## <誌上発表>

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

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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  $\leq 3$ months had the highest rate (49%), and children aged 1 to 4 years had the lowest rate (16%, p < 0.01 vs. infants aged  $\leq 3$  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  $\leq 3$  months  $(p \ge 0.06)$ . Our observations indicate that similar to infants, preteens and teens are at high risk of *B. pertussis* infection.

ODefining the Genome Features of *Escherichia* albertii, an Emerging Enteropathogen Closely Related to Escherichia coli •T. Ooka<sup>1)</sup>, Y. Ogura<sup>2)</sup>, K. Katsura<sup>3)</sup>, K. Seto<sup>4)</sup>, H. Kobayashi<sup>5)</sup>, K. Kawano<sup>6)</sup>, E. Tokuoka<sup>7)</sup>, M. Furukawa<sup>7</sup>), S. Harada<sup>7</sup>), S. Yoshino<sup>6</sup>), J. Seto<sup>8</sup>), T. Ikeda<sup>9)</sup>, K. Yamaguch<sup>i9)</sup>, K. Murase<sup>3)</sup>, Y. Gotoh<sup>3)</sup>, N. Imuta<sup>1)</sup>, J. Nishi<sup>1)</sup>, Ta<sup>^</sup> nia A. Gomes<sup>10)</sup>, Lothar Beutin<sup>11)</sup>, and Tetsuya Hayashi<sup>2)</sup> <sup>1)</sup>Department of Microbiology, Graduate School of Medical and Dental Sciences, Kagoshima University, Japan, <sup>2)</sup>Department of Bacteriology, Faculty of Medical Sciences, Kyushu University, Fukuoka, Japan, <sup>3)</sup>Division of Microbiology, Department of Infectious Diseases, Faculty of Medicine, University of Miyazaki, Japan, <sup>4)</sup>Division of Bacteriology, Osaka Prefectural Institute of Public Health, Osaka, Japan, <sup>5)</sup>Center for Animal Disease Control and Prevention, National Institute of Animal Health, Ibaraki, Japan, <sup>6)</sup>Department of Microbiology, Miyazaki Prefectural Institute for Public Health and Environment, Miyazaki, Japan, <sup>7)</sup>Division of Microbiology, Kumamoto Prefectural Institute of Public Health and Environmental Science, Kumamoto, Japan, <sup>8)</sup>Department of Microbiology, Yamagata Prefectural Institute of Public Health, Yamagata, Japan, <sup>9)</sup>Department of Infection Diseases Bacteriology, Hokkaido Institute of Public Health, Hokkaido, Japan, <sup>10)</sup>Departamento de Microbiologia, Imunologiae Parasitologia, Universidade Federal de Sa<sup>o</sup> Paulo-Escola Paulista de Medicina, Brazil, <sup>11)</sup>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