28 days. Regarding immune parameters, Cd-exposure lowered the lysozyme activity and difference was significant after 28 days of exposure, compared to control. Alternative complement pathway activities were slightly higher in Cd-exposed group upto 14 days and thereafter it reduced; however, immunoglobulin M levels were slightly lower in Cd-exposed group at any point of time. Peroxidase activity was always higher in Cd exposed group but the increment was not significant at any time point, and Cd exposure had not significant effect on phagocytic activity. The serum glutamic –pyruvic transaminase and serum alkaline phosphatase activities were significantly higher in fish exposed to Cd for 14 to 28 days. Further, Cd had an immunosuppressive effect and leading to down- regulation ($P < 0.05$) of IL-10 and IFN-γ mRNA. However, Cd-exposure led to the up- regulation of HSP47, HSP60, HSP70, HSP78, and HSP90 mRNA indicating Cd-induced cellular stress.

Conclusions: Overall, Cd-exposure in *L. rohita* affects the immune system and this make the fish immunocompromised and could increase the susceptibility of fish to pathogen infection.

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O-003

Molecular detection and phylogenetic analysis of *Borrelia afzelii* in ticks infested on Korean water deer

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Introduction: Lyme borreliosisis one of the most prevalent infectious vector-borne diseases in Europe, America and Asia. It is a multi-organ systemic disease which is caused by spirochetes of the *Borrelia burgdorferi* sensu lato group with its species (Lee et al. 2000). Among them, *B. burgdorferi* sensu stricto, *B. garinii* and *B. afzelii* are the major etiological agents of human Lyme disease (Chu et al. 2008). In Korea, *B. afzelii* has been detected from environmental ticks (*Ixodes persulcatus*, *I. nipponesis*, *I. granulatus*), wild rodents (*Apodemus agarius*) and sera of febrile disease patients (Kee et al. 1994). However, there is no report on the detection of *B. afzelii* from infested ticks yet. Thus, this study assessed the presence of *B. afzelii* in the ticks infested on Korean water deer.

Materials and Methods: A total of 48 ticks attached to Korean water deer were collected from Gyeongbuk province in Korea from 2013 to 2015. Identification of tick species was done by microscopy. Nested PCR was performed with the primers designed to amplify the *Borrelia* specific 5S–23S intergenic spacer region (*rrf-rrl*), with the expected sizes of 226-266 bp depending on the *Borrelia* strain (Chu et al. 2008). For the positive sample, DNA sequencing and phylogeny was assessed by comparing the sequences from NCBI GenBank database.

Results: From the microscopic examination, all the collected ticks were identified as *Haemaphysalis longicornis*. By nested PCR, the *Borrelia* specific DNA fragment was amplified in 1 out of 48 ticks (2.1%) with the amplicons at 246 bp of *B. afzelii rff-rrl* gene. The amplicon revealed a high sequence homology (96-100% similarity) to *B. afzelii* spirochetes deposited in the GenBank database.

Conclusions: The result indicates that *B. afzelii* was detected from *H. longicornis* in Korea. To the extent of our knowledge, this report is the first molecular detection of *B. afzelii* in ticks infested on Korean water deer. Since ticks can act as vectors for a number of pathogens, knowledge on their characteristics is important to humans and also in veterinary practices. Moreover, changes of environmental temperature may also cause changes in the proliferation of wild animals and the arthropod vectors as well as the pathogens they transmitted. Thus, further screening ticks for disease-causing pathogens using molecular epidemiological tools would be necessary for the data about the distribution and prevalence of tick-borne pathogens.

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O-004

Effect of polymorphisms of GBP1, Mx1 and CD163 genes in pigs infected with PRRSV

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