



Serologic Evidence of Leptospirosis in Humans, Union of the Comoros, 2011

Yann Gomard, Rahamatou Silai, Géraldine Hoarau, Ketty Bon, Florelle Gonneau, Amina Yssouf, Alain Michault, Koussay Dellagi, Pablo Tortosa

► To cite this version:

Yann Gomard, Rahamatou Silai, Géraldine Hoarau, Ketty Bon, Florelle Gonneau, et al.. Serologic Evidence of Leptospirosis in Humans, Union of the Comoros, 2011. *Emerging Infectious Diseases*, 2014, 20 (4), pp.720-722. 10.3201/eid2004.131207 . hal-01285431

HAL Id: hal-01285431

<https://hal.univ-reunion.fr/hal-01285431>

Submitted on 21 Jun 2018

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

**Julie Haendiges, Marvin Rock,
Robert A. Myers,
Eric W. Brown, Peter Evans,
and Narjol Gonzalez-Escalona**

Author affiliations: Department of Health and Mental Hygiene, Baltimore, Maryland, USA (J. Haendiges, M. Rock, R.A. Myers); and Food and Drug Administration, College Park, Maryland, USA (E.W. Brown, P. Evans, N. Gonzalez-Escalona)

DOI: <http://dx.doi.org/10.3201/eid2004.130818>

References

- González-Escalona N, Cachicas V, Acevedo C, Rioseco ML, Vergara JA, Cabello F, et al. *Vibrio parahaemolyticus* diarrhea, Chile, 1998 and 2004. *Emerg Infect Dis.* 2005;11:129–31. <http://dx.doi.org/10.3201/eid1101.040762>
- González-Escalona N, Martínez-Urtaza J, Romero J, Espejo RT, Jaykus LA, DePaola A. Determination of molecular phylogenetics of *Vibrio parahaemolyticus* strains by multilocus sequence typing. *J Bacteriol.* 2008;190:2831–40. <http://dx.doi.org/10.1128/JB.01808-07>
- Nair GB, Ramamurthy T, Bhattacharya SK, Dutta B, Takeda Y, Sack DA. Global dissemination of *Vibrio parahaemolyticus* serotype O3:K6 and its serovariants. *Clin Microbiol Rev.* 2007;20:39–48. <http://dx.doi.org/10.1128/CMR.00025-06>
- DePaola A, Kaysner CA, Bowers J, Cook DW. Environmental investigations of *Vibrio parahaemolyticus* in oysters after outbreaks in Washington, Texas, and New York (1997 and 1998). *Appl Environ Microbiol.* 2000;66:4649–54. <http://dx.doi.org/10.1128/AEM.66.11.4649-4654.2000>
- Abbott SL, Powers C, Kaysner CA, Takeda Y, Ishibashi M, Joseph SW, et al. Emergence of a restricted bioserovar of *Vibrio parahaemolyticus* as the predominant cause of vibrio-associated gastroenteritis on the West Coast of the United States and Mexico. *J Clin Microbiol.* 1989;27:2891–3.
- Jolley KA, Maiden MC. BIGSdb: scalable analysis of bacterial genome variation at the population level. *BMC Bioinformatics.* 2010;11:595. <http://dx.doi.org/10.1186/1471-2105-11-595>
- Jolley KA, Hill DM, Bratcher HB, Harrison OB, Feavers IM, Parkhill J, et al. Resolution of a meningococcal disease outbreak from whole-genome sequence data with rapid Web-based analysis methods. *J Clin Microbiol.* 2012;50:3046–53. <http://dx.doi.org/10.1128/JCM.01312-12>

- Jolley KA, Maiden MC. Automated extraction of typing information for bacterial pathogens from whole genome sequence data: *Neisseria meningitidis* as an exemplar. *Euro Surveill.* 2013;18:20379.
- Bryant D, Moulton V. Neighbor-net: an agglomerative method for the construction of phylogenetic networks. *Mol Biol Evol.* 2004;21:255–65. <http://dx.doi.org/10.1093/molbev/msh018>
- Makino K, Oshima K, Kurokawa K, Yokoyama K, Uda T, Tagomori K, et al. Genome sequence of *Vibrio parahaemolyticus*: a pathogenic mechanism distinct from that of *V. cholerae*. *Lancet.* 2003;361:743–9. [http://dx.doi.org/10.1016/S0140-6736\(03\)12659-1](http://dx.doi.org/10.1016/S0140-6736(03)12659-1)

Address for correspondence: Narjol Gonzalez-Escalona, Food and Drug Administration, Center for Food and Applied Nutrition, 5100 Paint Branch Pkwy, College Park, MD 20740, USA; email: narjol.gonzalez-escalona@fda.hhs.gov

Serologic Evidence of Leptospirosis in Humans, Union of the Comoros, 2011

To the Editor: Leptospirosis is a worldwide bacterial zoonosis caused by infection with pathogenic *Leptospira* spp. (Spirochaetales, Leptospiraceae). Most mammals can be infected, but rats are considered the main reservoir, maintaining *Leptospira* spirochetes in the lumen of renal tubules and contaminating the environment with bacteria-infected urine. Transmission to humans is accidental, occurring through contact with animal secretions or with contaminated environmental materials.

In temperate countries, human leptospirosis is a sporadic disease; incidence is much higher in the tropics because climate and environmental conditions are conducive to the survival

of bacteria, resulting in increased exposure of humans to leptospirosis-causing pathogens (1). Among islands in the southwestern Indian Ocean, human leptospirosis is endemic to Mayotte, France, and La Réunion (2–4) and to the Seychelles, where the incidence of leptospirosis is one of the highest worldwide (5). Leptospirosis is poorly documented in other islands in the region, including Mauritius, Madagascar, and the Union of the Comoros (2,6–8). Whether the scant documentation indicates underdiagnosis or reflects local epidemiologic specificities is unknown. To improve knowledge of *Leptospira* infection in the region, we conducted a study in the Union of the Comoros to serologically assess the presence or absence of leptospirosis in humans. The Union of the Comoros consists of 3 islands: Grande-Comore, Mohéli, and Anjouan. Together with a fourth, southern island, Mayotte, these islands form the Comoros Archipelago.

For feasibility reasons, we used excess serum samples. Seventy-six samples were from healthy volunteers who gave informed consent; 318 clinical blood samples from patients had been obtained by private laboratories and by the surveillance laboratory of the National Malaria Control Programme (PNLP) during August 1–October 8, 2011. The Ministère de la Santé, de la Solidarité et de la Promotion du Genre of the Union of the Comoros, authorized the serologic investigation (authorization no. 1175/MSSPG/DNS).

We used the microscopic agglutination test (MAT) to test serum samples; the MAT was based on a panel of 15 *Leptospira* strains, enabling the screening of all recently reported serogroups for human and animal cases on neighboring Mayotte (2,4,9). A list of the tested strains follows, shown as *Genus species* Serogroup/Serovar (type strain): *L. borgpetersenii* Ballum/Castellonis (Castellon 3), *L. borgpetersenii* Sejroe/Hardjovovis (Sponselee), *L. borgpetersenii* Sejroe/Sejroe (M 84),

L. borgpetersenii Tarassovi/Tarassovi (Perepelicin), *L. interrogans* Australis/Australis (Ballico), *L. interrogans* Autumnalis/Autumnalis (Akiyami A), *L. interrogans* Bataviae/Bataviae (Van Tienen), *L. interrogans* Canicola/Canicola (Hond Utrecht IV), *L. interrogans* Hebdomadis/Hebdomadis (Hebdomadis), *L. interrogans* Icterohaemorrhagiae/Copenhageni (Wijnberg), *L. interrogans* Pyrogenes/Pyrogenes (Salinem), *L. kirschneri* Cynopteri/Cynopteri (3522C), *L. kirschneri* Grippotyphosa/Grippotyphosa (Moskva V), *L. kirschneri* Mini/Undetermined serovar (200803703) (9), *L. noguchii* Panama/Panama (CZ214K). Each serum sample was tested at dilutions ranging from 1:50 to 1:3,200 and considered positive when the MAT titer was ≥ 100 .

Our serologic findings showed evidence of *Leptospira* infection in humans on the 3 islands of the Union

of the Comoros (MAT titers 100–1,600, geometric mean titer [GMT] 194). The positivity rate was 10.3% (95% CI 4.8–15.9) for samples from Mohéli, 4.2% (95% CI 1.4–7.0) for samples from Grande-Comore, and 3.4% (95% CI 0.1–6.7) for samples from Anjouan; no significant difference was found between islands or by the age or sex of residents ($p > 0.05$, Fisher exact test). *Leptospira* infection was more prevalent and MAT titers were higher among serum samples from the patient group than the healthy donor group (20 positive samples/318 total vs. 3 positive samples/76 total; GMT 207 vs. GMT 126), but the difference was not significant ($p > 0.05$, Fisher exact test). In 78% of seropositive serum samples, antibodies reacted with serogroups Australis, Bataviae, Grippotyphosa, Panama, Pomona, Pyrogenes, Mini, and/or Sejroe.

MAT titers > 100 , which are suggestive of more specific antibodies to *Leptospira*, were observed for all serogroups except Australis and Sejroe. Pyrogenes serogroup was identified in one third of positive samples from Mohéli and was associated with the highest agglutination titers (Figure).

Our data indicate that *Leptospira* infections do occur in humans in the Union of the Comoros; this finding is consistent with those in studies reporting leptospirosis in persons returning from travel in the Union of the Comoros (2,8) and with the detection of pathogenic *Leptospira* spp. in bats sampled on these islands (10). The human leptospirosis-related serologic findings in Union of Comoros are most comparable to those from neighboring Mayotte, where leptospirosis is mainly caused by serogroups Mini/Sejroe/Hebdomadis complex, Pyrogenes,

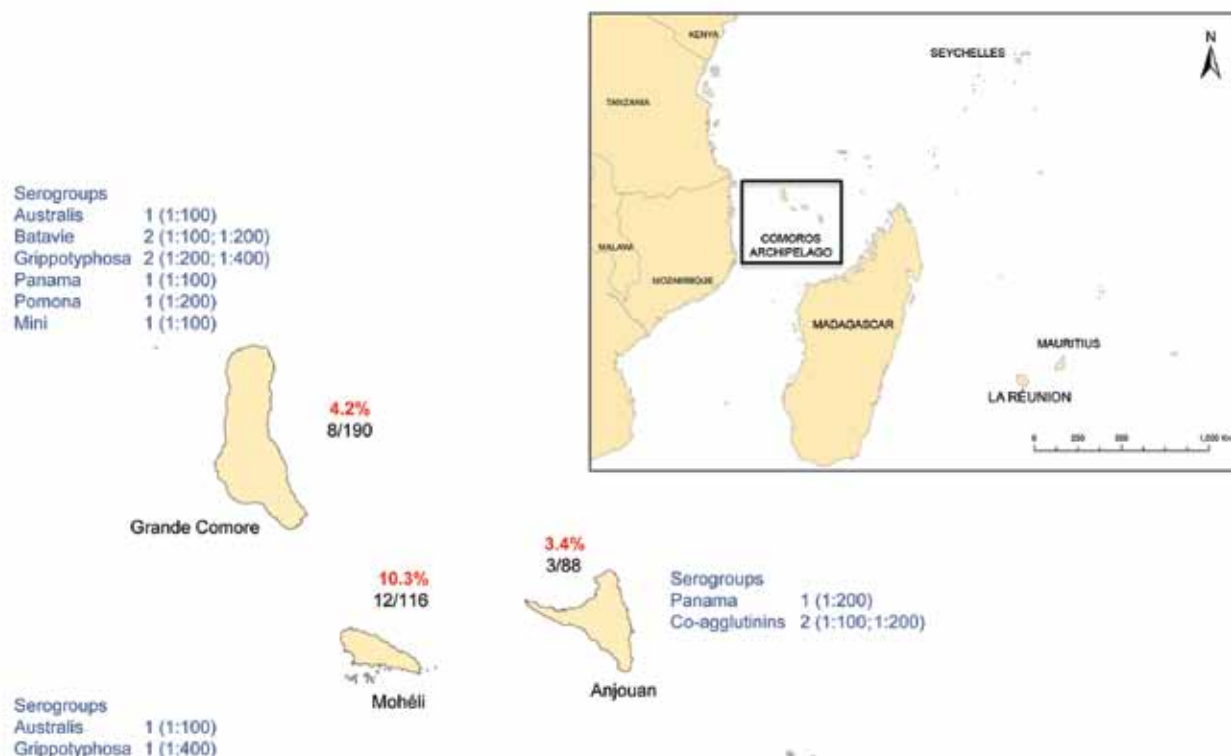


Figure. Microagglutination test results, showing serologic evidence of leptospirosis in humans, Union of the Comoros, 2011. The percentage of positive cases is shown for each island; the number below the percentage indicates the number of positive serum samples/total number tested. The serogroups identified on each island are shown; numbers represent the number of positive serum samples and, in parentheses, the number of corresponding titers. When agglutination was observed with > 1 serogroup, the serogroup with a titer difference ≥ 2 relative to other serogroups was considered to be the infecting serogroup; when no serogroup had a titer difference ≥ 2 relative to other serogroups, coagglutinins were considered to be present in the serum sample. Data for Mayotte Island are from previous studies (2,4).

Grippotyphosa, and Pomona and where serogroup Icterohaemorrhagiae is not detectable (2). These findings contrast with human leptospirosis findings from La Réunion and the Seychelles, where the Icterohaemorrhagiae serogroup is most common (3).

Our MAT-derived data cannot discriminate between recent and past *Leptospira* infections, nor can these data be used to determine the severity of the disease in the Union of the Comoros. Nonetheless, the data strongly support the presence of human leptospirosis on the 3 islands of the Union of the Comoros and emphasize the need for a proper diagnosis to ascertain the number of leptospirosis cases among the acute febrile illnesses in this country.

Acknowledgments

We thank Lisa Cavalerie and Marina Béral for their help with statistical analysis and with preparing the figure.

This work was supported by European Regional Development Funds ERDF-POCT; Réunion, *LeptOI* project.

**Yann Gomard,
Rahamatou Silai,
Géraldine Hoarau, Ketty Bon,
Florelle Gonneau,
Amina Yssouf, Alain Michault,
Koussay Dellagi,
and Pablo Tortosa**

Author affiliations: Centre de Recherche et de Veille sur les Maladies Emergentes dans l'Océan Indien (CRVOI), Ste. Clotilde, La Réunion, France (Y. Gomard, K. Dellagi, P. Tortosa); Programme National de Lutte contre le Paludisme (PNLP), Moroni, Comoros (R. Silai, A. Yssouf); Centre Hospitalier Universitaire, St. Pierre, La Réunion (G. Hoarau, K. Bon, F. Gonneau, A. Michault); Université de La Réunion, Ste. Clotilde (Y. Gomard, P. Tortosa); Unité de Recherche sur les Maladies Infectieuses et Tropicales Emergentes, Marseille, France (A. Yssouf); and Institut de Recherche pour le Développement, Ste Clotilde (K. Dellagi)

DOI: <http://dx.doi.org/10.3201/eid2004.131207>

References

1. Levett PN. Leptospirosis. Clin Microbiol Rev. 2001;14:296–326. <http://dx.doi.org/10.1128/CMR.14.2.296-326.2001>
2. Bourhy P, Collet L, Lernout T, Zinini F, Hartskeerl RA, van der Linden H, et al. Human *Leptospira* isolates circulating in Mayotte (Indian Ocean) have unique serological and molecular features. J Clin Microbiol. 2012;50:307–11. <http://dx.doi.org/10.1128/JCM.05931-11>
3. Picardeau M. Diagnosis and epidemiology of leptospirosis. Med Mal Infect. 2013;43:1–9. <http://dx.doi.org/10.1016/j.medmal.2012.11.005>
4. Bourhy P, Collet L, Clément S, Huerre M, Ave P, Giry C, et al. Isolation and characterization of new *Leptospira* genotypes from patients in Mayotte (Indian Ocean). PLoS Negl Trop Dis. 2010;4:e724. <http://dx.doi.org/10.1371/journal.pntd.0000724>
5. Pappas G, Papadimitriou P, Siozopoulou V, Christou L, Akritidis N. The globalization of leptospirosis: worldwide incidence trends. Int J Infect Dis. 2008;12:351–7. <http://dx.doi.org/10.1016/j.ijid.2007.09.011>
6. Simon F, Morand G, Roche C, Coton T, Kraemer P, Fournier P-E, et al. Leptospirosis in a French traveler returning from Mauritius. J Travel Med. 2012;19:69–71. <http://dx.doi.org/10.1111/j.1708-8305.2011.00573.x>
7. Rahelinirina S, Léon A, Harstskeerl RA, Sertour N, Ahmed A, Raharimanana C, et al. First isolation and direct evidence for the existence of large small-mammal reservoirs of *Leptospira* sp. in Madagascar. PLoS ONE. 2010;5:e14111. <http://dx.doi.org/10.1371/journal.pone.0014111>
8. Socolovschi C, Angelakis E, Renvoisé A, Fournier P-E, Marié JL, Davoust B, et al. Strikes, flooding, rats, and leptospirosis in Marseille, France. Int J Infect Dis. 2011;15:e710–5. <http://dx.doi.org/10.1016/j.ijid.2011.05.017>
9. Desvars A, Naze F, Voure'h G, Cardinale E, Picardeau M, Michault A, et al. Similarities in *Leptospira* serogroup and species distribution in animals and humans in the Indian Ocean island of Mayotte. Am J Trop Med Hyg. 2012;87:134–40. <http://dx.doi.org/10.4269/ajtmh.2012.12-0102>
10. Lagadec E, Gomard Y, Guernier V, Dietrich M, Pascalis H, Temmam S, et al. Pathogenic *Leptospira* spp. in bats, Madagascar and Union of the Comoros. Emerg Infect Dis. 2012;18:1696–8. <http://dx.doi.org/10.3201/eid1810.111898>

Address for correspondence: Pablo Tortosa, CRVOI, Plateforme de recherche CYROI, 2 rue Maxime Rivière, 97490 Ste Clotilde, France; email: pablo.tortosa@univ-reunion.fr

Nosocomial Drug-Resistant Bacteremia in 2 Cohorts with Cryptococcal Meningitis, Africa

To the Editor: Cryptococcal meningitis is the second leading cause of AIDS-related deaths in Africa. The prolonged hospitalization necessary for optimal management may predispose severely immunocompromised persons to hospital-acquired infections. Limited data are available for sub-Saharan Africa regarding multidrug-resistant infections (1,2). We hypothesized that bacteremia was a major cause of death.

We reviewed bacteremia episodes in cryptococcal meningitis cohorts in Kampala, Uganda (n = 115 episodes) and Cape Town, South Africa (n = 72) during November 2010–April 2013. Data were obtained from the prospective cryptococcal optimal antiretroviral therapy timing trial (www.clinicaltrials.gov/NCT01075152), a randomized strategy trial assessing optimal antiretroviral therapy timing (n = 142) and another prospective observational cohort in Cape Town (n = 45).

We enrolled HIV-infected adults who had a first episode of cryptococcal meningitis diagnosed by cerebrospinal fluid culture or cryptococcal antigen testing. Standardized treatment was in accordance with World Health Organization (WHO) guidelines: amphotericin deoxycholate, 0.7–1.0 mg/kg/d for 14 days, and fluconazole, 800 mg/d, requiring a minimum 14-day hospitalization (3). Each person provided written informed consent. Institutional review board approval was obtained.

Blood cultures were obtained in accordance with physician discretion, typically with new onset fever (>38°C) unrelated to amphotericin. Two aerobic blood cultures were obtained from 1 peripheral site and not