

## 【他誌発表論文(所員が First Author)】

### 四国初記録のヒロハマツナ(ヒユ科)

黒田 啓太, 小澤 潤

絶滅のおそれのある希少な塩生植物の一種, ヒロハマツナ *Suaeda malacosperma* H.Hara (ヒユ科) を愛媛県今治市で発見した. これは四国からの初めての記録でもある.

植物研究雑誌 96: 180- 182 (2021)

### A Collecting Record of *Ischnura asiatica* (BRAUER, 1865) (Odonata: Coenagrionidae) from Shiroiwa-do Cave in Kochi Prefecture.

Keita Kuroda, Ryosuke Okano

トンボが洞窟内で採集された例はこれまで世界各地で散発的な記録がある. その多くが偶然洞内に迷い込んだ例である一方, 洞窟内の水源を利用するトンボも少数ながら記録されている. しかしながら, そのどちらにおいてもこれまでの知見は限られたものであり, 日本からの報告もなかった. 本稿では高知県白岩洞内からのアジアイトトンボ *Ischnura asiatica* の採集記録を報告する. 採集された成虫はテネラル個体であり, 地表の川と繋がる地下水源の近くで採集されたことから, おそらく洞内に偶然流された幼虫が成虫になったものであろう.

Speleological Society of Japan 46: 49- 50 (2021)

## 【他誌発表論文(所員が First Author 以外)】

### 新型コロナウイルスオミクロン株のスクリーニング PCR 法の検出感度の違いについて

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稲崎 倫子, 佐賀 由美子, 川尻千賀子, 谷 英樹,  
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我々は SARS-CoV-2 陽性検体を用いて, L452R 変異 PCR 法と G339D 変異 PCR 法によるオミクロン株のスクリーニング PCR 法の検出感度を比較検討した. G339D 変異検査は L452R 変異検査と比較して高い検出感度があり, 通常 PCR 検査と同程度であることが分かった. 一方, L452R 変異検査では, 本来オミクロン株である可能性のある検体に対し判定不能と判定される頻度が高く, オミクロン株の推定がより不正確になることが示唆された. 以上のことから, 変異株スクリーニングにおいては, 判定不能例を少なくするために, より検出感度の高い検査を組み合わせて柔軟に対応できる検査体制を構築することが重要である.

IASR 43 (3), 76- 77 (2022)

### Detection of Jingtmenviruses in Japan with Evidence of Vertical Transmission in Ticks.

Kobayashi D, Kuwata R, Kimura T, Shimoda H, Fujita R, Faizah AN, Kai I, Matsumura R, Kuroda Y, Watanabe S, Kuniyoshi S, Yamauchi T, Watanabe M, Higa Y, Hayashi T, Shinomiya H, Maeda K, Kasai S, Sawabe K, Isawa H.

Jingtmen tick virus (JMTV) and the related jingtmenvirus-termed Alongshan virus are recognized as globally emerging human pathogenic tick-borne viruses. These viruses have been detected in various mammals and invertebrates, although their natural transmission cycles remain unknown. JMTV and a novel jingtmenvirus, tentatively named Takachi virus (TAKV), have now been identified during a surveillance of tick-borne viruses in Japan. JMTV was shown to be distributed across extensive areas of Japan and has been detected repeatedly at the same collection sites over several years, suggesting viral circulation in natural transmission cycles in these areas. Interestingly, these

jingmenviruses may exist in a host tick species-specific manner. Vertical transmission of the virus in host ticks in nature was also indicated by the presence of JMTV in unfed host-questing *Amblyomma testudinarium* larvae. Further epidemiological surveillance and etiological studies are necessary to assess the status and risk of jingmenvirus infection in Japan.

Viruses. 13 (12):2547 (2021)

#### Increased Transmissibility of the SARS-CoV-2 Alpha Variant in a Japanese Population.

Tanaka H, Hirayama A, Nagai H, Shirai C, Takahashi Y, Shinomiya H, Taniguchi C, Ogata T.

To assess the relative transmissibility of the SARS-CoV-2 Alpha variant compared to the pre-existing SARS-CoV-2 in Japan, we performed a cross-sectional study to determine the secondary attack rate of COVID-19 in household contacts before and after the Alpha variant became dominant in Osaka. We accessed 290 household contacts whose index cases were diagnosed between 1 and 20 December 2020 (the third epidemic group), at a time when Osaka was free of the Alpha variant. We also accessed 398 household contacts whose index cases were diagnosed between 20 April and 3 May 2021 (the fourth epidemic group), by which time the Alpha variant had become dominant. We identified 124 household contacts whose index case was determined positive for the Alpha variant (Alpha group) in this fourth group. The secondary attack rates in the fourth group (34.7%) and the Alpha group (38.7%) were significantly higher than that in the third group (19.3%,  $p < 0.001$ ). Multivariable Poisson regression analysis with a robust error variance showed a significant excess risk in the fourth group (1.90, 95% CI = 1.47-2.48) and the Alpha group (2.34, 95% CI = 1.71-3.21). This finding indicates that the SARS-CoV-2 Alpha variant has an approximately 1.9-2.3-fold higher transmissibility than the pre-existing virus in the Japanese population.

Int J Environ Res Public Health. 18(15): 7752 (2021)

The incubation period of the SARS-CoV-2 B.1.1.7 variant is shorter than that of other strains.

Homma Y, Katsuta T, Oka H, Inoue K, Toyoshima C, Iwaki H, Yamashita Y, Shinomiya H.

The analysis included 30 patients infected with the B.1.1.7 variant strain in March 2021, of whom 28 were infected in bars and late-night restaurants (3C environments). The mean age of the 30 patients infected with the B.1.1.7 variant was 32.4 years, and the mean (median) incubation period was 3.53 (3.0) days. The mean age of the 42 patients infected with other strains was 56.2 years, and the mean (median) incubation period was 5.71 (5.0) days. Of the patients infected with other strains, 20 were infected in 3C environments, such as bars and late-night restaurants, and the other 22 were infected at workplaces or in households. The mean age of the 20 patients infected in 3C environments was 53.2 years, and the mean (median) incubation period was 4.30 (4.0) days. Poisson regression analysis showed that the incubation period of the B.1.1.7 variant was 0.66 times shorter than that of other strains (95% CI: 0.38, 0.71). Among the patients infected in 3C environments, the incubation period of the B.1.1.7 variant was 0.63 times shorter than that of other strains (95% CI: 0.504, 0.797). After adjusting for age and sex, the incubation period of the B.1.1.7 variant was 0.62 times shorter than that of other strains in 3C environments (95% CI: 0.47, 0.82).

J Infect. 83 (2) : e15- e17 (2021)

#### Subtype Screening of *bla*<sub>IMP</sub> Genes Using Bipartite Primers for DNA Sequencing.

Kawahara R, Watahiki M, Matsumoto Y, Uchida K, Noda M, Masuda K, Fukuda C, Abe Y, Asano Y, Oishi K, Shibayama K, Shinomiya H.

Genes conferring carbapenem resistance have spread worldwide among gram-negative bacteria. Subtyping of these genes has epidemiological value due to the global cross-border movement of people. Subtyping of *bla*<sub>IMP</sub> genes that frequently detected in Japan appears to be important in

public health settings; however, there are few useful tools for this purpose. We developed a subtyping screening tool based on PCR direct sequencing, which targets the internal sequences of almost all *bla*<sub>IMP</sub> genes. The tool used bipartite multiplex primers with M13 universal sequences at the 5'-end. According to in silico analysis, among the 78 known IMP-type genes, except for *bla*<sub>IMP-81</sub>, 77 detected genes were estimated to be differentiated. In vitro evaluation indicated that sequences of amplicons of IMP-1, IMP-6, IMP-7, and IMP-20 templates were identical to their respective subtypes. Even if the amplicons were small or undetectable through the first PCR, sufficient amplicons for DNA sequencing were obtained through a second PCR using the M13 universal primers. In conclusion, our tool can be possibly used for subtype screening of *bla*<sub>IMP</sub>, which is useful for the surveillance of bacteria with *bla*<sub>IMP</sub> in clinical and public health settings or environmental fields.

Jpn J Infect Dis. 74(6): 592- 599 (2021)

#### Evaluating Methods for Detecting *Escherichia albertii* in Chicken Meat.

Arai S, Ohtsuka K, Konishi N, Ohya K, Konno T, Tokoi Y, Nagaoka H, Asano Y, Maruyama H, Uchiyama H, Takara T, Kudo Y.

*Escherichia albertii* is an emerging foodborne pathogen. The source of the *E. albertii* infection in most foodborne outbreaks is unknown because *E. albertii* is difficult to isolate from suspected food or water. *E. albertii* has a broad host range among birds and can be isolated from chicken meat. In this study, PCR assay, enrichment, and isolation conditions for detecting *E. albertii* in chicken meat were evaluated. The growth of 47 *E. albertii* strains isolated in Japan between 1994 and 2018 and a type strain was evaluated in modified EC broth (mEC) and mEC supplemented with novobiocin (NmEC) and on media containing carbohydrates. The enzyme used for the nested PCR, the enrichment conditions, the most-probable-number (MPN) method, and agar media were also evaluated with chicken meat. To distinguish *E. albertii* from presumptive non-*E. albertii* bacteria, desoxycholate hydrogen sulfide lactose agar (DHL), MacConkey agar (MAC), and these agars supplemented with rhamnose and xylose (RX-DHL and RX-

MAC, respectively) were used. All *E. albertii* strains grew in mEC and NmEC at both 36 and 42°C and did not utilize rhamnose, sucrose, or xylose. Both the first and nested PCRs with TaKaRa Ex Taq, which was 10 to 100 times more active than the other enzymes, produced positive results in enrichment culture of 25 g of chicken meat inoculated with >20 CFU of *E. albertii* and incubated in mEC and NmEC at 42°C for 22 ± 2 h. Thus, the first PCR was sensitive enough to detect *E. albertii* in chicken meat. The MPN values in mEC and NmEC were 0.5- and 2.3-fold higher than the original inoculated bacterial levels, respectively. *E. albertii* in chicken meat was more efficiently isolated with enrichment in NmEC (70.1 to 100%) and plating onto RX-DHL (85.4%) and RX-MAC (100%) compared with enrichment in mEC (53.5 to 83.3%) and plating onto DHL (70.1%) and MAC (92.4%). Thus, optimized conditions for the surveillance of *E. albertii* contamination in food and investigations of *E. albertii* outbreaks, including the infectious dose, were clarified.

J. Food Prot. 84(4): 553- 562 (2021)

Predation by the carrion crow *Corvus corone* (Passeriformes: Corvidae) on the apple snail *Pomacea canaliculata* (Architaenioglossa: Ampullariidae) in different locations in Japan.

Haruka Uehara, Hiroshi Murakami, Yoichi Yusa

スクミリンゴガイを捕食するハシボソガラスを奈良県, 福岡県, 愛媛県で調査し, 捕食サイズや捕食方法等の地域間差を明らかにした.

Applied Entomology and Zoology 56: 385- 392 (2021)

#### 愛媛県の農業用土水路における絶滅危惧種マツカサガイ残存個体群

畑 啓生, 井上 幹生, 東垣 大祐, 小笠原 康太, 松本 浩司, 山本 貴仁, 村上 裕, 中島 淳

道前平野で新たに確認されたマツカサガイ個体群を調査し, 個体サイズ分布等を既存産地と比較し, 再生産をしていることが明らかになった.

保全生態学研究 26: 315- 322 (2021)