＜誌上発表＞

○Laboratory-based surveillance of pertussis using multitarget real-time PCR in Japan: evidence for *Bordetella pertussis* infection in preteens and teens

・K. Kamachi[1)], S. Yoshino[2)], C. Katsukawa[3)], N. Otsuka[1)], Y. Hiramatsu[1)] and K. Shibayama[1)]

[1)] Department of Bacteriology II, National Institute of Infectious Disease, Tokyo, [2)] Department of Microbiology, Miyazaki Prefectural Institute for Public Health and Environment, Miyazaki and [3)] Department of Infectious Diseases, Osaka Prefectural Institute of Public Health, Osaka, Japan

New Microbe New Infect 2015; 8: 70–74

Between January 2013 and December 2014, we conducted laboratory-based surveillance of pertussis using multitarget real-time PCR, which discriminates among *Bordetella pertussis*, *Bordetella parapertussis*, *Bordetella holmesii* and *Mycoplasma pneumoniae*.

Of 355 patients clinically diagnosed with pertussis in Japan, *B. pertussis*, *B. parapertussis* and *M. pneumoniae* were detected in 26% (n = 94), 1.1% (n = 4) and 0.6% (n = 2), respectively, whereas *B. holmesii* was not detected. It was confirmed that *B. parapertussis* and *M. pneumoniae* are also responsible for causing pertussis-like illness. The positive rates for *B. pertussis* ranged from 16% to 49%, depending on age. Infants aged ≤ 3 months had the highest rate (49%), and children aged 1 to 4 years had the lowest rate (16%, $p < 0.01$ vs. infants aged ≤ 3 months). Persons aged 10 to 14 and 15 to 19 years also showed high positive rates (29% each); the positive rates were not statistically significant compared with that of infants aged ≤ 3 months ($p \geq 0.06$). Our observations indicate that similar to infants, preteens and teens are at high risk of *B. pertussis* infection.

○Defining the Genome Features of *Escherichia albertii*, an Emerging Enteropathogen Closely Related to *Escherichia coli*

・T. Ooka[1)], Y. Ogura[2)], K. Katsura[3)], K. Seto[4)], H. Kobayashi[5)], K. Kawano[6)], E. Tokuoka[7)], M. Furukawa[7)], S. Harada[7)], S. Yoshino[6)], J. Seto[8)], T. Ikeda[9)], K. Yamaguchi[9)], K. Murase[3)], Y. Gotoh[3)], N. Imuta[1)], J. Nishi[1)], Taˆ nia A. Gomes[10)], Lothar Beutin[11)], and Tetsuya Hayashi[2)]

[1)]Department of Microbiology, Graduate School of Medical and Dental Sciences, Kagoshima University, Japan, [2)]Department of Bacteriology, Faculty of Medical Sciences, Kyushu University, Fukuoka, Japan, [3)]Division of Microbiology, Department of Infectious Diseases, Faculty of Medicine, University of Miyazaki, Japan, [4)]Division of Bacteriology, Osaka Prefectural Institute of Public Health, Osaka, Japan, [5)]Center for Animal Disease Control and Prevention, National Institute of Animal Health, Ibaraki, Japan, [6)]Department of Microbiology, Miyazaki Prefectural Institute for Public Health and Environment, Miyazaki, Japan, [7)]Division of Microbiology, Kumamoto Prefectural Institute of Public Health and Environmental Science, Kumamoto, Japan, [8)]Department of Microbiology, Yamagata Prefectural Institute of Public Health, Yamagata, Japan, [9)]Department of Infection Diseases Bacteriology, Hokkaido Institute of Public Health, Hokkaido, Japan, [10)]Departamento de Microbiologia, Imunologiae Parasitologia, Universidade Federal de Sa˜o Paulo—Escola Paulista de Medicina, Brazil, [11)]National Reference Laboratory for Escherichia coli, Federal Institute for Risk Assessment (BfR), Berlin, Germany

Genome Biol Evol. 2015 Nov 3;7(12):3170-9. doi: 10.1093/gbe/evv211.

Escherichia albertii is a recently recognized close relative of *Escherichia coli*. This emerging enteropathogen possesses a type III secretion system (T3SS) encoded by the locus of

enterocyte effacement, similar to enteropathogenic and enterohemorrhagic *E. coli* (EPEC and EHEC). Shiga toxin-producing strains have also been identified. The genomic features of *E. albertii*, particularly differences from other *Escherichia* species, have not yet been well clarified. Here, we sequenced the genome of 29 *E. albertii* strains (3 complete and 26 draft sequences) isolated from multiple sources and performed intraspecies and intragenus genomic comparisons. The sizes of the *E. albertii* genomes range from 4.5 to 5.1 Mb, smaller than those of *E. coli* strains. Intraspecies genomic comparisons identified five phylogroups of *E. albertii*. Intragenus genomic comparison revealed that the possible core genome of *E. albertii* comprises 3,250 genes, whereas that of the genus *Escherichia* comprises 1,345 genes. Our analysis further revealed several unique or notable genetic features of *E. albertii*, including those responsible for known biochemical features and virulence factors and a possibly active second T3SS known as ETT2 (*E. coli* T3SS 2) that is inactivated in *E. coli*. Although this organism has been observed to be nonmotile in vitro, genes for flagellar biosynthesis are fully conserved; chemotaxis-related genes have been selectively deleted. Based on these results, we have developed a nested polymerase chain reaction system to directly detect *E. albertii*. Our data define the genomic features of *E. albertii* and provide a valuable basis for future studies of this important emerging enteropathogen.

○口蹄疫埋却地周辺水質調査について

・赤﨑いずみ，中山能久，三坂淳一，溝添光洋，坂元勇太，坂本祥子，島田玲子，中村公生，阿波野祥司，山田亨，津曲洋明，福留智子，萩平敦朗，元明秀成

全国環境研会誌　Vol.41　No1.　2016

平成 22 年 4 月に宮崎県で発生した口蹄疫では，約 30 万頭の家畜が殺処分・埋却され，埋却地周辺環境への影響が懸念された．埋却地が周辺地下水へ与える影響を確認するため，口蹄疫埋却地周辺水質調査を実施した．これまでの調査で，埋却地からの影響を受けていると推定された地点は 4 地点であった．調査開始当初は，下水のような臭気が強く，有機物量を示す TOC が高い値であった．また，水質は 4 地点とも大きく変動し，水質が悪化している時期と比較的良好な時期を繰り返しており，その変動は降水量に左右されていることがわかった．ただし，埋却から約 2 年経過後，水質は比較的良好な状態が継続しており，埋却地からの影響が落ち着いてきたものと考えられた．

＜学会及び研究発表会＞

○宮崎県における*Escherichia albertii*の分布について

・津曲 洋明, 永野 喬子, 吉野 修司, 水流 奈己, 元明 秀成

「平成27年度 日臨技九州支部医学検査学会（平成27年11月14日　鹿児島市）」

Escherichia albertii(Ea)はヒトに下痢症を起こす可能性がある菌として2003 年に新たに報告された菌で, 近年食中毒報告が相次ぎ注目されてきた菌種である. 本菌の病原性や感染源, 自然宿主についてはほとんど解明されてない. 今回, 当所に保存してある菌株のさかのぼり調査と環境水からのEaの検出を試み, 本県におけるEaの分布調査を行った.

さかのぼり調査の材料は1993年6月から2015年4月までに分離されたEPEC 144株, 1995年までに分離された赤痢菌16株の計160株を用いた. Eaの検出はHymaらが報告したDuplex PCR 法でスクリーニング後, 生化学的性状試験を実施した. また, Eaと同定された4株の薬剤感受性試験は米国臨床検査標準委員会(CLSI)の勧告に準拠した市販のK-Bディスク(BD)を用いて18薬剤について行った.

環境分布調査は2013年8月から2014年9月までの1年間に当所に搬入された事業場排水(295検体), 井戸水・湧水(51検体）ならびに県内河川水（22検体）の計368検体を材料としてインチミン(*eae*)をターゲットとしたMultiplex PCR 法でスクリーニング後，Ea検出用プライマーを用いたDuplex PCR法で確認し, 菌の分離を試みた.