ST1-t127 MRSA clinical strains and of 1 nasal strain belonging to ST398 lineage. Nasal colonization by different ST398 genetic lineages and by other lineages of MRSA as ST1-t127 seems to be frequent in persons living in close proximity to farm animals. Dissemination of MRSA ST398 (and probably also MRSA ST1) in humans who have contact with farm animals, is an emerging problem in Spain.

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Carmen Aspiroz, Carmen Lozano, Ana Vindel, Juan J. Lasarte, Myriam Zarazaga, and Carmen Torres

Author affiliations: Hospital Royo Villanova, Zaragoza, Spain (C. Aspiroz); Universidad de La Rioja, Logroño, Spain (C. Lozano, M. Zarazaga, C. Torres); Centro Nacional Microbiología, Madrid, Spain (A. Vindel); and Centro Salud San Mateo de Gállego, Zaragoza (J.J. Lasarte)

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Address for correspondence: Carmen Torres, Area Bioquímica y Biología Molecular, Universidad de La Rioja, Madre de Dios 51, 26006 Logroño, Spain; email: carmen.torres@unirioja.es

Identification of a Rotavirus G12 Strain, Indonesia

To the Editor: Group A rotavi-ruses are the most common etiologic agents of acute gastroenteritis in infants and young children, each year resulting in ≈100 million diarrhea episodes and 600,000 deaths worldwide (1). The genome of rotavirus comprises 11 segments of double-stranded RNA, which encode 6 structural viral proteins (VPs) and 6 nonstructural proteins (NSPs). Recent scientific reports have identified novel rotavirus strains, such as G12 (2–5), which were first described in 1987 among Filipino children with diarrhea (6). In Indonesia, a rotavirus study showed that a broad variety of VP7 types (G1, G2, G3, G4, G8, G9) and VP4 types (P[4], P[6], P[8], P[9], P[10], P[11]), especially G9 and P[8] and G9P[8], were the genotype combinations most frequently encountered (7).

From 2005 through 2008, we conducted a nationwide surveillance study among children who had diarrhea to determine etiologies among Indonesian children seeking health services for diarrhea at hospitals and health clinics. Patients were enrolled after obtaining consent from parents/guardians of those eligible in accordance with an institutional review board protocol approved by the US Naval Medical Research Unit No. 2 (NAMRU-2) and the Ethical Committee of the Indonesian National Health Research and Development Institute. Stool specimens and clinical enrollment data were collected for each eligible patient, and all collected items were transported to NAMRU-2 in Jakarta, Indonesia. In December 2007, a stool specimen was collected from a 14-day-old afebrile infant brought to Sumber Waras Hospital in West Jakarta with diarrhea, vomiting, moderate dehydration, and malnutrition. This patient was infected with the rotavi-
The Indonesia G12 clustered into the lineage II composed of rotavirus G12 reference strains from Japan, Argentina, South Korea, and Thailand (Figure). Lineage II is a minority cluster when compared with lineage III, which consists of rotavirus G12 from the United States (US6588, Se585), Saudi Arabia (MD844), India (13B2), Bangladesh (RV161), and other Thailand strains (MS051) (4). The nucleotide sequence divergence between lineage II and lineage III ranges from 2.6% to 3.2%. Analysis of the deduced amino acid sequence alignment on the neutralization epitopes that code for the antigenic regions A, B, and C show high conservation of the most immunodominant sites (data not shown). Antigenic regions A, B, C, D, E, and F of Indonesia SWJ0806 show 100% amino acid similarity to Japan G12 strains; K12 and CP727 (9). The amino acid residue at position 142 of the antigenic region B has characterized lineage I and II (Val) and lineage III (Leu).

Phylogenetic analysis showed that the virus clusters into lineage II and that the deduced amino acid sequence is highly conserved compared with other reported rotavirus G12 strains identified. The combination of the P[6] genotype in this rotavirus strain suggests the possibility of a zoonotic transmission (10). Continued surveillance for rotavirus is an essential component of a country’s public health infrastructure and diarrhea prevention programs. Rotavirus genotyping from the data obtained provides necessary information for vaccine development and identification of novel and emerging rotavirus strains.

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**Figure.** Phylogenetic analysis of the viral protein (VP) 7 genotype G12 rotavirus of Indonesia, with reference strains downloaded from GenBank. The GenBank accession numbers of each strain appear next to the strain. The multiple alignment was constructed by using ClustalX version 1.81 (www.clustal.org). The phylogenetic tree was based on the 971 nt sequence of the VP7 gene and constructed by using the neighbor-joining method and applying the Kimura 2-parameter method with 1,000 bootstrap replicates of the neighbor-joining model. The isolate identified in this study is shown in **boldface.** Bootstrap values <50% are not shown. Scale bar indicates nucleotide substitutions per site.
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Wahyu N. Wulan, Erlin Listiyaningsih, Kiki M.K. Samsi, Magdarina D. Agtini, Matthew R. Kasper, and Shannon D. Putnam

Author affiliations: US Naval Medical Research Unit No. 2, Jakarta, Indonesia (W.N. Wulan, E. Listiyaningsih, M.R. Kasper, S.D. Putnam); Sumber Waras Hospital, Jakarta (K.M.K. Samsi); and Indonesian Ministry of Health, Jakarta (M.D. Agtini)

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Address for correspondence: Matthew R. Kasper, US Embassy Jakarta UNIT 8132 NAMRU-2, FPO AP 96520; email: kasper@namruwo.org

Age-based Human Influenza A Virus (H5N1) Infection Patterns, Egypt

To the Editor: In April 2009, a representative of the World Health Organization in Cairo voiced concern about the changing age-based pattern of human influenza A virus (H5N1) infection in Egypt compared with the pattern for earlier influenza seasons. Confirmation reports by the World Health Organization generally indicate associations with dead and sick poultry for these recent cases among children. The cultural patterns and customs of poultry husbandry have not changed in Egypt since the first human cases of influenza A (H5N1) were confirmed in 2006; thus, it is not clear why more children have been infected since December 2008. One explanation may be the increased recognition of the clinical signs of nonfatal influenza A (H5N1) among children and increased confirmation by laboratory testing. The lack of influenza A virus (H5N1) infection among the infected children’s parents and caregivers suggests that the virus is still not easily transmissible among humans in Egypt.

The results for 1-way analysis of variance indicate that the age at time of virus subtype H5N1 infection in Egypt differs significantly among these 4 periods (Kruskal–Wallis test statistic = 20.732, p<0.0004 ).

Further analysis shows that persons infected from August 1, 2008 through July 31, 2009, were much younger than those infected in the preceding 12-month period (Mann-Whitney U test statistic = 328.500, p<0.001). The median age of the 12 confirmed case-patients from August 1, 2007, through July 31, 2008, was 23.5 years, but the median age of the 33 confirmed case-patients from August 1, 2008, through July 31, 2009, was 3.0 years. The Table shows the distribution of case-patients by age group, the median age of each group, and the case-fatality ratio (CFR) for the 4 seasonal 12-month periods.

This recent rise of subtype H5N1 influenza cases among children represents a major change in the pattern of human influenza A virus (H5N1) infections in Egypt compared with the pattern for earlier influenza seasons. Confirmation reports by the World Health Organization generally indicate associations with dead and sick poultry for these recent cases among children. The cultural patterns and customs of poultry husbandry have not changed in Egypt since the first human cases of influenza A (H5N1) were confirmed in 2006; thus, it is not clear why more children have been infected since December 2008. One explanation may be the increased recognition of the clinical signs of nonfatal influenza A (H5N1) among children and increased confirmation by laboratory testing. The lack of influenza A virus (H5N1) infection among the infected children’s parents and caregivers suggests that the virus is still not easily transmissible among humans in Egypt.

Not only has there been a recent increase in infections of influenza A (H5N1) among children, but there has also been a recent decline in deaths.