

This study was partially supported by Ministerio de Sanidad y Consumo, Instituto de Salud Carlos III, Spanish Network for the Research in Infectious Diseases (REIPI RD06/0008).

**Raquel Abad,* Rocío Enríquez,*
Celia Salcedo,*
and Julio A. Vázquez*.**

*National Institute of Health Carlos III, Madrid, Spain

References

1. Urwin R. Nucleotide sequencing of antigen genes of *Neisseria meningitidis*. In: Pollard AJ, Maiden MCJ, editors. Meningococcal disease: methods and protocols. Totowa (NJ): Humana Press, Inc.; 2001. p. 157–72.
2. Van der Ley P, Heckels JE, Virji M, Hoogerheut P, Poolman JT. Topology of outer membrane porins in pathogenic *Neisseria* spp. *Infect Immun*. 1991;59:2963–71.
3. Frasch CE, Zollinger WD, Poolman JT. Serotype antigens of *Neisseria meningitidis* and proposed scheme for designation of serotypes. *Rev Infect Dis*. 1985;7:504–10.
4. Sacchi CT, Lemos APS, Whitney AM, Solari CA, Brant ME, Melles CEA, et al. Correlation between serological and sequence analysis of the PorB outer membrane protein in the *Neisseria meningitidis* serotyping scheme. *Clin Diagn Lab Immunol*. 1998;5:348–54.
5. Abdillahi H, Poolman JT. Typing of group-B *Neisseria meningitidis* with monoclonal antibodies in the whole-cell ELISA. *J Med Microbiol*. 1988;26:177–80.
6. Abad R, Alcalá B, Salcedo C, Enríquez R, Uría MJ, Díez P, et al. Sequencing of the *porB* gene: a step toward a true characterization of *Neisseria meningitidis*. *Clin Vaccine Immunol*. 2006;13:1087–91.
7. Cooke SJ, Jolley K, Ison CA, Young H, Heckels JE. Naturally occurring isolates of *Neisseria gonorrhoeae*, which display anomalous serovar properties, express PIA/PIB hybrid porins, deletions in PIB or novel PIA molecules. *FEMS Microbiol Lett*. 1998;162:75–82.
8. Carbonetti NH, Simnad VI, Seifert HS, So M, Sparling PF. Genetics protein I of *Neisseria gonorrhoeae*: construction of hybrid porins. *Proc Natl Acad Sci U S A*. 1988;85:6841–5.
9. Carbonetti N, Simnad V, Elkins C, Sparling PF. Construction of isogenic gonococci with variable porin structure—effects on susceptibility to human serum and antibiotics. *Mol Microbiol*. 1990;4:1009–18.

Address for correspondence: Julio A. Vázquez, Reference Laboratory for Meningococci, Servicio de Bacteriología, National Centre for Microbiology, National Institute of Health Carlos III, 28220 Majadahonda (Madrid), Spain; email: jvazquez@isciii.es

West Nile Virus in Birds, Argentina

To the Editor: West Nile virus (WNV), genus *Flavivirus*, family *Flaviviridae* has been rapidly dispersing through the Americas since its introduction in 1999 in New York (1). By 2004, serologic studies detected WNV-specific antibodies in birds and horses from Canada to northern South America (2–4). The first report of WNV activity in the Southern Cone of South America surfaced in April 2006, when 3 horses died in Argentina (5). However, established transmission foci in Argentina are unknown. We report evidence for the introduction and establishment of WNV in Argentina as early as January 2005.

Serum samples from free-ranging birds were collected from 5 locations in Argentina and screened for generic flavivirus antibodies by using a blocking ELISA with monoclonal antibody 6B6C-1 (6). Positive serum specimens were further characterized by plaque-reduction neutralization test (PRNT). We identified the etiologic agent responsible for the previous flavivirus infection by using the following criteria: 80% neutralization of reference virus (WNV NY99-4132 or an Argentinean strain of St. Louis encephalitis virus [SLEV CbaAr4005]) in serum diluted at least 1:40 and 4-fold greater titer compared with the other virus.

Overall, 474 (25.6%) of 1,845 serum specimens from 117 bird species collected from January to June

2006 tested positive when using the blocking ELISA; 30% inhibition was the threshold for a positive test. SLEV infections were confirmed in 105 birds by PRNT; WNV infections were confirmed in 43 birds. Anti-WNV antibody titers ranged from 40 to 2,560 in birds collected as early as January 2005 in Córdoba City and as late as June 2006 in Mar Chiquita (Table). Recent WNV activity was indicated by seroconversion in 3 banded rufous horned in Córdoba City between January and March 2005. Although 1.5% of 659 serum samples were positive for SLEV, no WNV infection was detected in free-ranging birds collected in 2004. After 2004, WNV activity was detected in all 5 sampling locations and in a variety of ecosystems: Córdoba, periurban thorn forest (1.1%, 6/543); Mar Chiquita, thorn forest (5.1%, 16/313); Monte Alto, semi-dry chaco forest (9.8%, 8/82); Montecristo, cropland (9.5%, 2/21) and San Miguel de Tucumán, periurban yungas foothills (4.9%, 12/227).

In 2006, WNV was isolated from equines in Buenos Aires province (5). WNV transmission to resident birds collected further north in Córdoba, Chaco, and Tucumán provinces was detected in 2005 and 2006. Our data suggest that WNV was introduced into Argentina before 2005 and maintained naturally in enzootic foci where numerous bird species from many families were exposed. Presumably, as in North America, locally abundant passerine birds such as turdids (thrushes) are amplifying hosts. If common species of the *Furnariidae* (a family absent from temperate North America) prove to be competent hosts, they could play an important role in WNV transmission in Argentina because of their frequent exposure to WNV. Twelve (12.5%) of 96 *F. rufus* sampled in 2005 and 2006 tested positive.

How WNV reached Argentina may never be known. Dispersal by migrating birds is a popular hypothesis, although relatively few North American breeding

Table. Prevalence of West Nile virus–neutralizing antibodies among birds grouped by taxonomic family, sampled in Chaco, Córdoba, and Tucumán Provinces, Argentina, 2004–2006*

| Bird family | No. positive | No. tested | % Positive (95% CI) | Range of PRNT ₈₀ titer† |
|-------------------------|--------------|------------|---------------------|------------------------------------|
| <i>Cardinalidae</i> | 2 | 54 | 3.7 (1.0–12.5) | 80–160 |
| <i>Columbidae</i> | 4 | 270 | 1.5 (0.6–3.8) | 80–1,280 |
| <i>Dendrocolaptidae</i> | 4 | 17 | 23.5 (9.6–47.3) | 320–2,560 |
| <i>Falconidae</i> | 3 | 5 | 60.0 (23.1–88.2) | 320–2,560 |
| <i>Furnariidae</i> | 12 | 201 | 6.0 (3.4–10.1) | 80–1,280 |
| <i>Icteridae</i> | 3 | 137 | 2.2 (0.7–6.2) | 40–320 |
| <i>Passeridae</i> | 1 | 87 | 1.1 (0.2–6.2) | 40 |
| <i>Phasianidae</i> | 2 | 8 | 25.0 (7.1–59.1) | 320 |
| <i>Poliopitidae</i> | 2 | 7 | 28.6 (8.2–64.1) | 80–640 |
| <i>Troglodytidae</i> | 1 | 17 | 5.9 (1.0–27.0) | 80 |
| <i>Turdidae</i> | 8 | 132 | 6.1 (3.1–11.5) | 40–1,280 |
| <i>Tyrannidae</i> | 1 | 370 | 0.3 (0.05–1.5) | 160 |

*Most of these families are of the order Passeriformes except for *Falconidae* (Falconiformes), *Phasianidae* (Galliformes), and *Columbidae* (Columbiformes). CI, confidence interval, determined by the Wilson score method for binomial proportions, without continuity correction.

†PRNT, plaque-reduction neutralization test. Titers are expressed as inverse of dilution.

birds migrate to Argentina, and austral migrants number fewer than boreal migrants. Komar and Clark (2) suggested that bird species in the order Charadriiformes, such as shorebirds and terns, are candidates for carrying WNV from North America to South America due to long lasting high-level viremias, occasional persistent infectious viral loads in skin, and direct, long-distance flights. WNV spread southward from the United States to northern South America between 1999 and 2004 following a stepping stone pattern, consistent with spread by birds. Moreover, introduction of WNV into Argentina by migratory birds could explain the presence of the virus in many places in a brief period. However, for migratory birds (211 serum samples tested) in this study, serologic test results were negative.

The high titers of WNV-reactive antibody are strongly indicative of WNV infections. Overall, 216 serum specimens reacted by PRNT test against SLEV, WNV or both at titers ≥ 20 . Sixty-eight serum samples remain unidentified. The large number of unidentified flavivirus-positive samples detected by PRNT, ELISA, or both (148/474) could be due to 1) false positives; 2) cross-reactions between WNV- and SLEV-reactive antibodies that prevented definitive diagnosis by PRNT; 3) cross-reactive antibody and multiple, heterologous flavivirus infections; 4) previous infections by both

WNV and SLEV; and/or 5) presence of other flaviviruses circulating in Argentina. SLEV is endemic throughout Argentina and, like WNV, belongs to the Japanese encephalitis virus serocomplex. Hemagglutination-inhibiting antibodies against several Brazilian flaviviruses (e.g., Bussuquara, Ilheus, Rocio viruses) have been reported in the neotropical region of extreme northern Argentina (7), but these viruses have not been isolated in Argentina.

Our serologic data suggest that WNV has established itself in 4 ecologic regions in Argentina in a brief period. Additional studies are needed to define the reservoir hosts and vectors of WNV in Argentina, and most importantly, to define the public health risk this virus represents.

Acknowledgments

We thank J. Rosa, A. Boris, R. Reynoso, C. Castillo, A. Zarco, N. Villafañe, S. Flores, M.A. Cortez, M.E. Alvarez, J.R. Torres-Dowdall, D. Serra, and E. Edwards. We also thank the Cordoba Environment Agency (Cordoba Province), Department of Wildlife (Chaco Province), Municipality of San Miguel de Tucumán City (Tucumán Province), and SENASA for permission to obtain and export bird samples.

This study was supported by grants from Agencia Nacional de Promoción Científica y Tecnológica – Fondo Nacional de Ciencia y Tecnología (ANPCYT–

FONCYT 01-12572 and 38060), Consejo Nacional de Investigaciones Científicas y Tecnológicas (CONICET), Roemmers Foundation, Secretaría de Ciencia y Técnica – Universidad Nacional de Córdoba (SECYT–UNC), Secretaría Nacional de Ciencia y Técnica – Universidad Nacional del Noreste (SECYT–UNNE), Centers for Disease Control and Prevention – Division of Vector-Borne Infectious Diseases (CDC–DVBID), International Society for Infectious Diseases, International Union of Microbiological Societies – Society for General Microbiology (UNESCO–IUMS–SGM), Ministry of Public Health of the Tucumán Province, and the Public Health Department of the School of Medicine, National University of Tucumán.

Luis Adrián Díaz,*
Nicholas Komar,†
Andres Visintin,*
María Julia Dantur Juri,‡
Marina Stein,§
Rebeca Lobo Allende,‡
Lorena Spinsanti,*
Brenda Konigheim,*
Javier Aguilar,*
Magdalena Laurito,*
Walter Almirón,*
and Marta Contigiani*

*Universidad Nacional de Córdoba, Córdoba City, Argentina; †Centers for Disease Control and Prevention, Fort Collins, Colorado, USA; ‡Universidad Nacional de Tucumán, Tucumán, Argentina; and §Universidad Nacional del Noreste, Chaco, Argentina

References

- Hayes EB, Komar N, Nasci RS, Montgomery SP, O'Leary DR, Campbell GL. Epidemiology and transmission dynamics of West Nile virus disease. *Emerg Infect Dis.* 2005;11:1167–73.
- Komar N, Clark GG. West Nile virus activity in Latin America and the Caribbean. *Rev Panam Salud Publica.* 2006;19:112–7.
- Morales-Betoulle ME, Morales H, Blitvich BJ, Powers AM, Davis EA, Klein R, et al. West Nile virus in horses, Guatemala. *Emerg Infect Dis.* 2006;12:1038–9.
- Bosch I, Herrera F, Navaro JC, Lentino M, Dupuis A, Maffei J, et al. West Nile virus, Venezuela. *Emerg Infect Dis.* 2007;13:651–3.
- Morales MA, Barrandeguy M, Fabbri C, Garcia GB, Vissani A, Trono K, et al. West Nile virus isolation from equines in Argentina, 2006. *Emerg Infect Dis.* 2006;12:1559–61.
- Blitvich BJ, Bowen RA, Marlenee NL, Hall RA, Bunning ML, Beaty BJ. Epitope-blocking enzyme-linked immunosorbent assays for detection of West Nile virus antibodies in domestic mammals. *J Clin Microbiol.* 2003;41:2676–9.
- Sabattini MS, Avilés G, Monath TP. Historical, epidemiological and ecological aspects of arbovirus in Argentina: Flaviviridae, Bunyaviridae and Rhabdoviridae. In: Travassos da Rosa APA, Vasconcelos PFC, Travassos da Rosa JFS, editors. An overview of arbovirology in Brazil and neighboring countries. Belem (Brazil); Instituto Evandro Chagas; 1998. p. 113–34.

Address for correspondence: Luis Adrián Díaz, Arbovirus Laboratory, Institute of Virology “Dr. J. M. Vanella” School of Medical Sciences, National University of Cordoba, Enfermera Gordillo Gómez s/n 5016, Ciudad Universitaria, Córdoba, Argentina; email: ladriandiaz@gmail.com



Clostridium difficile Surveillance Trends, Saxony, Germany

To the Editor: Vonberg et al. (1) recently commented on the increase of *Clostridium difficile* seen in US hospitals by using discharge diagnoses and confirmed the observation from the United States (2) with hospital discharge data from Germany during 2000 through 2004. *C. difficile* ribotype 027 has recently been isolated in Germany (3). We further contribute to the assessment of *C. difficile* as an emerging threat by looking at population surveillance data.

C. difficile is not a federal notifiable disease in Germany, which limits our ability to analyze national surveillance trends. However, in 2002 the state of Saxony implemented additional mandatory surveillance of community- and hospital-acquired infectious enteritis caused by laboratory-confirmed *C. difficile*.

To check for an increase in notifications due to reporting bias of gastroenteric diseases, we compared the quarterly incidence data from 2002 through 2006 with data on *Salmonella* spp. infections (usually reported by local general practitioners) and rotavirus

and norovirus infections (both usually reported by clinics). The potential problem of reporting bias for gastroenteric diseases has been addressed recently (4). Information about age and sex of *C. difficile* patients was available for 2006 only.

Quarterly incidences for *C. difficile* in Saxony were from 1.7–3.8 per 100,000 population in 2002 and 2003 and continued to increase to 14.8 cases per 100,000 population in 2006 (Figure). This constitutes a 6-fold increase of the yearly average of *C. difficile* incidence rates between 2002 and 2006. The third quarter of 2005 experienced a sharp drop that could not be explained retrospectively and might have resulted from transition to new procedures for data collection and management.

Gastroenteric infections showed clear seasonality with a slightly decreasing yearly trend for *Salmonella* spp. and seasonal values from 13.8 cases per 100,000 in winter to summer peaks of 56.8. Rotavirus infections displayed an even stronger seasonality, with values from 7.0 cases per 100,000 in summer to winter peaks of 140.3. Norovirus infections peaked again during winter, at 137.2 cases per 100,000 but had as few as 11.0 cases per 100,000 during summer. Notification does not suggest reporting bias of gastroenteric infections.

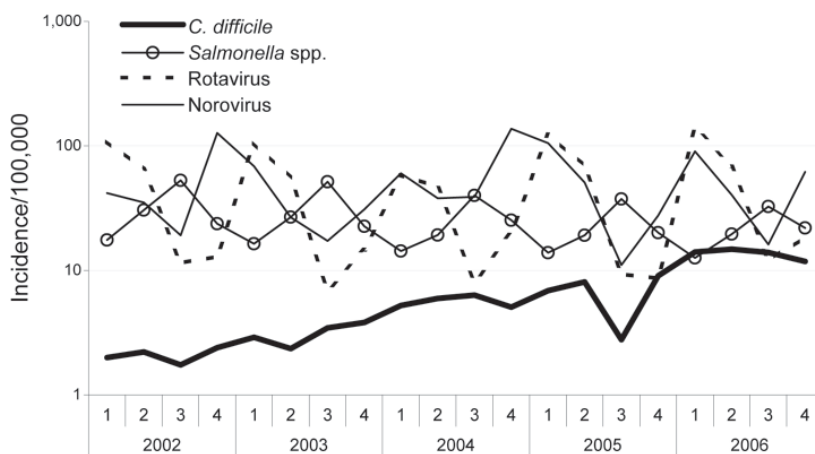


Figure. Quarterly incidence per 100,000 population of *Clostridium difficile* infections compared with gastroenteric infections caused by *Salmonella* spp., rotaviruses, and noroviruses in Saxony, Germany, 2002–2006. Note the log scale on the y axis.