References

1. Pokharel BM, Koirala J, Dahal RK, Mishra SK, Khadga PK, Tuladhar NR. Multidrug-resistant and extended-spectrum β-lactamase (ESBL)-producing Salmonella enterica (serotypes Typhi and Paratyphi A) from blood isolates in Nepal: surveillance of resistance and a search for newer alternatives. Int J Infect Dis. 2006;10:434–8. DOI: 10.1016/j. ijid.2006.07.001

2. Gröbner S, Linke D, Schütz W, Fladerer C, Madlung J, Autenrieth IB, et al. Emergence of carbapenem-non-susceptible extended-spectrum β-lactamase (ESBL)-producing Klebsiella pneumoniae isolates at the university hospital of Tübingen, Germany. J Med Microbiol. 2009;58:912–22.

3. Jacoby GA, Walsh KE, Mills DM, Walker VJ, Oh H, Robicsek A, et al. qnrB, another plasmid-mediated gene for quinolone resistance. Antimicrob Agents Chemother. 1999;43:2131–7.

4. Giraud E, Brisabois A, Martel JL, Chaslus-Dancla E. Comparative studies of mutations in animal isolates and experimental in vitro- and in vivo-selected mutants of Salmonella spp. suggest a counterselection of highly fluoroquinolone-resistant strains in the field. Antimicrob Agents Chemother. 1999;43:2131–7.

5. Carattoli A, Miriagou V, Bertini A, Loli C, Colinon C, Villa L, et al. Replicon typing of plasmids encoding resistance to newer beta-lactams. Emerg Infect Dis. 2008;14:1957–9. DOI: 10.3201/eid1412.080494

6. Pokharel BM, Koirala J, Dahal RK, Mishra SK, Khadga PK, Tuladhar NR. Multidrug-resistant and extended-spectrum β-lactamase (ESBL)-producing Salmonella enterica (serotypes Typhi and Paratyphi A) from blood isolates in Nepal: surveillance of resistance and a search for newer alternatives. Int J Infect Dis. 2006;10:434–8. DOI: 10.1016/j. ijid.2006.07.001

7. Gröbner S, Linke D, Schütz W, Fladerer C, Madlung J, Autenrieth IB, et al. Emergence of carbapenem-non-susceptible extended-spectrum β-lactamase (ESBL)-producing Klebsiella pneumoniae isolates at the university hospital of Tübingen, Germany. J Med Microbiol. 2009;58:912–22.

8. Jacoby GA, Walsh KE, Mills DM, Walker VJ, Oh H, Robicsek A, et al. qnrB, another plasmid-mediated gene for quinolone resistance. Antimicrob Agents Chemother. 1999;43:2131–7.

9. Giraud E, Brisabois A, Martel JL, Chaslus-Dancla E. Comparative studies of mutations in animal isolates and experimental in vitro- and in vivo-selected mutants of Salmonella spp. suggest a counterselection of highly fluoroquinolone-resistant strains in the field. Antimicrob Agents Chemother. 1999;43:2131–7.

Address for correspondence: Yvonne Pfeifer, Robert Koch Institute, Burgstr. 37, 38855 Wernigerode, Germany; email: pfeifery@rki.de

Gordonia sp.
Bacteremia

To the Editor: In November 2007, a 69-year-old man with fever was hospitalized at the Northern Hospital in Marseilles, France. He also had diabetes, high blood pressure, and alcohol and tobacco addictions. In September 2007, he had received a diagnosis of laryngeal cancer, which required 2 chemotherapy treatments through a central venous catheter (CVC), the second of which he had received 6 days before his November visit. Prostatic cancer, diagnosed 1.5 years earlier, had been treated by radiotherapy. At the time of the November admission, he had leukopenia (1.77 × 10^9 leukocytes/L with 0.49 × 10^9 polymorphonuclear cells/L) and an elevated C-reactive protein level (151 mg/L). The patient was admitted with a preliminary diagnosis of drug-induced febrile granulocytosis; the origin of his fever remained unclear. Blood for culture was first collected from a peripheral vein and on the next day was collected from the CVC. The day after hospital admission, the patient was empirically treated with Rhodococcus spp. in Kuwait. Emerg Infect Dis. 2008;14:1957–9. DOI: 10.3201/ eid1412.080494

The genus Gordonia was first described in 1971, for coryneform bacteria isolated from sputum of patients with pulmonary disease or from soil (1). It is a member of the mycotic acid–containing group consisting of genera Corynebacterium, Dietzia, Gordonia, Mycobacterium, Nocardia, Rhodococcus, and Tsukamurella. The genus has been revised several times by rearrangements with the genera Rhodococcus and Nocardia, and the name Gordonia was changed to Gordonia in 1997. The genus belongs to suborder Corynebacterineae within the order Actinomycetales and currently contains 27 recognized species; only 7 have been described in human disease. Species are identified by molecular analysis.

Gordonia spp. cause a wide spectrum of disease in humans (2–10; Table). Neurologic and vascular infections in immunocompromised and immunocompetent patients have been reported. Cutaneous and respiratory infections, otitis externa, osteitis, and arthritis have reportedly occurred only in immunocompetent patients. Bacteria have most often been isolated from blood samples. Bacteremia has started from underlying disease such as a sequestrated lung (4) or acute cholecystitis (5) or has been related to coronary artery surgery (2) and frequently to CVCs (2,3,6). Catheter removal has been recommended for treatment of
Gordonia spp. infections in children (6), but the recommendation varied for adults. Six cases of infection in children have been described (6), appearing as bacteremia, ventriculitis, and brain abscess.

Microbiologic diagnosis of Gordonia spp. remains difficult. Biochemical profiles can lead to incorrect identification of isolates as Rhodococcus spp. (2,4–6,9) and sometimes Corynebacterium spp. (3) or Nocardia spp. (6). Identification at the genus and species levels is presently obtained by 16S rRNA sequence comparisons.

No recommendation for antimicrobial drug susceptibility testing has been unanimously approved, but these microorganisms seem to be susceptible to many antimicrobial drugs (6). Previous studies suggest a combination of penicillins and aminoglycosides as a suitable therapy for Gordonia-related bacteremia (3). Carbapenem or fluoroquinolone in combination with an aminoglycoside can also be used (6).

Antimicrobial drug susceptibility is similar to that of Rhodococcus spp., for which Gordonia spp. are usually incorrectly identified. However, although vancomycin is often used to treat Rhodococcus spp. infections, in a previous study 11% of Gordonia spp. isolates were resistant (6). Treatment must therefore be evaluated specifically for each patient.

Gordonia spp. are environmental bacteria whose implication in human disease seems to be increasing. Phenotypic identification of bacteria included in this genus is difficult, and they are often poorly identified as Rhodococcus spp. or Corynebacterium spp. Molecular identification of Gordonia spp. by using 16S rRNA gene sequence comparison enables their characterization in human disease because the method is more accurate. The fact that these bacteria are often associated with medical devices highlights their role as nosocomial agents. Gram-positive bacilli must, therefore, not be systematically considered as contaminants, especially if associated with medical devices, and should be thoroughly identified by molecular methods in addition to biochemical tests.

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Aurélie Renvoise,
Jean-Robert Harle, Didier Raoult, and Véronique Roux

Author affiliations: Hôpital de la Timone, Marseille, France (A. Renvoise, D. Raoult, V. Roux); and Hôpital de La Conception, Marseille (J.-R. Harle)

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References

1. Tsukamura M. Proposal of a new genus, Gordona, for slightly acid-fast organisms occurring in sputa of patients with pulmonary disease and in soil. J Gen Microbiol. 1971;68:15–24.
Cross-reactive Antibodies against Avian Influenza Virus A (H5N1)

To the Editor: Intravenous immunoglobulin (IV Ig) is used to treat bacterial and viral infections in patients with primary immunodeficiency disease and those with autoimmune and inflammatory disorders (1). IV Ig contains pooled IgG from >1,000 blood donors and antibodies against various common human pathogens, including influenza virus A.

We tested the efficacy of commercial preparations of IV Ig (50 mg/mL of highly purified immunoglobulin) against homosubtypic influenza viruses A (H1N1 and H3N2) and their cross-reactivity against avian influenza virus A (H5N1). IV Ig preparations (Octagam; Octapharma, Vienna, Austria and Flebogamma; Instituto Grifols, Barcelona, Spain) had hemagglutination inhibition (HI) titers against subtypes H1N1 and H3N2 ranging from 20 to 40. Human Immunoglobulin, pH 4.0, (Harbin Sequel Bio-Engineering Pharmaceutical, Harbin, People’s Republic of China) had lower HI titers against avian influenza viruses (10 for subtype H3N2 and <10 for subtype H1N1). As expected, we did not detect antibodies against hemagglutinin (HA) of subtype H5N1 (A/duck/Germany 1207 H2N3) and observed no effect (NI titer <10). The N3 subtype belongs to avian influenza NA. Thus, antibodies against NA in IV Ig appear to be specific for those circulating human influenza viruses (human N1 and human N2).

Unlike HA and NA, virus matrix 2 ectodomain (M2e) is highly conserved. Its presence on the surface of the viral particle makes it a potential target of antibody response similar to that for HA and NA (5,6). We assessed reactivity of IV Ig preparations against a consensus M2e peptide derived from human influenza viruses of H1, H2, and H3 subtypes (MSLLTEVETPROMEWRGCRNDSSD) and those derived from A/Hong Kong/156/97 H5N1 (MSLLTEVETLRNGCGRNDSSD) and A/Thailand/SP-83/2004 H5N1 (MSLLTEVETPROMEWRGCRNDSSD) by using ELISA (7). Antibody titer was defined as the reciprocal of the highest dilution that had an optical density of 0.5 at 414 nm in our assay.

Results showed considerable variation among IV Ig preparations, caused by M2e peptides derived from different influenza viruses (titer range 88–23,614). Among the 3 preparations, Human Immunoglobulin, pH 4.0, IV Ig showed the highest titers against subtype H1N1 range 258–986) and human N2 (NI titer against subtype H3N2 range 1,309–3,274).

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Enzyme activity of avian N1 (7:1 reassortant; PR8 + NA [A/Vietnam/DT-0361/05 H5N1]) was inhibited by all IV Ig preparations (NI titer range 143–231). These findings support the recent observation of neutralizing antibodies against human N1 in human serum, which could inhibit enzyme activity of avian N1 from subtype H5N1 (3,4). We also tested IV Ig preparations against reverse genetics subtype H5N3 virus in which the N3 NA was derived from H2N3 virus (6:1:1 reassortant; 6 internal genes from PR8 + HA [A/Vietnam/DT-0361/05 H5N1] + NA [A/duck/Germany 1207 H2N3]) and observed no effect (NI titer <10). The N3 subtype belongs to avian influenza NA. Thus, antibodies against NA in IV Ig appear to be specific for those circulating human influenza viruses (human N1 and human N2).

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