＜誌上発表＞

○Simple and specific detection of *Bordetella holmesii* by using a loop-mediated isothermal amplification assay.

・Otsuka N[1)], Yoshino S[2)], Kawano K[2)], Toyoizumi-Ajisaka H[1)], Shibayama K[1)], Kamachi K[1)].

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A loop-mediated isothermal amplification (LAMP) assay for simple detection of *Bordetella holmesii* was developed. This assay discriminates between *B. holmesii* and other Bordetella species and successfully detect *B. holmesii* DNA in nasopharyngeal swab samples from subjects with suspected pertussis. The LAMP assay results were in complete agreement with the results of previously published real-time PCR assay, indicating that the former is a powerful tool for the accurate diagnosis and surveillance of *B. holmesii.*

○Transmission of *Bordetella holmesii* during Pertussis Outbreak, Japan.

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We describe the epidemiology of a pertussis outbreak in Japan in 2010-2011 and *Bordetella holmesii* transmission. Six patients were infected; 4 patients were students and a teacher at the same junior high school. Epidemiologic links were found between 5 patients. *B. holmesii* may have been transmitted from person to person.

○*Stx* genotype and molecular epidemiological analyses of Shiga toxin-producing *Escherichia coli* O157:H7/H− in human and cattle isolates

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The relationship between human diseases caused by infection with Shiga toxin (Stx)-producing *Escherichia coli* (STEC) O157 strains and O157 strains isolated from cattle was investigated in an area where stockbreeding is prolific. For this purpose, the *stx* genotypes, the molecular epidemiological characteristics of 268 STEC O157 strains including 211 human-origin strains and 57 cattle-origin strains, and clinical manifestations of 210 STEC-infected people were analyzed. Of 211 human-origin strains, 92 strains (44%) were of the *stx1/stx2* genotype, and 74 strains (35%) were of the *stx2c* genotype. Most of the people infected with *stx2c* genotype strains presented no symptoms or mild symptoms such as slight diarrhea, except for 3 patients with bloody diarrhea. Of the 57 cattle-origin strains, 27 strains (47%) were of the *stx2c* genotype and 17 strains (30%) were of the *stx1/stx2* genotype. Pulsed-field gel electrophoresis (PFGE) and insertion sequence (IS) analysis demonstrated that 11 isolates (41%) of the 27 cattle isolates of the stx2c genotype had high homology (>95% identity) with human isolates. These results suggest that some genetic patterns of the *stx2c* genotype strains might be preserved in cattle or their surrounding environment for several years, and during these periods, they might have opportunities to infect people through