Study of recently identified porcine parvoviruses in pig herds of Japan and Thailand

(日本とタイの養豚に感染している新規豚パルボウイルスの研究)

Abstract of Doctoral Thesis

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I have been studying porcine parvoviruses during the PhD course. The initially identified parvovirus in pigs is porcine parvoviruses (PPV), which was reported in the 1960s and is now endemic in most pig-producing countries. PPV mainly causes reproductive failure in naïve dams, and manifestation characterized by stillbirth, mummification, embryonic death and infertility. In contrast, PPV infection of adult pig causes only a subclinical or mild disease.

Besides the classical PPV, several other parvoviruses or their genomes have been recently identified in pigs. These newly identified porcine parvoviruses have not been well characterized. I therefore investigated several porcine parvoviruses infecting pig herds of Japan and Thailand by isolating and characterizing viral DNAs.

These parvoviruses appear to share common biological properties such as resistance to antiseptic substances and extreme environmental conditions like heat and pH. They also have common biological properties in their DNA replication; they require the mitotic S phase of cells to replicate their DNA genome. These properties are related both to difficulty in eradicating the PPV-associated diseases at the pig farms and to its pathogenesis.

In the chapter I, I describe my study of the characterization of porcine parvovirus 2 (PPV2) detected in Japanese pig herds. PPV2 genome was first detected in Myanmar in 2001. The genome was subsequently reported from several countries. The prevalence of Japan was 58% in healthy pigs. I cloned a near complete genome of PPV2 from a healthy pig. I sequenced a region of 41 PPV2s and compared them with those of other countries using the phylogenetic analysis. The analysis showed that diverged PPV2 strains exist in Japan and 7 of the 10 pig farms carried clearly distinct strains of PPV2. Circulating multiple strains within a farm may be a risk for generating emerging virus as reported in other parvoviruses.

In the chapter II, I describe my study of the five newly identified porcine parvoviruses detected in the Chiangmai area of Thailand. I examined the 80 tonsil samples, and the prevalence of the five porcine parvoviruses (PPV、PPV2、PPV3、PPV4、PBo-likeV) were 23～73%. The phylogenetic analyses for PPV2 and PPV3 indicated the existence of two and one clade(s) of viruses, respectively, suggesting an invasion from a limited source for each virus.

In the chapter III, I describe the characterization of the infection status of the four porcine parvoviruses (PPV, PPV3, PPV4, and PBo-likeV) and PCV2 which is a causative agent of PCVAD. The prevalences of these viruses in 120 apparently healthy pigs aged about 6 months were 33～80%, and the detection of PCV2 was significantly coincidental with each detection of PPV, PPV2 and PPV3, and PPV and PPV4 were also coincidentally detected. The exact reason for the coincidental detection remains unknown, but the coinfection we observed in the field samples of the subclinical pigs may relate to the mechanisms leading to severe PCVAD in which the coinfection with PCV2 and other viral and bacterial agents may promote the PCV2 infection by stimulating immune cells and providing target cells for PCV2 replication or suppressing PCV2 clearance by alteration of the cytokine production and profiles.

Finally, this study shows the infection status of newly identified porcine parvoviruses in pig herds of Japan and Thailand. Since these viruses are not known regarding the association with any disease, our investigation will provide useful information for further studies.