sons and persons born in the United States), for whom the difference from NHANES III to NHANES 1999–2000 data reached statistical significance at p<0.05 in the t test, but the 95% confidence intervals (CIs) for the prevalence estimates for these groups still overlapped between NHANES III and NHANES 1999–2000 (i.e., the t test is a less conservative measure of association than CI).

After this correction, the overall age-adjusted *T. gondii* antibody prevalence according to NHANES 1999–2000 data changed from 15.8% (95% CI 13.5%–18.1%) to 14.3% (95% CI 12.3%–16.2%). The Table shows the overall and stratified seroprevalence rates for NHANES 1999–2000 (corrected) compared with NHANES III (no corrections needed).

### Table. Comparison of *Toxoplasma gondii* IgG antibody seroprevalence, NHANES 1999–2000 and NHANES III (1988–1994)†

| Race/ethnicity          | NHANES 1999–2000 | NHANES III (1988–1994) |
|-------------------------|------------------|-----------------------|
|                         | N‡               | Prevalence | 95% CI | N‡               | Prevalence | 95% CI |
| Sex                     |                  |          |        |                  |          |        |
| Male                    | 2,013            | 15.2     | 12.4–18.0 | 5,144           | 16.7     | 14.8–18.6 |
| Female                  | 2,221            | 13.4     | 11.2–15.5 | 5,988           | 15.3     | 13.5–17.0 |
| Race/ethnicity          |                  |          |        |                  |          |        |
| Non-Hispanic white      | 1,293            | 10.8     | 8.1–13.6 | 3,304           | 14.3     | 12.5–16.2 |
| Non-Hispanic black      | 1,027            | 16.8     | 13.4–20.3 | 3,674           | 18.0     | 16.1–19.8 |
| Mexican American        | 1,553            | 14.2     | 10.1–16.4 | 3,661           | 18.3     | 16.7–20.0 |
| Age group, y            |                  |          |        |                  |          |        |
| 12–19                   | 2,105            | 7.3      | 4.7–10.0 | 2,749           | 8.5      | 6.4–10.5 |
| 20–29                   | 735              | 11.9     | 9.5–14.4 | 3,100           | 15.2     | 12.1–18.3 |
| 30–39                   | 726              | 17.0     | 12.9–21.2 | 2,960           | 16.1     | 14.6–17.6 |
| 40–49                   | 668              | 18.7     | 15.0–22.3 | 2,323           | 22.2     | 19.4–25.0 |
| Country of birth        |                  |          |        |                  |          |        |
| United States           | 3,211            | 10.5     | 8.3–12.8 | 8,606           | 14.1     | 12.7–15.5 |
| Not United States       | 995              | 32.0     | 24.0–39.9 | 2,493           | 27.9     | 24.1–31.7 |

†IgG, immunoglobulin G; NHANES, National Health and Nutrition Examination Survey; CI, confidence interval.

‡Sex, race/ethnicity, country of birth, and total values are age-adjusted to the 2000 census–estimated population using the 4 age categories shown.

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Address for correspondence: Jeffrey L. Jones, Centers for Disease Control and Prevention, Mailstop F22, 4770 Buford Highway, Atlanta, GA 30341, USA; email: JLIones@cdc.gov

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**Human Infection with Schineria larvae**

To the Editor: Myiasis remains prevalent worldwide (1,2) and is infestation by larvae from fly species of live or dead tissues from vertebrate hosts (1,3,4). In humans, myiasis most frequently causes infection of exposed ulcers or traumatic wounds (1). In industrialized countries, most cases occur in tourists returning from tropical and subtropical areas (5,6), but autochthonous cases still exist. Several bacterial species have been associated with fly larvae, including species of the family *Enterobacteriaceae* and, more recently, *Schineria larva* (7,8). *S. larva*, a gram-negative bacterium, has been grown from larvae of *Wohlfahrtia magnifica*, a fly species responsible for myiasis (7,8). Its 16S rRNA gene has been amplified from a bacterial community of species involved in aerobic thermophilic bioprocesses (9). We report a case of *S. larva* bacteremia in a man with wound myiasis.

On June 12, 2006, a 76-year-old man who had type 2 diabetes mellitus was examined at the emergency
continued for 7 more days. The patient was discharged 27 days after initiation of antimicrobial therapy, which he continued for 7 more days. The patient lived alone in a rural, crowded area and had received no medical care. He reported owning sheep and denied any recent travel outside France. At the time of admission, his body temperature was 37.8°C, he was malodorous, and he had swelling and painful wounds on both legs. Maggots were found infected in the leg wounds, scrotum ulcers, and on the anal margin. A radiographic examination of both legs did not show any osteolytic lesion. Laboratory data were as follows: C-reactive protein 71 mg/L (reference value, <5 mg/L), leukocyte count 18.2 × 10⁹/L (81% granulocytes), platelet and erythrocyte counts within normal limits, glucose 200 mg/dL, hemoglobin A1c level 13.8%. Serum protein electrophoresis showed hypoalbuminemia (16.9 g/L) but no monoclonal gammopathy. Two blood samples and a 2 blood cultures yielded methicillin-susceptible Staphylococcus aureus, and the 2 blood cultures yielded the same S. aureus strain and an oxidative gram-negative bacterium (Romans strain). The Romans strain was sent to the bacteriology laboratory at Grenoble University Hospital for identification. Using the API 20NE and Vitek II ID-GNB systems (bioMérieux, Marcy L’Etoile, France), we obtained, respectively, a “good” identification of Psychrobacter phenylpyruvicus and a “very good” identification of Oligella ureolytica. The nearly complete 16S rRNA gene of the Romans strain was amplified and sequenced; primers were Fd1 and rp2 (10) (GenBank accession no. EF120377). A BLAST search that used the network service of the National Center for Biotechnology Information (www.ncbi.nlm.nih.gov) showed 99.6% identity between the determined gene sequence of 16S rRNA and that of S. larvae type strain L1/68T (accession no. AJ252143). The 16S rRNA gene sequences from several species belonging to the Gamma Proteobacteria order were aligned by using the ClustalW package (www.ncbi.nlm.nih.gov). A consensus phylogenetic tree was constructed from Jukes-Cantor evolutionary distances based on the neighbor-joining method using Bacillus subtilis as the root. The Romans strain clustered with previously characterized S. larvae strains (Figure).

Our report demonstrates that S. larvae can induce bacteremia in humans. Because S. larvae has been associated with only fly larvae, we can speculate that bacteremia originated from maggots infesting the patient’s wounds. We cannot affirm that W. magnifica was the fly species involved because maggots were not saved for identification. Phenotypic identification of S. larvae is tedious (7). Because it is an asaccharolytic species, erroneous identification may occur. We can speculate that difficulties in phenotypic identification of this species may explain why it has not been previously reported as a potential human or animal pathogen.

In conclusion, myiasis remains an unresolved problem in animals and humans worldwide. Physicians and microbiologists should be aware of the possibility of S. larvae bacteremia and should specifically search for S. larvae infection in myiasis patients. Also, animal myiasis is still responsible for severe economic losses to the livestock industry worldwide. The occurrence of S. larvae bacteremia in animals with myiasis may explain the evolution from disease to death, especially in chronically infected animals.

Max Maurin,* Jeanne Noelle Delbano,* Léandre Mackaya,† Henri Colomb,† Christophe Guier,† Aziza Mandjee,† Christine Recule,* and Jacques Croize*

Figure. Phylogenetic position of the Romans strain within the Gamma Proteobacteria, determined by using Jukes-Cantor evolutionary distance calculation and neighbor-joining tree method. Bootstrap values (based on 500 steps) are indicated. GenBank accession no. of 16S rRNA gene of each bacterial species is indicated in parentheses.
Isolation of Schineria sp. from a Man

To the Editor: Schineria larvae has been isolated from maggots of the fly Wohlfahrtia magnifica (1), which cause myiasis in animals and people in Eurasia and northern Africa. In industrialized nontropical countries, a range of species in the order Diptera cause facultative myiasis in patients with neglected wounds (2). Since the recent description of S. larvae, Schineria sp. isolates and clones have been detected in diverse environmental and animal sources, but in all cases a relation with flies could be established. We describe a case of bacteremia due to Schineria sp. in a human patient with myiasis.

In July 2005, a 39-year-old homeless man with medical history of polynuropathy related to alcohol abuse was examined at Montpellier Hospital, Montpellier, France, and found to be in poor general health and to have an abnormal electrocardiogram, mild fever (38°C), metabolic disorders, increased C-reactive protein (254 mg/L) and fibrinogen (18.23 mg/L), and a normal leukocyte count (7.8 × 10^9/L). Removal of his shoes and socks, which he had worn continuously for 2 months, showed advanced maceration of his feet (trench foot) with wounds invaded by maggots. The following organisms were found in wound samples: Proteus mirabilis, Providentia stuartii, group G Streptococcus, Streptococcus sp., and Enterococcus sp. Aerobic blood culture, after 1 day of incubation, was positive for strain ADV4155.05, which displayed the same phenotype as strain ADV1107.05 except for tetracycline resistance. Clinical improvement was observed after 2 weeks of the same local and systemic treatments as initially prescribed. The patient was transferred to an addiction care center and received oral antimicrobial therapy (ciprofloxacin 500 mg/day plus amoxicillin/clavulanic acid 3 g/day) for 20 days.

The 16S rDNA amplification and sequencing were performed with universal primers 27f and 1492r as described (3). The 1,414-bp sequences of the 2 isolates were identical and showed similarity level of 99.6% with the sequence of Schineria sp. 010793816 isolated from human urine (M. Vanechaoutte, pers. comm.) but only 98.3% with S. larvae L1/68T 16S rDNA. This finding differed from the biochemical identification and underlined the usefulness of sequencing to precisely identify gram-negative bacilli that assimilate only a few

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