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Comparison of prevalence of *Theileria orientalis* infection in Holstein cattle before and after grazing on selected farm in the Republic of Korea

Du-Gyeong Han[1], Ji-Hyung Ryu[1], Jin-Ho Park[2], Jeong-Byoung Chae[3], Joon-Seok Chae[3], Do-Hyeon Yu[4], Bae-Keun Park[5], Hyeon-Cheol Kim[6], Kyoung-Seong Choi[*1]

[1]Deparment of Animal Science and Biotechnology, College of Ecology and Environmental Science, Kyungpook National University, Sangju 37224, Republic of Korea; [2]College of Veterinary Medicine, Chonbuk National University, Iksan 54596, Republic of Korea; [3]Laboratory of Veterinary Internal Medicine, BK21 PLUS Program for Creative Veterinary Science Research, Research Institute for Veterinary Science and College of Veterinary Medicine, Seoul National University, Seoul 08826, Republic of Korea; [4]College of Veterinary Medicine, Gyeongsang National University, Jinju 52825, Republic of Korea; [5]College of Veterinary Medicine, Chungnam National University, Daejeon 34134, Republic of Korea; [6]College of Veterinary Medicine, Kangwon National University, Chuncheon 24341, Republic of Korea

Introduction: Tocompare the prevalence of *Theileriaorientalis* genotypes Chitose, Ikeda, and Buffeli in Holstein cattlebefore grazing and after two months spent atpasture, and investigate theassociation between *T. orientalis* infectionand hematological changes.

Materials and Methods: Bloodsamples were collected from Holstein cattle beforegrazing (n=40) and after two monthsspent at pasture (n=40) and screenedfor *T. orientalis* genotypes using major piroplasmsurface protein (MPSP) gene-based PCR amplification. The changes in hematological parameters such as red blood cell (RBC) count, hemoglobin (Hb) concentration,and hematocrit (HCT) from these animals were also performed.

Results: Six (6/40, 15%) and seven(7/40, 17.5) animals were positive for *T.orientalis* infection before and after two months spent at pasture,respectively. Of the 13 total positive samples, Chitose, Ikeda, anothergenotype, and co-infection with Chitose and Ikeda were detected in four, seven,one, and one animal, respectively. Infection with the Buffeli was notidentified in this study. To our knowledge, this is the first reportidentifying co-infection with Chitose and Ikeda inHolstein cattle in the Republic of Korea. Although RBC count, Hb, and HCT in *T. orientalis*-infected cattle were significantly decreased aftertwo months spent at pasture (as compared to values obtained before grazing),these hematologic parameters remained within the normal reference ranges.

Conclusions: These results suggest that theIkeda of *T. orientalis* is endemic inthis region and that *T. orientalis*infection is not necessarily associated with anemia. Our findings indicate thatthe prevalence of *T. orientalis*infection is closely related to the seasonal activity of ticks. Further studiesshould focus on blood samples obtained from various climaticregions to identify the distribution of*T. orientalis* genotypes as well as the association between *T. orientalis* infection and anemia.

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Molecular surveillance of *Taylorella equigenitalis* from Thoroughbred horses since the first report in South Korea

Soo-Kyoung Lee[1], Hye-Young Jeoung[1], Jee-Yong Park[1], Sung-Hee Kim[1], Hyun-Jeong Kim[1], Ji-Hye Lee[1], Sun-Joo Yang[2], Sang Kyu Lee[2], Hae-Eun Kang[1], Jun-Gu Choi[*1]

[1]Foreign Animal Disease Division, Animal and Plant Quarantine Agency, Gimcheon 39660, Republic of Korea; [2]Korea Racing Authority, Gwacheon 13822, Republic of Korea

Introduction: Contagious equine metritis (CEM) caused by the organism *Taylorella equigenitalis* (*T. equigenitalis*) is a notifiable animal disease of the equid species. In South Korea, a subsequent country-wide surveillance on CEM was implemented since the first CEM report in 2015.

Materials and Methods: A total of 4,259 swab samples were screened using real-time polymerase chain reaction (qPCR) over the 2 year period from 2015 to 2016. The specimens placed in Amies charcoal transport media (BD, New Jersey, USA) were kept cool, and transported to thelaboratory no later than 48 h after sampling. Genomic DNA was extracted from suspensions (400 μl of phosphate-buffered saline) of each swab sample using a commercial Maxwell®16 DNA Purification Kit (Promega, Wisconsin, USA) and the qPCR assay was tested in duplicate using primers capable of amplifying *T. equigenitalis* 16S rDNA amplicons.

Results: The nationwide surveillance of consecutive 2 years showed that the infection rate of CEM was decreased from 2.13 % (46 out of 2,171) in 2015 to 0.96 % (20 out of 2,086) in 2016. In detail, 46 (2 stallions and 44 mares) out of 2,171 Thoroughbred horses surveyed in 2015 were positive against CEM. The causative agents were detected in Jeju (95.65 %, 2 stallions and 42mares), a major Thoroughbred horse breeding area in South Korea, and in inland Jeonbuk province (4.35%, 2 mares). In 2016, CEM was detected in 3 out of 74 stallions and 17 out of 2,012 mares. Most of positive results were from Jeju (2 stallions and 15 mares) and other positive results were detected in 1 stallion in Jeonbuk, 1 mare in Gyeongbuk, and 1 mare in Gyeonggi, respectively.

Conclusions: This surveillance showed the extent of *T. equigenitalis* infection in Thoroughbred horses in South Korea and how molecular tools can be utilized during a national surveillance and subsequent infection management. At the same time, this national surveillance demonstrated that molecular-based assays were useful in detecting *T. equigenitalis* from a large population of Thoroughbred horses. PCR assay can help in curtailing the spread of the infection by early detection and subsequent quarantine and the proper treatment.

References

[1] Anzai T. et al. Development of a PCR test for rapid diagnosis of contagious equine metritis. J. Vet. Med. Sci., 1999. 61(12): 1287-92.

[2] Wakeley P.R. et al. Development of a real time PCR for the detection of *Taylorella equigenitalis* directly from genital swabs and discrimination from *Taylorella asinigenitalis*. Vet. Microbiol., 2006. 118(3-4): 247-54.

[3] Jeoung H.Y. et al. First Isolation of *Taylorella equigenitalis* from Thoroughbred Horses in South Korea. J. equine Vet. Sci., 47: 42-6.

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The prevalence of severe fever with thrombocytopenia syndrome virus in cats

Joon-Seok Chae*, Jun-Gu Kang, Yoon-Kyoung Cho, Young-Sun Jo, Jeong-Byeong Chae, Sun-Woo Han

Laboratory of Veterinary Internal Medicine, BK21 Plus program for Creative for Veterinary Science Research, Research Institute of Veterinary Science and College of Veterinary Medicine, Seoul National University, Seoul 151-742, Korea

Introduction: Severefever with thrombocytopenia syndrome virus (SFTSV) is a novel phlelbovirus inthe family of Bunyaviridae and a causative agent of an emerging disease in China,Japan, and the Republic of Korea (ROK) and is mainly characterized by fever,leukopenia and thrombocytopenia (1, 2). In the ROK, theinvestigations about SFTSV infection rate in Korean water deer, wild boars, andferal cats were conducted (3, 4).

Materials and Methods: Serum collectedfrom feral and house cats in the ROK. Usingsera samples, SFTSV-specific genes were amplified by one-step reversetranscription (RT)-PCR and nested PCR and sequenced. The sequence data wereanalyzed using Chromas and were aligned using CLUSTAL X. The phylogenetic analysis was constructed using theneighbor-joining method in MEGA7.

Results: A total of 196serum samples were collected from 103 feral cats and 93 house cats between Mayand September of 2017 in Seoul. Eleven of 196 (5.6%) samples were positive forSFTSV using RT-PCR targeting the S segment RNA. The size of amplified productwas 346 bp. The obtained SFTSV sequences were included in Korean/Japanese SFTSVclade and could be classified into three sub-clades.

Conclusions: Ourresult provides data that SFTSV may have been circulating in house cats as wellas feral cats.

References

[1] Yu XY, Liang MF, Zhang SY, Liu Y, et al. Fever with thrombocytopeniaassociated with a novel Bunyavirus in China. N Engl J Med 2011;364:1523–1532.

[2] Kim KH, Yi JY, Kim GY, Choi SJ, et al. Severe fever with thrombocytopeniasyndrome, South Korea, 2012. Emerg Infect Dis 2013;19:1892–1894.

[3] OhSS, Chae JB, Kang JG, Kim HC, Chong ST, Shin JH, Hur MS, Suh JH, Oh MD, JeongSM, Shin NS, Choi KS, Chae JS. Detection of severe fever with thrombocytopenia syndromevirus from wild animals and Ixodidae ticks in the Republic of Korea. VectorBorne Zoonotic Dis. 2016; 16(6):408-414.

[4] HwangJ, Kang JG, Oh SS, Chae JB, Cho YK, Cho YS, Lee H, Chae JS. Molecular detectionof severe fever with thrombocytopenia syndrome virus (SFTSV) in feral cats fromSeoul, Korea. Ticks Tick Borne Dis. 2017; 8(1):9-12.

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Triclosan exposure affects the neural development of zebrafish embryos (*Danio rerio*)

Jin Kim[1], Hanseul Oh[1], Bokyeong Ryu[1], Ukjin Kim[1], Ji Min Lee[1], Cho-Rok Jung[2], C-yoon Kim[3], Jae-Hak Park*[1]

[1]Laboratory Animal Medicine, College of Veterinary Medicine, Seoul National University, Seoul, Korea; [2]Korea Research Institute of Bioscience and Biotechnology, Daejeon, Korea; [3]Stem Cell Biology, School of Medicine, Konkuk University, Seoul, Korea

Introduction: Triclosan (TCS) is a compound with a wide range of antibiotic activity and has been widely used in items ranging from hygiene products to cosmetics; however, it has recently been suggested to have several adverse effects. In particular, TCS can be passed to both fetus and infants, and evidence suggests cellular-level neurotoxicity, but there is little *in vivo* research describing whether this neurotoxicity can affect neural development.

Materials and Methods: Therefore, this study aimed to clarify the effect of TCS on neural development by analyzing morphological changes, fluorescent alterations using HuC-GFP and Olig2-dsRED transgenic zebrafish, and neurodevelopmental gene expression.

Results: TCS exposure decreased the body length, head size, and eye size in a concentration-dependent manner in zebrafish embryos. It particularly affected the structure of the central nervous system (CNS), resulting in decreased synaptic density and shortened axon length. In addition, it increased apoptosis in the CNS and significantly altered the expression of genes related to multiple steps of neural development.

Conclusions: Collectively, these changes indicate that TCS is toxic to neurodevelopmental stages, especially in axonogenesis. This is the first study to demonstrate the toxicity of TCS during neurogenesis, and suggests a possible mechanism underlying the neurotoxic effects of TCS in developing vertebrates.