

Detection of bovine rotavirus C and study on its genetic properties

Abstract of Doctoral Thesis

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In the virus taxonomically, bovine had not generally been included in the natural host of Rotavirus C (RVC). However, the first detection of RVC from cattle in the world is a Shintoku strain isolated from diarrhea of adult cattle in Hokkaido in 1991. Following it, RVC Yamagata strain was detected from diarrhea cases of dairy cattle caused the outbreak in a farm in Yamagata prefecture in April 2002. Since then, the presence of bovine RVC was recognized and, in addition, multiplex RT-PCR to detect major diarrhea-related viruses including bovine RVCs was developed. Therefore, diarrhea cases on bovine RVC were reported one after another. In order to elucidate the occurrence state of bovine RVCs in the field, major diarrhea-related pathogenic microorganisms were detected from the case of diarrhea occurred on farms in Yamagata Prefecture for ten years and the information was organized for the occurrence state and clinical symptoms.

Bovine RVC was suggested to be one of the major pathogenic microorganisms that cause outbreak of diarrhea in dairy cattle from autumn to early spring. High incidence seasons and occurrences of bovine RVC disease showed a common tendency to bovine coronavirus (BCoV) disease and bovine rotavirus B (RVB) disease, and clinical symptoms of bovine RVC disease was similar to bovine RVB disease and slightly different from BCoV disease. The occurrences of bovine RVC in the field have been

gradually elucidated, but genetic properties of bovine RVC have not been clarified because of little genetic information. Therefore, all 11 gene segments of RVC 6 strain detected in Chapter 2 were analyzed on genetic diversity, genetic dynamics and ecology of bovine RVC in the field. As a result, it was recognized for the first time that VP4 genes of various bovine RVC strains were resulted in the low homology with nucleotide deletion and insertions. These results indicate that there are various genetic diversities. In addition, it shows that strains belonging to the same genotype acquire genetic diversity by repeating reassortants independently for each segment.

These results lead us to the conclusion that several strains possessing different genetic backgrounds are widely distributed in Japan and are involved in bovine diarrhea. Also, this study revealed at the genetic level for the first time that the same strain or new strain resulted in occurrence repeatedly with bovine RVC disease in neighboring farms and re-occurred in the same farm.