

reported. Badgers and binturong have been housed in zoological gardens for decades without incidence of influenza. Increased surveillance for influenza by the scientific community during the pandemic may have resulted in the novel recognition of infection in these species. Alternatively, the current pandemic (H1N1) 2009 virus may have a broader host range and stronger virulence than viruses in the past.

Pandemic (H1N1) 2009 was first detected in humans in March 2009 and reached pandemic levels by June of that year, rapidly establishing a rich pool for the development of genetic variants. Naturally acquired disease has now been described in 10 animal species, and experimental infection has been reported in an additional 2 animals (mice and cynomolgus macaques) (9). The ubiquity of pandemic (H1N1) 2009 and its ability to infect a diverse range of hosts is worrisome for the health of wildlife and for the possibility of creating additional reservoirs that could alter the evolution of subtype H1N1 viruses by applying varied selection pressures and establishing new ways of generating unique reassortant strains.

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**Mark D. Schrenzel,
Tammy A. Tucker, Ilse H. Stalis,
Rebecca A. Kagan,
Russell P. Burns,
Amy M. Denison,
Clifton P. Drew,
Christopher D. Paddock,
and Bruce A. Rideout**

Author affiliations: San Diego Zoo Global, Escondido, California, USA (M.D. Schrenzel, T.A. Tucker, I.H. Stalis, R.A. Kagan, R.P. Burns, B.A. Rideout); and Centers for Disease Control and Prevention, Atlanta, Georgia, USA (A.M. Denison, C.P. Drew, C.P. Paddock)

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Address for correspondence: Mark D. Schrenzel, San Diego Zoo Global, Beckman Bldg, 15600 San Pasqual Valley Rd, Escondido, CA 92027, USA; email: mschrenzel@sandiegozoo.org

Hemagglutinin 222 Variants in Pandemic (H1N1) 2009 Virus

To the Editor: The biologic role of amino acid variants at position 222 of the hemagglutinin (HA) gene of pandemic (H1N1) 2009 virus in severe infections has been extensively discussed. A recent series of studies (1–3) confirm the initial suggestions that G or N in this position might confer greater pathogenic potential to the virus than to the wild type. In contrast, their data suggest that no particular pathogenicity is associated with the 222E variant because it occurs at the same frequency in severe and mild infections. Most authors also seem to agree that D222G or N appears sporadically in phylogenetically distant viruses, with limited transmissibility.

However, Puzelli et al. (4) reported transmission of a 222G mutant from son to father (with the appearance of an additional G155E mutation). In Italy, the pattern of D222 variants has been peculiar, with extremely rare appearances of 222G and high diffusion of 222E isolates. At the National Institute for Infectious Diseases in Rome, 82 isolates (GenBank accession nos. CY063455–CY063469 for new sequences in this study) were monitored for D222 variants. No 222G or N variants were detected, even in 24 severe infections, nor was the G155E mutation detected. This finding was not surprising, given the worldwide low frequency of this mutation, even in severe infections.

Conversely, D222E was detected in 12 of the 82 cases, peaking in September 2009, when it was present in most of the infections, with no overrepresentation in severe cases. Subsequently, it was substituted by different 222D viruses during the autumn–winter outbreak. The analysis of publicly available sequences from

other centers in Italy confirmed the trend: 222E was the dominant variant during the summer, 222G was detected only in 4 cases, and 222N was never detected. As we previously reported (5), phylogenetic analysis of 222E variants allowed identification of them as an authentic circulating subclade of clade 7 (6) or cluster 2 (7), rather than as sporadically occurring variants.

To further investigate the origin and the evolution of 222 variants, we have extended the phylogenetic analysis (neighbor-joining) to 2,492 complete HA sequences from the

Global Initiative on Sharing All Influenza Data database (expanded Figure online, www.cdc.gov/EID/content/17/4/749-F.htm), confirming the clustering of all the worldwide 222E variants in a well-defined subclade (Figure; expanded Figure online). The same analysis showed that D222G variants could be reconciled with 2 different phylogenetic patterns. The first less frequent pattern includes sequences appearing sparsely throughout the tree, confirming the mentioned hypothesis of sporadic mutation. In contrast, the second

pattern (the majority) relates to small groups of sequences appearing in monophyletic microclusters. Among these microclusters, 2 are particularly interesting because they include only 222G sequences, isolated in different parts of the world (expanded Figure online). This finding is still compatible with sporadic mutation; bootstrap values are low because of the low general variability of these sequences. However, the possibility that D222G variants are transmissible and might sustain small epidemics of their own or that they might arise more easily from specific, phylogenetically related backgrounds, is intriguing. In a few countries, such as Italy, Norway, or Sweden, where the 222E virus has been circulating as a substantial proportion of the total virus, the 222G variants appeared more frequently in the genetic context of the 222E virus (1,4), as demonstrated by phylogenetic analysis and confirmed by the analysis of codon 239 (the codon determining the 222 residue specificity): GAA to GGA (E to G), instead of GAT to GGT (D to G). In these cases, the correct definition of 222G variants would therefore be E222G rather than D222G. From this point of view, the 222N variant would have a higher genetic barrier to change from E because it would require 2 mutations (GAA to AAT) instead of 1 (GAT to AAT), and indeed none of the 16 available (worldwide) 222N full-length variants clustered with the 222E virus. On the basis of these findings, 2 different amino acids, D and E, might be considered polymorphic variants at position 222, and the potentially more pathogenic mutants or circulating variants would be G or N.

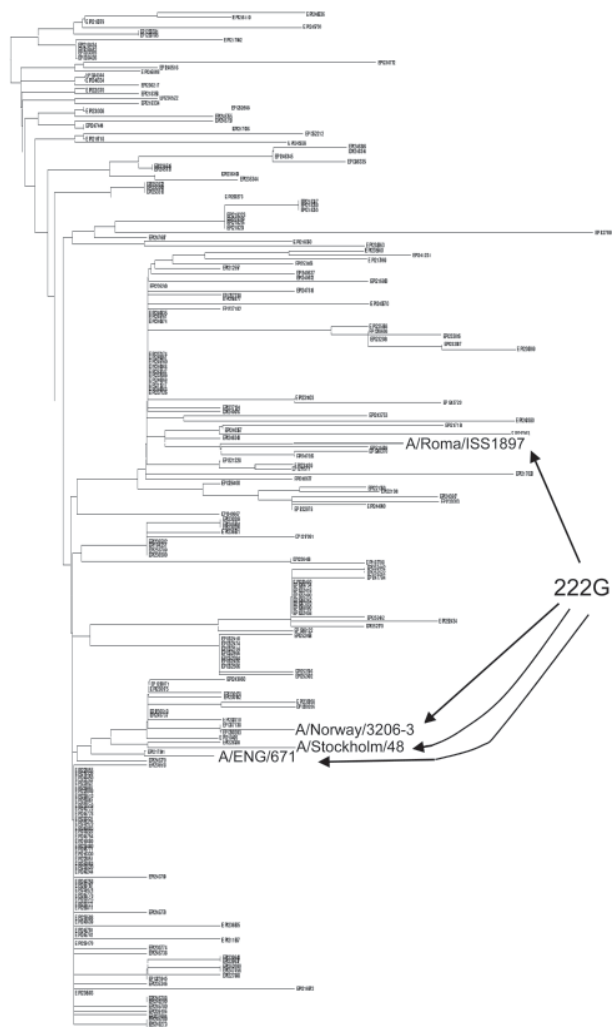


Figure. Monophyletic pandemic (H1N1) 2009 virus D222E cluster, including 98% of the global 222E isolates. E222G variant isolates, as examples, respectively, from Italy (4), Norway (1), Sweden, and the United Kingdom, are indicated by arrows. The sequence labels represent the Global Initiative on Sharing Avian Influenza Data serial numbers; those of particular interest for this study are indicated by the strain name or country of origin. An expanded, color version of this figure is available online (www.cdc.gov/EID/content/17/4/749-F.htm).

**Maria Beatrice Valli,
Marina Selleri, Silvia Meschi,
Paola Zaccaro,
Donatella Vincenti,
Eleonora Lalle,
Maria Rosaria Capobianchi,
and Stefano Menzo**

Author affiliation: National Institute for Infectious Diseases, Virology, Rome, Italy

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Address for correspondence: Stefano Menzo, National Institute for Infectious Diseases–Virology, via Portuense 292, Rome 00149, Italy; email: stefano.menzo@inmi.it



Effect of School Closure from Pandemic (H1N1) 2009, Chicago, Illinois, USA

To the Editor: On April 28, 2009, the Chicago Department of Public Health received notification of 1 student at an elementary school with a probable pandemic (H1N1) 2009 virus infection; the infection was subsequently laboratory confirmed. This case was one of the first pandemic (H1N1) 2009 cases in Chicago. To prevent transmission of influenza and with guidance from the Chicago Department of Public Health, the school closed on April 29; it reopened on May 6 after the Centers for Disease Control and Prevention (CDC) revised its recommendations (1). We conducted an investigation to evaluate psychosocial and economic effects of the school closure on the students' families and to assess whether students complied with mitigation recommendations. In the early pandemic, Chicago's number of pandemic (H1N1) 2009 cases was one of the highest in the United States (2).

Households were surveyed if ≥ 1 child in the household was enrolled in the school and contact was made with an adult (parent/guardian). We made a minimum of 3 attempts to contact eligible households by telephone in English or Spanish. Households without working telephone numbers were visited, but only 1 visit yielded a completed interview. The school had an enrollment of 744 students (609 households, of which 439 were reachable by telephone) during April–May 2009. The final sample comprised 170 households (39% of reachable households). Fifty-four (31%) respondents were employed full-time and 37 (22%) part-time; 78 (46%) were unemployed, homemakers, students, or retired. Households had a median

of 2 adults and 2 children in grades prekindergarten through eight.

In contrast with findings of Johnson et al. (3) in an investigation of an influenza B virus outbreak, where 89% of students visited ≥ 1 public location during the school closure, results from our investigation (Table) indicate that most students complied with recommended social distancing measures. Johnson et al. highlighted the potential for transmission in public areas during a school closure. However, with only approximately one third of households in this investigation reporting their children went to public areas during the school closure, the same level of concern of public transmission was not found.

The results from this investigation indicate the economic effect of the school closure was minimal for survey respondents. These results were similar to those found by Johnson et al. (3), which had only 18% from 220 households (with 315 employed adults) report missing work to stay home because of school closure. However, the number of families losing work time in our investigation was much lower than the 53% of families in central Virginia reported by Nettleman et al. (4) using a survey of school absenteeism and employment status for adults who stayed home to care for an ill child. This might have been because 31% of respondents surveyed in this investigation were homemakers, and an additional 10% were unemployed or retired. Therefore, many parents and legal guardians from this investigation did not need to noticeably change their daily routine to care for their children during the closure. Moreover, compliance has been shown to vary by income and employment status (5).

CDC guidance issued on April 27, 2009, recommended closing any school that had a laboratory-confirmed case of pandemic (H1N1) 2009 (1). As new information became available, CDC updated its recommendations,