

### 3・3 誌上发表論文抄録

A confirmation of sapovirus re-infection gastroenteritis cases with different genogroups and genetic shifts in the evolving sapovirus genotypes, 2002–2011

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At present, there is no clear evidence for gastroenteritis cases caused by re-infection with SaV. We found that two individuals were sequentially infected with SaVs of two different genogroups and had gastroenteritis after each infection, although in one of the subsequent cases, both SaV and norovirus were detected. We also found a genetic shift in SaVs from gastroenteritis outpatients in the same geographical location. Our results suggest that protective immunity may be at least genogroup-specific for SaV.

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Follow-up survey of Japanese encephalitis virus infection in Kumamoto Prefecture, South-West Japan: status during 2009–2011

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The present follow-up survey in Kumamoto Prefecture during the 2009–2011 period found that annual infection rates estimated by NS1 antibody prevalence and the percentage of population that was neutralizing antibody- positive but had no history of JE vaccination were similar to those obtained in 2004–2008 in the same prefecture. Although correlations were not always observed among the yearly JE incidence, JEV antibody prevalence in swine, and annual infection rates estimated in this study, these results provide strong evidence of continuous JEV circulation in Kumamoto and suggest a recent exposure of the human population in south-west Japan to JEV infection.

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Molecular and serological investigation of *Leptospira* and leptospirosis in dogs in Japan.

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Among 283 clinically suspected cases of canine leptospirosis diagnosed from August 2007 to March 2011 in Japan, 83 cases were laboratory diagnosed as leptospirosis by blood culture, a rise in antibody titres in paired sera using a microscopic agglutination test (MAT) and/or DNA detection using *flaB*-nested PCR. The infected dogs comprised hunting dogs (31 dogs) and companion animals (50 dogs) and two unknown; 63.4% of the infected dogs were males. The mortality rate was 53.2%. A rise of at least fourfold in MAT titre was detected in 30 dogs whose paired serum samples were obtained, and the predominant reactive serogroup was Hebdomadis (53.3 %), followed by Australis (16.7%) and Autumnalis (16.7 %).

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Molecular epidemiology of the attachment glycoprotein (G) gene in respiratory syncytial virus in children with acute respiratory infection in Japan in 2009/2010.

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This study performed a detailed genetic analysis of the glycoprotein (G) gene of respiratory syncytial virus (RSV) detected in 50 Japanese children with acute respiratory infection (ARI) in the

2009/2010 season. A phylogenetic tree constructed by the neighbour-joining method showed that 34 and 16 of the RSV strains could be classified into subgroups A and B, respectively. Strains belonging to subgroups A and B were further subdivided into GA2 and BA, respectively. The nucleotide and deduced amino acid sequence identities were relatively high among these strains (>90 %). The deduced amino acid sequences implied that a relatively high frequency of amino acid substitutions occurred in the C-terminal 3rd hypervariable region of the G protein in these strains. In addition, some positively selected sites were estimated. The results suggest that RSV with genotypes GA2 and BA was associated with ARI in Japanese children in 2009/2010.

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#### Genetic analysis of the VP4/VP2 coding region in human rhinovirus species C in patients with acute respiratory infection in Japan.

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Detailed genetic analysis was carried out of the VP4/VP2 coding region in human rhinovirus species C (HRV-C) strains detected in patients with acute respiratory infection in Japan. Phylogenetic trees were constructed by the neighbour-joining (NJ) and maximum-likelihood (ML) methods. The NJ phylogenetic tree assigned 11 genotypes to the present strains, whilst the ML tree showed that the strains diversified sometime in the early 1870s. Moreover, the pairwise distance among the present strains was relatively long, and the rate of molecular evolution of the coding region was rapid ( $3.07 \times 10^{-3}$  substitutions per site per year). The results suggest that the present HRV-C strains have a wide genetic divergence and a unique evolutionary timescale.

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# Determination of Nitenpyram and Its Metabolites in Agricultural Products by Using Hydrophilic Interaction Liquid Chromatography-Tandem Mass Spectrometry

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A simple and rapid method for the measurement of a neonicotinoid pesticide, nitenpyram, and its metabolites, CPMA and CPMF, was investigated. The three compounds were determined individually and simultaneously by simple ultrasonic extraction followed by hydrophilic interaction liquid chromatography – tandem mass spectrometry (HILIC-MS/MS). Good chromatograms were obtained using a non-modified silica gel column. The calibration curves were straight ( $R^2 > 0.999$ ) for each compound; they were 0.002–2 mg/kg for 5 g of agricultural product sample with limits of detection ( $S/N=3$ ) of 0.24–0.36 µg/kg (nitenpyram), 0.12–0.19 µg/kg (CPMA), and 0.13–0.18 µg/kg (CPMF). Good recoveries were obtained for sweet pepper, mandarin orange, onion, and brown rice (93.0–106.6% in recovery). For contaminated samples, data by the presented method agreed well with nitenpyram data by HPLC-UV and the total of CPMA and CPMF by derivatization followed by gas chromatography – flame thermionic detection.

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## 九州中部の山岳における光化学オキシダント濃度の挙動および高濃度要因について

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光化学オキシダント（以下、「Ox」という）濃度上昇要因とされている大陸越境移流、地域内汚染および成層圏オゾン沈降について、その各寄与の程度を観測により見積もることを目的として、2011年度に九州中部に位置する標高 930 m の阿蘇カルデラの外輪山にて自動計測器により Ox 濃度を通年観測した。Ox 濃度の平均日変化の振幅は小さく、夜間に観測される Ox 濃度は、バックグラウンド Ox とみなされた。春季は、地上局と外輪山が、日中ほぼ同じ濃度レベルとなっていたことから、平均的に見れば、この時期は、上層のバックグラウンド Ox 気塊が、鉛直混合により、日中の地表 Ox 濃度レベルを主に決定しているものと推測された。外輪山の平均日変化の振幅より、日中最大濃度に対する地域内 Ox 平均生成量の寄与割合を見積もったところ、夏季を除けば、その影響は平均的には 10% 以下であった。ただし、個別の高濃度事例で見れば、大陸越境移流時においても 20 ppb を超える地域内 Ox 生成の寄与もあり得る可能性が見られた。春季の Ox 日平均値に対して、比湿および硫酸塩濃度を変数とする重相関分析を行ったところ、この時期のバックグラウンド Ox 濃度は、成層圏オゾン沈降分をベースに、大陸越境移流分が上乘せされたものと考えられた。