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

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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/H1− 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