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

	NHANES 1999–2000			NHANES III (1988–1994)		
	N‡	Prevalence	95% CI	N‡	Prevalence	95% CI
Total	4,234	14.3	12.3–16.2	11,132	16.0	14.5–17.5
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	10.1–18.4	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.
‡Totals for the race/ethnicity and country-of-birth categories do not add up to the total number because an "other" race/ethnicity category was included in the totals but not shown in these categories or because persons did not provide a response to country-of-birth questions.

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).

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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 larvae* (*7,8*). *S. larvae*, 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. larvae* 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

department of Drôme North Hospitals, Romans, France, for inflammation of chronic cutaneous ulcers of both legs and intermittent fever. 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 in the leg wounds, scrotum ulcers, and at 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 18.2×10^9/L (81% granulocytes), platelet and erythrocyte counts within normal limits, glucose 200 mg/dL, hemoglobin A1c level 13.8%. Serum protein electrophoresis showed hypoalbuminemia (20 g/L) and hypergammaglobulinemia (16.9 g/L) but no monoclonal gammopathy. Two blood samples and exudate from the leg wounds were collected for microbial cultures.

The patient was given a combination of amoxicillin-clavulanate and ofloxacin, and his cutaneous wounds were cleaned. After 24 h of incubation, leg wound cultures grew 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 found to be highly susceptible to β-lactams, aminoglycosides, chloramphenicol, cotrimoxazole, fluoroquinolones, and colistin. The antimicrobial drug therapy was changed to oxacillin and ofloxacin. The patient's condition improved rapidly, and his leg wounds healed progressively during hospitalization. He was discharged 27 days after initiation of antimicrobial therapy, which he continued for 7 more days. The patient was reexamined 1 month later and was considered cured.

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 L1/68^T (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.

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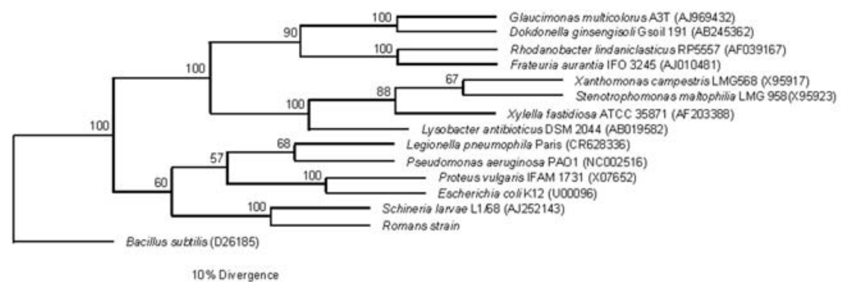

Figure. Phylogenetic position of the Romans strain within the Gamma Proteobacteria, determined by using Jukes-Cantor evolutionary distance calculation and neighbor-joining tree method. Bootstrap values (based on 500 steps) are indicated. GenBank accession no. of 16S rRNA gene of each bacterial species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

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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 polyneuropathy 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 μmol/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 2 days of incubation, was positive for a gram-negative rod, strain ADV1107. 05. Subculture on MacConkey medium showed positive reactions for oxidase, catalase, and gamma-glutamyltransferase. Positive malate reaction with API 20NE system (bioMérieux, Marcy l'Etoile, France) identified the strain as *Oligella urethralis,* whereas VITEK2 (bioMérieux) with ID-GN card failed to identify the strain. Disk diffusion assay showed the strain to be susceptible to β-lactams, aminoglycosides, fluoroquinolones, tetracyclines, erythromycin, rifampin, and colistin but resistant to nalidixic acid and fosfomycin. Local therapy of debridement, bandaging, and sulfadiazin argentic, along with systemic antimicrobial therapy (ofloxacin 400 mg/day plus cefotaxime 6 g/day) for 2 weeks, led to clinical improvement and sterilization of the blood cultures. The local therapy was continued, and ofloxacin (400 mg/day) was prescribed for 15 days while the patient was in a rehabilitation center.

In October 2005, the patient was readmitted with the same symptoms. *P. mirabilis*, group A and group G streptococci, *Morganella* sp., *Bacteroides fragilis*, and *Candida albicans* were cultured from maggot-invaded wounds. 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. Vaneechoutte, pers. comm.) but only 98.3% with *S. larvae* L1/68^T 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