

<誌上発表>

**○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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Yoshino S<sup>2</sup>), Kawano K<sup>2</sup>), Takahashi H<sup>3</sup>), Nishida  
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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

various routes. Because of the mild virulence of the *stx2c* genotype strains, they seemed to be transmitted asymptotically from cattle to humans and then spread from person to person. It may be a public health concern. Further, they occasionally cause severe symptoms in humans; therefore, caution is warranted for infections by *stx2c* genotype O157 strains, in addition to *stx2*-possessing genotype O157 strains.

**○Comparison of real-time reverse-transcription loop-mediated isothermal amplification and real-time reverse-transcription polymerase chain reaction for detection of noroviruses in municipal wastewater**

・ Yoshihiro Suzuki<sup>1)</sup>, Shogo Narimatsu<sup>1)</sup>, Takashi Furukawa<sup>1)</sup>, Akira Iwakiri<sup>2)</sup>, Miho Miura<sup>2)</sup>, Shogo Yamamoto<sup>2)</sup>, Hiroyuki Katayama<sup>3)</sup>

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The monitoring of NVs in municipal wastewater by both real-time RT-LAMP and real-time RT-PCR, and the comparison of these two methods with respect to NV detection were carried out. The change in NVs detected by real-time RT-LAMP agreed well with that detected by real-time RT-PCR. In contrast, the correlation between the copy number determined by real-time RT-PCR and the threshold time (T<sub>t</sub>) determined by real-time RT-LAMP obtained during monitoring was not significant (0.1<p) for both NV-GI and NV-GII.

<学会及び研究発表会>

**○宮古列島における *Orientia tsutsugamushi* の分離および遺伝子解析**

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「第64回日本衛生動物学会大会

(平成24年3月29日~31日 長野県上田市信州大学)」

2008年6月, 沖縄県宮古島市の恙虫病患者初発後, 2011年7月までの野外調査の中で, 野鼠の脾臓や吸着 *Leptotrombidium deliense* (*Ld*) から *Orientia tsutsugamushi* の検索を試み, 45頭中13頭の脾臓が分離陽性, 1頭が遺伝子検出陽性, また, 個体毎の吸着 *Ld* プール試料35件中1件が分離陽性で本調査初の *Ld* 由来株となったほか, 2件が遺伝子検出陽性となった. 分離・検出は池間島という限られた地域由来ながら 56kDa 抗原遺伝子は多様で, 系統解析では台湾系 Gilliam 株, Saitama 株, Karp 株, TA678 株に一致または近縁な4グループに分かれた. うち分離株が得られた3グループにおける必須遺伝子11領域の Multi Locus Sequence 解析では, 国内主要株と異なる1つのクラスタを形成し, 3つのサブクラスタに別れ, さらに各サブクラスタの 56kDa 抗原遺伝子が一致したことから, *Ld* をベクターとして最低3種のクローンが共進化していると思われる. 今後, 宮古列島における感染環や東南アジアとの疫学的関連を解明したい.

**○宮古島の恙虫病に関する調査—池間島のネズミとツツガムシから検出された病原体—**

・ 北野智一<sup>1)</sup>, 平良勝也, 岡野祥<sup>2)</sup>, 角坂照貴<sup>3)</sup>, 藤田博己<sup>4)</sup>, 高田伸弘<sup>5)</sup>, 高橋守<sup>6)</sup>, 安藤秀二<sup>7)</sup>, 高野愛<sup>7)</sup>, 川端寛樹<sup>7)</sup>, 御供田睦代<sup>8)</sup>, 本田俊郎<sup>9)</sup>, 林哲也<sup>10)</sup>, 山本正悟<sup>10)</sup>

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