-clinical. Besides Japan, presence of HEV infection among wild boars has been reported in some European countries (Spain, Hungary, Germany, Italy and the Netherlands). Even though HEV positive serology has been described in farm and backyards pigs in Serbia, no data about wild boars are available. So, the aim of this study was to find out if HEV is present in wild boars in Serbia.

Materials and Methods:

For that purpose, we determined the presence of specific IgG antibodies against HEV in 201 blood samples and of HEV RNA in 298 liver samples from wild boars culled during hunting seasons from January 2010 until February 2011. The blood and liver samples were collected from 27 hunting grounds located on the territory of 7 counties/regions from the whole Vojvodina province (northern part of Serbia), as well as from some central and southern parts of the country. Tested animals were of different age and gender. For the detection of HEV specific antibodies collected blood serum samples were tested by a commercial indirect ELISA (PrioCHECK HEV Ab porcine, Prionics, Switzerland) and by in house ELISA based on baculovirus expressed ORF2 recombinant proteins. For HEV RNA detection in liver samples, in house TagMan based one step RT-qPCR was used. Results:

The overall seroprevalence rate was 34.33% (69/201), but ranges greatly between different hunting grounds (0 - 93.33%) and different counties/regions (4.55%- 48.65%) analyzed. RT-qPCR analysis revealed a relative high prevalence of 9.40 % (28/298) of positive animals with regional differences. Notably, a high proportion of adult wild sows and wild boars were positive for the presence of HEV RNA.

Conclusions:

The high prevalence of HEV found in wild boars population in Serbia may represent a risk for human health, as human alimentary infection after consuming undercooked wild boar livers has been documented. Besides that, the high HEV prevalence found in wild boars found in some areas of Serbia implies a possible direct risk for environmental contamination and, thus, an additional risk for public health. Further research on the presence of HEV in humans, wild boars and domestic pigs as well as molecular characterization of isolates from all these species is necessary to study the possible connection and transmission between them.

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