V217G), which were coded genes of PCV3show up at least 1 non nsynonymous substitution. At present, the significanceof these non-synonymous substitutions are not almost obscured among PCV3strains.

Conclusions: Thisstudy clearly demonstrated that best phylogenetic tree model for futureresearch, and not yet able to distinguish clusteres of PCV3 strains. And PCV3evolutionary analysis, evolutionary researchers might enough to merit closeattention.

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O-002

Extensive drug resistant *Escherichia coli* isolated from companiondogs

Myoung-Han Lee, Ji-Wung Han, Seo-Jin Lee, Tae-Soo Kim, Joong-Bok Lee, Seung-Yong Park, Chang-Seon Song, In-Soo Choi, Hun-Young Yoon, Sang-Won Lee*

College of Veterinary Medicine, Konkuk University, Seoul, Republic of Korea

Introduction: Multi drug-resistant bacteria became a seriousconcern in public health. Livestock were intensively monitored as sauces of multidug-resistant bacteria, whereas companion animals were overlooked. We report the isolation of extensive drug-resistant(XDR) *Escherichia coli* (*E. coli*) strains with colistinresistance from canine patients. For the isolated *E. coli* strains, the minimum inhibitory concentration (MIC) of 18antibiotics belonging to 12 classes was determined.

Materials and Methods: Clinicalsamples were collected from different individual canine patients, and *E. coli* were isolated from the samples. TheMIC of antibiotics for the *E. coli*isolates was determined using broth micro-dilution method or MIC strip test andpresence of the colistin resistance genes, mcr-1 and mcr-2 in genome of theisolates were screened using PCR.

Results: Theresults of MIC tests showed that all of the isolates have strong resistance to morethan 10 antibiotics. Surprisingly, most of the *E.coli* isolates were resistant to imipenem and polymyxin B,fortunately, some strains were susceptible to colistin and most resistantstrains has not colistin resistance genes.

Conclusions: The*E. coli* strains isolated fromcompanion dogs in University teaching hospital could be classified as XDR orMDR *E. coli*. The emergence of XDR *E. coli* in companion animals is apotential risk to public health. To prevent the emergence and spread of XDRbacteria in companion animals, should be performed antibiotic susceptibilitytest before antibiotics treatment in clinics and, shotgun treatment should beavoided.

O-003

Cabbage (Brassica oleracea var. capitata) protects against H_2O_2-induce doxidative stress by preventing mitochondrial dysfunction in H9c2 cardiomyoblasts

Jong Suk Kim, Hyung-Sub Kang*

College of Veterinary Medicine, Korea Zoonoses Research Institute and Bio-Safety Research Institute, Chonbuk National University, Iksan, 54596, Republic of Korea

Introduction: Oxidative stress plays an important role in the progression ofcardiac diseases, including ischemia/ reperfusion injury, myocardial infarction,and heart failure. Growing evidence indicates that cabbage has variouspharmacological properties against a wide range of diseases, such ascardiovascular diseases, hepatic diseases, and cancer. However, little is knownabout its effects on oxidative stress in cardiomyocytes or the underlyingmechanisms. Therefore, the present study examined the effects of cabbageextract on oxidative stress in H9c2 cardiomyoblasts.

Materials and Methods: To elucidate the effect ofcabbage extract on oxidative stress in H9c2 cardiomyoblasts, the cells werepretreated with 100,200, and 300 μg/ml cabbageextract for 24 h and treated then with 500 μM H_2O_2 for anadditional 24 h. Cell viability, reactive oxygen species (ROS) production, apoptosis, mitochondrial functions, and expression levels of mitogen-activatedprotein kinase (MAPK) proteins were analyzed to elucidate the antioxidanteffects of cabbage extract.

Results: Cabbage extract protected against H_2O_2-inducedcell death and did not elicit any cytotoxic effects. In addition, cabbageextract suppressed ROS production and increased expression of antioxidantproteins (superoxide dismutase-1, catalase, and glutathione peroxidase) in adose-dependent manner. TUNEL and Hoechst staining and western blotting analysisof apoptosis regulators showed that cabbage extract inhibited the apoptoticresponses. The cabbage extracts also restored the mitochondrial functions fromthe mitochondrial membrane potential and qRT-PCR analysis of mitochondrialbiogenesis-related genes. Finally, cabbage extract blocks the activation ofMAPK proteins (extracellular signal-regulated kinase 1/2, c-Jun N-terminalkinase, and p38) upon oxidative stress for their underlying mechanisms ofantioxidant effects.

Conclusions: Thisstudy provides new evidence that cabbage extract protects against oxidativestress in H9c2 cardiomyoblast by inhibiting ROS production and apoptosis and bypreserving mitochondrial functions. In addition, the present study demonstratesthat cabbage suppresses activation of pro-apoptotic MAPK proteins in H9c2 cellsexposed to oxidative stress. Thus,

we propose that cabbage is a potentialantioxidant-agent to protect against oxidative stress.

O-004

Evaluation of Haematogenous Oxidation Therapy as an alternative therapy in alloxan-induced diabetic rabbits

Gareeballah Adam[1], Gi-Beum Kim[2], Jin-Shang Kim[1], Hyung-Sub Kang[*1]

[1]Department of Pharmacology, College of Veterinary Medicine, Chonbuk National University, Iksan Campus, 79 Gobong-ro, Iksan-si, Jeollabuk-do 54596 Republic of Korea; [2]Department of R&D Planning, Institute of Jinan Red Ginseng, Jinan, Jeonbuk, 55442, Republic of Korea

Introduction: Diabetes emerges as the disease causing social problems, because it has a very high prevalence as a typical chronic metabolic disease characterized by high blood glucose levels and many implications. In the mid of the last century. Daily treatment of diabetic patients is uncomfortable for many people. Hematogenous Oxidation Therapy (HOT) is the most intensive form of UV light treatment method for blood, and the entire process generally takes short time. Within the blood, activated oxygen molecules arise, which have a very strong biological effect and a number of functions in thebody, including positively influencing the metabolic processes. HOT device was made to identify effects of ultraviolet blood irradiation on the blood in a diabetic animal model. This study evaluated the effects of HOT blood irradiation on the diabetes by using physical methods with UV light rather than drug therapy such as insulin injection in order to get over diabetes causing serious problems.

Materials and Methods: Ten rabbits weighing between 2 to 2.5 kg were made diabetic by injecting intravenously 110 mg/kg body weight of alloxan monohydrate (A7413, Aldrich). It is confirmed that the diabetes is induced by measuring blood glucose levels in rabbits at 72 hours (3 days) after alloxan is injected. HOT device was made by connecting infusion pump with a box containing UV lamp at a wave length of 260 nm. The blood was perfused with oxygen for 10seconds before subjected to UV light. The blood was collected, treated in HOT device, and transfused back to the original rabbit in a clean environment. Treatment was done weekly for 10 weeks.

Results: Complications of diabetes were observed in diabetic rabbits as changes in liver, renal, and lipid parameters. In addition, a turmoil in blood pH, electrolytes and gases was noticed in diabetic rabbits. Glucose and insulin levels were significantly increased and decreased in diabetic rabbits respectively. AST, ALT, ALP, and LDH as liver indicators were significantly increased in diabetic rabbits. Kidney function was evaluated as well, Creatinine, BUN, UA, and CK were significantly increased in diabetic rabbits. T-CHO, LDL, TG, T-PRO, and albumin levels in serum were increased. In contrast, LDH level was decreased. Interestingly, these parameters were completely or partially corrected in rabbits under HOT treatment.

Conclusions: HOT sessions for 10times significantly reduced complications in alloxan-induced diabetes in rabbit model.

O-005

Isolation and characterization of a novel bat paramyxovirus in Korea

Ji Yeong Noh[1,2], Dae Gwin Jeong[1,3], Sun-Woo Yoon[1,3], Ji Hyung Kim[1], Yong Gun Choi[4], Shien-Young Kang[2], Hye Kwon Kim[*1]

[1]Infectious Diseases Research Center, Korea Research Institute of Bioscience and Biotechnology, Daejeon, Republic of Korea; [2]College of Veterinary Medicine, Chungbuk National University, Cheongju 28644, Republic of Korea; [3]Bio-Analytical Science Division, University of Science and Technology (UST), Daejeon, Republic of Korea, 4The Korean Institute of Biospeleology, Daejeon, Republic of Korea

Introduction: In many respects, bats are typical the reservoir for emerging zoonotic pathogens. Bats as a source of zoonotic disease became obvious with the emergence of human viruses, such as severe acute respiratory syndrome coronavirus (SARS-CoV), Middle East respiratory syndrome coronavirus (MERS-CoV), Nipah virus, Hendravirus, Hendra virus and Ebola virus. In Korea, there are diverse coronaviruses in the feces of domestic bats based on the investigation data in 2015 (Kim et al., 2016). In this study, we first isolated and characterized a bat paramyxovirus from a domestic bat.

Materials and Methods: Virus isolation was performed from samples including feces, urine and oropharyngeal swab of bats. After the sample was inoculated to MARC 145 cell, blind passage was performed up to three times. A virus isolate showing CPE was identified asa paramyxovirus by paramyxoviruses-specific RT-PCR (Tong, Suxiang, et al.,2008). Viral RNA was extracted using Trizol LS reagent and genomic sequence was obtained by RT-PCR with designed primer. Hem-adsorption assay with 0.5% chicken RBC and neuraminidase assay tested using NA-Fluor influenza neuraminidase assay kit(Thermo) to investigate the characterization of HN protein. Cross-reaction and Cross-neutralization was tested using mouse serum against bat paramyxovirus and human parainfluenzavirus 1, respectively.

Results: From the second passage, CPE was observed in the infected cell and novel bat paramyxovirus was isolated from bat sample. A result of sequencing paramyxovirus genomic RNA, it was closely related with a bat paramyxovirus (Bat Ms-ParaV-2/Anhui2011,KC154054) in China and it include seven genes in the order 3'-N-P-M-F-TM-HN-L-5'. Phylogenetic analysis of each gene revealed that bat paramyxovirus isolated in this study was in the group of Beilong virus and J-virus. Notably, amino acids identity of the HN protein was more