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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 ($7.8 \times 10^9$/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

sugars. Phylogenetic analysis linked the 2 strains to the genus *Schineria* in the class Gamma Proteobacteria (Figure). However, whether the isolates are species *S. larvae* remains in doubt. Enterobacterial repetitive intergenic consensus–PCR and repetitive extragenic palindromic–PCR fingerprints (*6*) showed that the 2 strains were unrelated, thereby demonstrating that the second episode of bacteremia was a reinfection with a new strain and not a relapse.

The 16S rDNA of our isolates is most related to an uncultured bacterium found in swine waste (*7*), but its presence in such an environment could be correlated with fly larvae proliferation. Because of the lifestyle of *Schineria* sp., thinking that the strains in our patient originated from his wounds' maggots is reasonable. Unfortunately, the maggots were thrown away and could be neither analyzed nor identified. *Schineria* sp. could not be cultivated from the patient's wounds, perhaps because of its close association to larvae or to the abundant associated flora. Despite the presence of virulent bacteria in the wounds, *Schineria* sp. was the sole bacterium recovered from blood during the 2 independent episodes of bacteremia, which suggests its invasive potential. Invasiveness may be enhanced by the maggots' acting as a vector as they move through the necrotic tissues toward the bloodstream. Invasiveness also may be a specific characteristic of the bacterium; phylogenetic methods placed the genus *Schineria* in a subgroup that included human pathogens *Cardiobacterium*, *Francisella*, *Coxiella*, and *Legionella*. Indeed, all the phylogenetic methods tested excluded *Schineria* spp. of the family *Xanthomonadaceae* (Figure), which conflicts with current classification (*8*).

No report has described bacteremia following myiasis with facultative parasites, but investigations of bacteria in reported myiasis cases have been conducted on cutaneous lesions and never on blood (*9*). Because of this association between maggots and risk for bacteremia, blood cultures should be performed for patients with myiasis and poor hygiene. Moreover, germ-free maggots bred for biosurgery use (*10*) should be checked, by molecular methods, for the absence of *Schineria* sp.

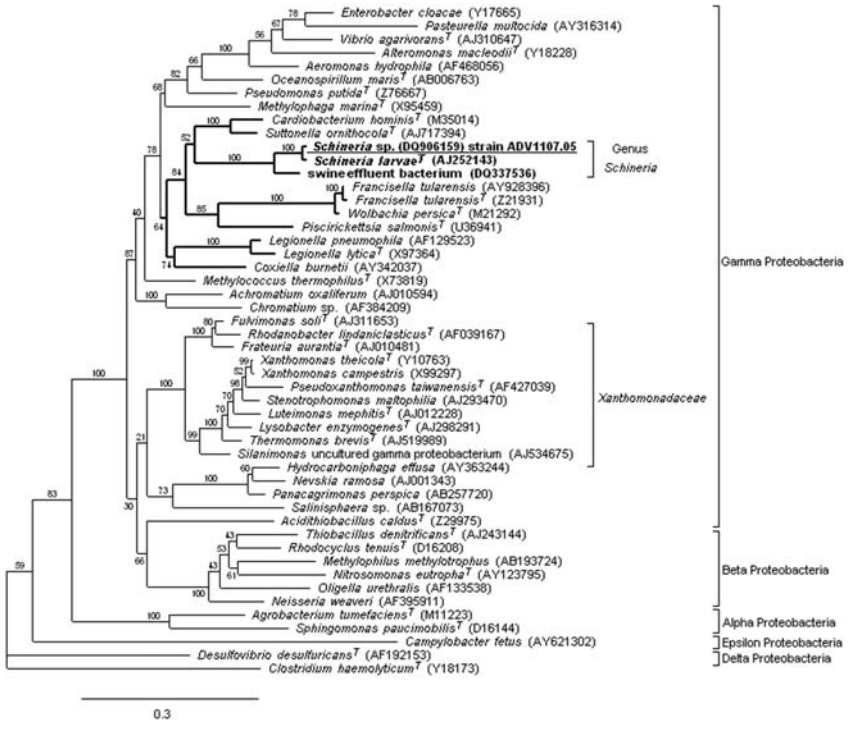


Figure. Maximum likelihood (ML) 16S rRNA gene phylogenetic tree showing the placement of the genus *Schineria* (**boldface**) and the isolate ADV1107.05 (underlined) in the phylum Proteobacteria. To reconstruct this tree, we used the strain ADV1107.05 sequence (DQ906159, 1441 bp) and 49 sequences selected from the GenBank database: 38 among the 15 orders of the Gamma Proteobacteria, 6 for the Beta Proteobacteria, 2 for the Alpha Proteobacteria, 1 for Delta Proteobacteria, 1 for Epsilon Proteobacteria and *Clostridium haemolyticum* (used as the outgroup organism). Accession nos. are in brackets. Alignment was performed with ClustalW 1.83 (*4*). ML phylogenetic analysis was performed by using PHYML v2.4.4 (*5*) with the general time-reversible plus gamma distribution plus invariable site (GTR + Γ + I) model found to be most appropriate according to Akaike information criteria. Bootstrap values given at the nodes are estimated with 100 replicates. The scale bar indicates 0.3 substitutions per nucleotide position. Strain ADV4155.05 sequence (DQ906158, 1414 bp) is not reported because it was identical to ADV1107.05. Trees were also obtained by distance methods (JC69, F84, and GTR models, and neighbor-joining), by parsimony, and by Bayesian inference. In all instances the genus *Schineria* branched out of the *Xanthomonadaceae* cluster.

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## *Salmonella* Kingabwa Infections and Lizard Contact, United States, 2005

**To the Editor:** Nontyphoidal *Salmonella* infections cause an estimated 1.4 million illnesses and 400 deaths in the United States annually (*1*). Among the >2,500 *Salmonella* serotypes, *Salmonella enterica* serotype Kingabwa rarely causes human illness. This serotype was first reported in a patient in the Belgian Congo in 1953 (*2*). From 1995 through 2004, only 30 human illnesses caused by *S.* Kingabwa were reported to the National *Salmonella* Surveillance System (*3*). No common source for *S.* Kingabwa human illnesses has been previously identified. We recently investigated an outbreak of *S.* Kingabwa infections associated with 2 lizard species: the water dragon and the bearded dragon.

Eighteen isolates of *S.* Kingabwa (antigenic formula: I 43:y:1,5) were received by PulseNet, the National Molecular Subtyping Network for Foodborne Disease Surveillance, from 2001 through 2005. When digested with restriction enzyme *Xba*I and subtyped by pulsed-field gel electrophoreisis (PFGE), 13 isolates produced a single, indistinguishable pattern (KINX01.0001). Of these, 1 (8%) was isolated in 2001, 4 (31%) were isolated in 2002, 2 (15%) were isolated in 2004, and 6 (46%) were isolated in 2005. We defined a case as illness during 2005 caused by *S.* Kingabwa that matched pattern KINX01.0001 by PFGE. Of the 9 *S.* Kingabwa isolates received by PulseNet in 2005, 6 matched KINX01.0001. Antimicrobial drug susceptibility of 3 isolates was determined by the National Antimicrobial Resistance Monitoring System (NARMS) for Enteric Bacteria at the Centers for Disease Control and Prevention (CDC), and the isolates were susceptible to each of 15 antimicrobial agents tested.

The 6 patients in the 2005 outbreak did not know each other and resided in 5 states: Maine (2 patients), Arizona, California, Idaho, and Ohio. Illness onset dates were in June, July, August, October (2 patients), and November 2005. Of the 6 patients, 4 (67%) were ≤1 year old (range <1–53 years), 4 were male, 2 were hospitalized, and none died.

Interviews with patients or their parents or guardians conducted during routine public health surveillance collected information on specific food items, water sources, restaurant venues, travel history, and animal contact. No common food or environmental source was identified. However, 4 (67%) of the 6 patients had known exposure to lizards: 3 water dragons (*Physignathus cocincinus*, Figure) and 1 bearded dragon (*Pogona* sp.). Of these 4 patients, 3 had >1 lizard in their own household as pets; the other patient was exposed to a lizard when visiting a family member. The 2 patients who did not recall lizard exposure might represent patients with background cases unrelated to lizards. Single cultures of the 2 lizards available for testing in February 2006 did not yield *S.* Kingabwa, which could mean that they did not carry this rare *Salmonella* serotype. However, this does not exclude lizards as the source of these illnesses because lizards intermittently shed salmonellae (*4*).

The lizards had been purchased from local pet shops and a traveling reptile show. Shipments of reptiles were mixed together at points of sale, and numerous distributors and importers were used, so determining the origin of individual reptiles was not feasible. However, water dragons and bearded dragons are imported into the United States from Asia and Australia and are rarely bred domestically.