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BOLLETTINO BIBLIOGRAFICO

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Ribeiro Júnior J.C., Alexandrino B., Fritzen Torres Tomazi J., Nino De Souza Lima B., Almeida K.S., Ribeiro J., Garcia J.L., Pretto-Giordano Garcia L., Fernandes Alfieri A., da Costa, L.B.S.B., Alfieri Amauri A.

Serological profile of infectious bovine rhinotracheitis, bovine viral diarrhea, leptospirosis, toxoplasmosis, and neosporosis in beef cattle herds in Tocantins, Northern Brazil

(2026) Veterinary Research Communications, 50 (1), art. no. 48

DOI: 10.1007/s11259-025-10989-1

ABSTRACT: Monitoring the health of cattle herds is essential for establishing prophylactic measures and reducing their impact on the production chain, especially in regions where beef cattle form the economic base. This study aimed to determine the serological profile of infectious bovine rhinotracheitis (IBR), bovine viral diarrhea (BVD), leptospirosis, toxoplasmosis, and neosporosis in beef cattle slaughtered in a federally inspected slaughterhouse in the state of Tocantins, northern Brazil. A total of 614 serum samples from 70 herds were evaluated for the presence of antibodies to Bovine alphaherpesvirus-1 and Bovine viral diarrhea virus by virus neutralization test, 12 serovars of Leptospira spp. by microscopic agglutination test, and to Toxoplasma gondii and Neospora caninum by indirect immunofluorescence reaction. The rates of seropositive animals for IBR, BVD, leptospirosis, toxoplasmosis, and neosporosis were 90.4, 50.8, 63.2, 6.2, and 7.3%, respectively. For herds, 100% had at least one animal serum positive for IBR and leptospirosis. Considering the seropositive rates for the five infectious diseases observed in slaughtered cattle, the number of beef cattle in Tocantins, and the intrinsic conditions of the etiological agents being by regional seasonality, it is essential to implement or improve animal health surveillance, prevention, and biosecurity programs to ensure better productivity and economic sustainability of beef cattle herds in the state.

LANGUAGE OF ORIGINAL DOCUMENT: English

Maaskant A., Morel M., Jean S.M., Koo B.-S., Noor S., da Silva Cavalcanti Pereira L.C., Chipangura, J.K., Vercammen F., Nederlof R.A., Bakker, J.

A guidance for diagnosis, control measures, and surveillance of leptospirosis in non-human primates from a veterinary perspective in a one-health approach

(2025) Journal of Medical Primatology, 54 (6), art. no. e70047

DOI: 10.1111/jmp.70047

ABSTRACT: Leptospirosis is an emerging zoonotic disease caused by pathogenic Leptospira spp., affecting a wide range of domestic and wild mammals including nonhuman primates (NHPs). Despite rising incidence rates in both NHPs and humans, there is a lack of comprehensive resources addressing leptospirosis in NHPs from a veterinary perspective in a One Health approach. The close phylogenetic relationship between NHPs, humans and the similarities in disease progression may reveal valuable insights into the pathophysiology, diagnosis, treatment, control measures, and surveillance of leptospirosis. This review synthesizes existing literature on leptospirosis in NHPs, focusing on diagnosis, control measures, and surveillance. It offers insights into the prevalence among NHPs, environmental and civilization factors affecting Leptospira spp. dynamics, and recommendations for the diagnosis, management, and monitoring of leptospirosis. The findings highlight the need for coordinated research efforts and integrated surveillance systems to reduce leptospirosis risk in NHPs.

LANGUAGE OF ORIGINAL DOCUMENT: English

Sánchez-Lerma L., Bernal Otalora J.C., Mattar A.S., Máttar S., Ramírez-Mora, M.

The unusual clinical presentation of leptospirosis is masked by Gilbert's syndrome

(2025) Infectio, 29 (4), pp. 269 - 271

DOI: 10.22354/24223794.1259

ABSTRACT: Leptospirosis is a zoonotic disease endemic to tropical regions, with flu-like symptoms that make early diagnosis difficult. This study describes the case of a 23-year-old man with a history of Gilbert's syndrome and mixed anxiety and depressive disorder who presented with headache radiating to the cervical region, jaundice, generalized abdominal pain, nausea, and vertigo. Initially, he was diagnosed with an exacerbation of Gilbert's syndrome; however, after 24 hours, he returned with persistent symptoms. The patient's history revealed that he had been in contact with his sick dog, which died a few days before the first consultation. Laboratory tests suggested acute febrile syndrome, and serological tests confirmed leptospirosis. Treatment with doxycycline was initiated, and the patient gradually improved, with persistent jaundice and hepatomegaly. Jaundice in leptospirosis could guide diagnosis, but Gilbert's syndrome, which causes intermittent jaundice, can mask this sign. Nevertheless, the patient's prognosis was favorable, given the absence of complications and good clinical outcome.

LANGUAGE OF ORIGINAL DOCUMENT: English

Kędzierska-Mieszkowska S., Arent Z.

Alternative sigma factors of RNA polymerase as master regulators in the pathogenic spirochaete *Leptospira interrogans*

(2025) Pathogens, 14 (11), art. no. 1100

DOI: 10.3390/pathogens14111100

ABSTRACT: This review summarizes the current knowledge on the role of alternative σ factors in the highly invasive spirochaete Leptospira interrogans, the causative agent of leptospirosis. This globally distributed zoonosis affects both animals and humans, resulting in substantial public health and economic consequences. Together with the primary σ70, alternative σ factors provide transcriptional flexibility essential for bacterial adaptation to environmental changes and host–pathogen interactions. Comparative genomic analyses have revealed that the L. interrogans genome encodes 14 σ factors, including one housekeeping σ70-like factor and three types of alternative σ factors: σ54, σ28, and 11 predicted extracytoplasmic function (ECF, σ^{E}-type) factors. This review discusses the characteristics of these regulators, with particular emphasis on the poorly understood ECF σ factors and their potential roles in gene regulation, adaptive responses, and pathogenicity.

LANGUAGE OF ORIGINAL DOCUMENT: English

Di Azevedo Nogueira M.I., Lilenbaum, W.

Genetic diversity and clonal expansion of pathogenic Leptospira in Brazil: a multi-host and multi-regional panorama

(2025) Microorganisms, 13 (11), art. no. 2512

DOI: 10.3390/microorganisms13112512

ABSTRACT: Leptospirosis is a globally distributed zoonosis of major public health and veterinary relevance, caused by pathogenic species of the genus Leptospira. Brazil is a hotspot for transmission due to its ecological diversity and complex host–environment interfaces. This study explored the genetic diversity and structure of circulating pathogenic Leptospira spp. in Brazil through a single-locus sequence typing (SLST) analysis based

on the secY gene. A total of 531 sequences were retrieved from GenBank and subjected to phylogenetic and haplotype diversity analyses. Maximum likelihood reconstruction revealed strongly supported clades for seven species, with L. interrogans being the most prevalent and broadly distributed across hosts and regions. This species showed evidence of clonal expansion, with a dominant haplotype (n = 242) shared by humans, domestic animals, and wildlife. In contrast, L. santarosai and L. noguchii exhibited high haplotypic diversity and reticulated network structures, reflecting greater evolutionary variability. The species L. kirschneri and L. borgpetersenii displayed reduced haplotypic variation, the latter mainly associated with cattle, consistent with its host-adapted profile. Host- and biome-based haplotype networks revealed both the broad ecological adaptability of certain lineages and the exclusive presence of haplotypes restricted to specific environments, such as those found in marine mammals from the Atlantic Ocean. Genetic distance analyses confirmed the strong taxonomic resolution of the gene secY, which effectively distinguished closely related species while capturing intraspecific diversity. These findings provide a comprehensive molecular overview of pathogenic Leptospira in Brazil, highlighting ecological connectivity across hosts and biomes, as well as the contrasting evolutionary dynamics among species. Beyond describing genetic patterns, our analyses emphasize evolutionary processes, host–environment connectivity, and the implications for One Health. This integrative framework strengthens the basis for surveillance and control strategies in other endemic regions in the world.
LANGUAGE OF ORIGINAL DOCUMENT: English

Liu Y., Zou T., Lu M., Li P., Xiang T.

Delayed psychiatric sequelae following multifocal central nervous system lesions in leptospirosis: a case report

(2025) IDCases, 42, art. no. e02435

DOI: 10.1016/j.idcr.2025.e02435

ABSTRACT: Leptospirosis is a zoonotic infectious disease that can involve multiple organ systems. Neurological involvement is uncommon, and long-term neuropsychiatric sequelae have rarely been described. We report the case of a previously healthy adult who developed acute leptospiral infection complicated by multifocal central nervous system (CNS) lesions. The patient presented with fever, convulsions, altered mental status. Chest computed tomography (CT) scan revealed diffuse ground-glass opacities and patchy consolidations in both lungs. Brain magnetic resonance (MRI) demonstrated multifocal CNS lesions. Cerebrospinal fluid Metagenomic Next-generation Sequencing (mNGS) confirmed leptospiral infection. The patient received appropriate antimicrobial therapy and recovered fully, with follow-up imaging showing resolution of cortical lesions. Three years later, the patient developed new-onset psychiatric symptoms, including delusions, hallucinations, or personality changes, without evidence of recurrent infection or other organic causes. This case highlights that leptospiral infection may cause multifocal CNS lesions and lead to delayed psychiatric sequelae years after apparent recovery.
LANGUAGE OF ORIGINAL DOCUMENT: English

Cardoso T.L., Hartwig D.D.

Recombinant chimeric proteins offer new hope to control of leptospirosis

(2026) Vaccine, 70, art. no. 128012

DOI: 10.1016/j.vaccine.2025.128012

ABSTRACT: Leptospirosis is an emerging zoonotic disease that causes over a million human cases and numerous fatalities annually, imposing substantial public health, economic, and veterinary burdens worldwide.

Despite its impact, control strategies remain limited, as commercial bacterin vaccines offer only short-term, serovar-specific protection. The extensive genetic and antigenic diversity of Leptospira species presents a major challenge to the development of broadly protective vaccines. In response, several alternative strategies have been explored, including DNA vaccines, viral-vectored platforms and multi-epitope recombinant chimeric proteins. Among these, chimeric constructs have emerged as promising candidates due to their ability to combine conserved immunogenic regions from multiple antigens, potentially eliciting broader and more effective immune responses. Advances in immunoinformatics, reverse vaccinology and structural modeling have enabled the rational design of these constructs, allowing for the identification of B- and T-cell epitopes with high antigenic potential and wide population coverage. This mini-review provides an overview of recent progress in the development of innovative vaccine strategies against leptospirosis, with particular focus on recombinant chimeric proteins. We discuss the advantages and limitations, highlighting their potential to enhance cross-protection and contribute to more effective control of leptospirosis.
LANGUAGE OF ORIGINAL DOCUMENT: English

Santi M., Marina R., Astuti E.P., Yuliasih Y., Fuadzy H., Hakim L., Dhewantara P.W.

Molecular detection of pathogenic Leptospira in rodents: a zoonotic threat in Bogor District, Indonesia

(2025) BIO Web of Conferences, 193, art. no. 00033

DOI: 10.1051/bioconf/202519300033

ABSTRACT: Leptospirosis is a neglected zoonotic disease with high mortality rates, particularly in tropical regions. Rodents are the primary reservoirs of pathogens and play a critical role in transmitting the pathogens to humans. This study aimed to assess rodent population density and detect pathogenic Leptospira in rodents captured in three villages in Bogor District. An observational cross-sectional study was conducted in Kota Batu, Mekar Jaya, and Parakan villages in September 2021. Rodents were captured using a single trap method over 15-16 hours 150 traps placed across the three villages. Captured rodents were identified by species, and their kidneys were dissected for molecular examination. Pathogenic Leptospira were detected using the ii-PCR method. A total of 88 rodents were captured, with Rattus tanezumi (54.5%) being the dominant species, followed by Bandicota indica (21.6%), Rattus norvegicus (20.5%), and Mus musculus (3.4%). Pathogenic Leptospira was detected in 22% of rodent kidneys, with Bandicota indica exhibited the highestinfection rate (68.4%). These findings underscore the need for improved rodent population control and increased public awareness of leptospirosis risks. Further studies are recommended to map the distribution and risk factors of Leptospira transmission in this region.
LANGUAGE OF ORIGINAL DOCUMENT: English

Le Turnier P., Oberlis M., Lavergne A., Epelboin L., Picardeau M.

Leptospirosis seroprevalence and exposure factors in three informal settlements of French Guiana: an opportunistic survey

(2025) PLOS Neglected Tropical Diseases, 19 (11), pp. e0013764

DOI: 10.1371/journal.pntd.0013764

ABSTRACT: BACKGROUND: Leptospirosis is a zoonotic disease of increasing importance in French Guiana. It particularly affects subjects living in precarious conditions. We aimed to determine the seroprevalence and the risk of exposure to leptospirosis among inhabitants of three informal settlements in French Guiana. METHODS: A serological investigation was conducted in 2022 in three informal settlements in the area of

Cayenne, the main city of French Guiana. Leptospirosis exposure factors were assessed in volunteers aged > 15 through a standardized questionnaire. Leptospirosis seroprevalence was evaluated with Microscopic Agglutination Test (MAT) using 17 pathogenic Leptospira antigens with a reactivity threshold of 1:100. RESULTS: In 266 participants, median [IQR] age was 42 [34-52] and male to female sex ratio was 0.9. Most participants were migrants (96%), mainly from Haiti (83%), and lived in the study area for at least 2 years (82%). Household rodent exposure (89%) and use of other water sources than collective standpoint (92%) were common. An at-risk occupation was reported for 68% of working participants. Leptospirosis seroprevalence was 7.5% (95% CI [4.7-11.4]) with Ballum and Icterohaemorrhagiae as the main serogroups. Foot skin exposure in wet environments was associated with reactive serum (OR 7.6, 95% CI [1.1 - 326.7]). CONCLUSION: Despite a high theoretical risk of leptospirosis exposure among informal settlements inhabitants, only a few participants were seroreactive for Leptospira. This may suggest that despite at-risk exposures the effective transmission of leptospirosis remains limited within the study area. Broader serological surveys and environmental studies should clarify the areas of at-risk leptospirosis transmission in French Guiana.
LANGUAGE OF ORIGINAL DOCUMENT: English

Schmitt K.G., Bergmann M., van der Linden H., Ahmed A.A., Straubinger R.K., Zablotski Y., Hartmann K.
Five Leptospira spp. antibody point-of-care tests in healthy dogs reveal different results after revaccination against leptospirosis
(2025) Microorganisms, 13 (11), art. no. 2604
DOI: 10.3390/microorganisms13112604
ABSTRACT: The microscopic agglutination test (MAT) is the diagnostic standard for canine leptospirosis. However, it is a time-consuming process and does not differentiate between infection- and vaccine-induced antibodies. Canine Leptospira spp.-specific antibody point-of-care (POC) tests provide the rapid detection of immunoglobulin M (IgM) and/or G (IgG). IgM POC tests are considered to become negative more rapidly after vaccination, making them more effective at diagnosing leptospirosis in not-recently vaccinated dogs. This study analysed 582 serum samples of 97 healthy dogs using five different POC tests and the MAT before vaccination and 2, 4, 12, 26, and 52 weeks afterwards. Among the POC tests, three detected IgM antibodies, one detected IgG antibodies, and one detected both IgM and IgG. The results were analysed using mixed-effects logistic regression. Before vaccination, only 2/291 IgM tests were positive (0.7%), compared to 45/194 IgG tests (23.2%). All the POC tests became positive after vaccination, but IgM positivity occurred significantly less frequently (59/1746), especially >4 weeks post-vaccination (7/59 positive results), with 94.5–99.6% specificity compared to 41.4–77.8% in IgG tests. These findings support the use of IgM POC tests in vaccinated dogs, while IgG POC tests are more difficult to interpret.
LANGUAGE OF ORIGINAL DOCUMENT: English

Ding Y., Zhang S., Zhang W., Sun S., Xie X., Cao Y.
Seroprevalence and molecular epidemiology of Leptospira spp. infecting dogs in the Yangtze River Region of China
(2025) Transboundary and Emerging Diseases, 2025 (1), art. no. 5728490
DOI: 10.1155/tbed/5728490

ABSTRACT: Leptospirosis, a globally re-emerging zoonosis caused by pathogenic Leptospira species, poses escalating public health challenges in rapidly urbanizing regions. Canines, as significant reservoir hosts, are increasingly regarded as effective sentinels for human leptospirosis risk. This study assessed the seroprevalence of pathogenic Leptospira in dogs across multiple provinces and regions along the Yangtze River in China. From 2021 to 2023, a total of 1517 canine serum samples were collected from Shanghai, Jiangsu, Anhui, Jiangxi, Hunan, Hubei, Chongqing, Sichuan, and Yunnan. In addition, a tissue sample was obtained from an infected dog, leading to the successful isolation and culture of one Leptospira strain. Microscopic agglutination test (MAT) results indicated an overall seroprevalence of 46.41% (704/1517), predominantly involving L. interrogans serogroups Canicola (72.73%, 512/704) and Icterohaemorrhagiae (28.68%, 202/704), followed by Ballum (18.04%, 127/704) and Australis (17.90%, 126/704). Organ examination and histopathological analysis identified severe pulmonary hemorrhage induced by the isolated strain as the primary cause of canine mortality. Whole-genome sequencing (WGS) and multilocus sequence typing (MLST) based on seven housekeeping genes classified the isolate as L. interrogans serovar Australis, sequence type (ST) ST93. These findings reveal a high seroprevalence of pathogenic Leptospira in dogs within the Yangtze River region, consistent with the distribution of locally prevalent serogroups, and underscore the potential public health risk posed by this zoonotic pathogen in the area.
LANGUAGE OF ORIGINAL DOCUMENT: English

Yang L.W., Tang X.G., Xiong B., Zhang Y.

A case report of leptospirosis complicated by severe pulmonary hemorrhage treated with venovenous extracorporeal membrane oxygenation

(2025) Frontiers in Medicine, 12, art. no. 1696005
DOI: 10.3389/fmed.2025.1696005
ABSTRACT: Leptospirosis is a zoonotic disease with diverse clinical manifestations, and its severe form can lead to life-threatening complications such as pulmonary hemorrhage. We present a novel case of a 57-year-old woman with leptospirosis who developed severe pulmonary hemorrhage and acute respiratory distress syndrome (ARDS) and was successfully managed with early venovenous extracorporeal membrane oxygenation (VV-ECMO), minimal anticoagulation, and lymphoplasmacyte exchange (LPE). This case highlights the importance of early ECMO initiation, individualized anticoagulation, and immunomodulatory therapy in improving outcomes for patients with leptospiral pulmonary hemorrhage syndrome (LPHS), a condition with mortality exceeding 50%. To our knowledge, this is the first reported case combining VV-ECMO with LPE in LPHS, offering a new therapeutic paradigm for critically ill patients at the intersection of infection and autoimmunity.
LANGUAGE OF ORIGINAL DOCUMENT: English

Bonilla-Sánchez C.A., Rivera-Tenorio A.D., Álvarez A., Cortés J., Faccini Á.A.

A case of disseminated intravascular coagulation by leptospirosis during the ongoing yellow fever outbreak in Colombia

(2026) New Microbes and New Infections, 69, art. no. 101684
DOI: 10.1016/j.nmni.2025.101684
LANGUAGE OF ORIGINAL DOCUMENT: English

Andrade-Silveira E., Segura-Correa J.C., Ortega-Pacheco A., Cárdenas-Marrufo M.F., Gutiérrez-Blanco E., Jiménez-Coello M.

Seroprevalence of pathogenic *Leptospira* in domiciled and stray dogs from subtropical Mexico

(2026) Veterinary Research Communications, 50 (1), art. no. 67

DOI: 10.1007/s11259-025-11016-z

ABSTRACT: Leptospirosis is a zoonotic bacterial disease of public health concern. Dogs are hosts that can carry and eliminate diverse serovars of Leptospira for long periods. Available vaccines can protect against only two to four serovars of Leptospira, and some additional virulent serovars not included in the vaccines may circulate in the environment. The objective of this study was to estimate the seroprevalence of circulating Leptospiras in owned vaccinated, owned unvaccinated, and stray dogs, and to assess the risk factors associated with the presence of antibodies. Owned vaccinated, and owned unvaccinated dogs were selected, which were randomly recruited from different veterinary clinics, and a questionnaire was given to their owners to obtain their background; samples from stray dogs were obtained from the animal control center of the municipality of Merida. The MAT test against 11 serovars was used. A total of 335 samples were obtained, 215 from domiciled dogs and 120 from stray dogs. The seroprevalence was 34.02% (33/97) in vaccinated domiciled dogs, 38.98% (46/118) in nonvaccinated domiciled dogs and 39.16% (47/120) in stray dogs. The main serovars found were Australis, Bratislava, Autumnalis, and Pyrogenes in the three groups of dogs. A high seroprevalence of Leptospira spp. was detected in all groups of evaluated dogs including pathogenic serovars not serovars not contained in the commercial vaccines; since no relevant risk factors were detected all pet and stray dogs are at the same risk to become in contact with pathogenic leptospiras.

LANGUAGE OF ORIGINAL DOCUMENT: English

Boodman C., Çimen C., Gupta N., Bottieau E.

Culture-negative bacteria: a blind spot in bacterial pathogen prioritization

(2026) International Journal of Infectious Diseases, 163, art. no. 108237

DOI: 10.1016/j.ijid.2025.108237

ABSTRACT: Culture-negative bacteria (CNB), including Bartonella spp., Coxiella burnetii, Rickettsia spp., Orientia tsutsugamushi, and Leptospira spp., are frequent yet underrecognized causes of febrile illness in low- and middle-income countries (LMICs). Although these pathogens cause significant morbidity and mortality, they often remain undetected because standard culture techniques fail to identify them, resulting in systematic underdiagnosis. This narrative review examines existing criteria used in infectious disease guidelines for pathogen recognition and prioritization, applying them to CNB to assess how these organisms fit, or fail to fit, within current frameworks. We discuss the diagnostic limitations that impede CNB detection, as well as the cognitive biases that lead clinicians and public health practitioners to overlook these infections. The disproportionate impact of CNB in LMICs, where diagnostic infrastructure is limited and pathogen diversity is high, further fragments epidemiological data and constrains research investment. Collectively, these factors perpetuate the neglect of CNB in clinical practice, public health policy, and global health research agendas.

LANGUAGE OF ORIGINAL DOCUMENT: English

Seguel M., Moeggenberg F., Arakawa N., Pavés H., Balaji S., Maboni G., Müller A., Gottdenker N.L.

Anthropogenic disturbance on island ecosystems promotes inflammation and zoonotic pathogens among invasive rats

(2026) Science of the Total Environment, 1010, art. no. 181089
DOI: 10.1016/j.scitotenv.2025.181089
ABSTRACT: Invasive species and landscape disturbance are major drivers of emerging infectious diseases, particularly in island ecosystems where native wildlife evolved in ecological isolation. However, the mechanisms linking anthropogenic disturbance, host immune function, and pathogen transmission on island systems remain poorly understood. We investigated how small-scale anthropogenic disturbance influences host diet, body condition, immunity, and zoonotic pathogen carriage among invasive black rats (Rattus rattus) on Guafo Island, a remote island in the northern Chilean Patagonia. Using a spatial mosaic of undisturbed and disturbed habitats, we combined field ecology, immunopathology, and molecular diagnostics to assess inflammation and infection risk. Rats from human-altered habitats had access to human food sources and exhibited higher population densities and improved body condition. Although body condition was higher, rats in these human-intervened habitats had increased systemic inflammation and more marked Th2-type inflammation compared to rats in more pristine areas of the island. These immunopathological changes were associated with increased prevalence of Leptospira interrogans and Calodium hepaticum infection. These effects were independent of rat abundance and body condition, suggesting that Th2 immune skewing in rats in disturbed island habitats may independently enhance pathogen shedding. Our findings indicate that even minimal landscape disturbance in an otherwise pristine ecosystem can alter invasive species' immunity and amplify zoonotic risk, highlighting the importance of early intervention and ecological monitoring in remote island systems undergoing human encroachment.
LANGUAGE OF ORIGINAL DOCUMENT: English

Tee Z.H., Forbes Z., Galloway L., Kazi S.S., McLeman L., Mukhopadhya A.

Leptospiral infection overlapping with autoimmune hepatitis: a diagnostic conundrum

(2025) Journal of the Royal College of Physicians of Edinburgh, 55 (4), pp. 295 - 298
DOI: 10.1177/14782715251394936
ABSTRACT: Autoimmune hepatitis (AIH) is characterised by the presence of circulating auto-antibodies, elevated serum globulin, lymphocytic and plasma cell infiltration on liver biopsy, in the absence of markers of viral hepatitis. Management typically involves use of oral or intravenous corticosteroids in combination with immunosuppressants. We report a rare case of a young patient with a background of AIH that failed to respond to such interventions and was diagnosed to have superadded leptospirosis. In this case report, we describe our challenges in localising the aetiology and management for his acute hepatitis. This report highlights the need to recognise alternative diagnosis in acute hepatitis, especially in AIH patients that fail to respond to conventional management.
LANGUAGE OF ORIGINAL DOCUMENT: English

Djafar L., Manyullei S.

Health literacy gaps in leptospirosis prevention: evidence from an analysis of knowledge, attitudes, practices, and perceptions in Limboto Lake, Gorontalo

(2025) Journal of Cultural Analysis and Social Change, 10 (2), pp. 1188 - 1194
DOI: 10.64753/jcasc.v10i2.1750
ABSTRACT: In Indonesia, leptospirosis is a zoonotic disease with rats as the main reservoir that remains a serious public health problem, especially in areas with high prevalence, including Lake Limboto and Gorontalo.

The purpose of this study was to identify the presence of Leptospira in rats and examine the relationship between knowledge, attitudes, practices, and perceptions (KAPP) and health literacy. This study used a cross-sectional design with laboratory examination using PCR on 34 rat samples and a survey of KAP, perceptions, and health literacy among 168 respondents in two villages along Lake Limboto. Analysis of the relationship between variables was performed using the chi-square test. A total of 14 of 34 rat samples (41.2%) were detected positive for Leptospira. The study findings showed a strong correlation between health literacy and perceptions (p=0.002), practices (p=0.023), attitudes (p=0.008), and knowledge (p<0.001). Significant gaps in health literacy are highlighted by these findings, underscoring the need for integrated community-based interventions aligned with the one health paradigm. Reducing the burden of leptospirosis in coastal communities requires increased knowledge, improved risk perception, and encouragement of ongoing preventive measures.
LANGUAGE OF ORIGINAL DOCUMENT: English

Manyullei S., Basir Wisudawan O.B., Sembiring D.Y., Purtanto R.H., Su'udi A.

Hotspots of infection: spatial analysis of rat populations and *Leptospira sp*. in South Sulawesi

(2025) Journal of Cultural Analysis and Social Change, 10 (2), pp. 3438 - 3447
DOI: 10.10.64753/jcasc.v10i2.2126

ABSTRACT: Leptospirosis is a zoonotic disease caused by the bacterium Leptospira sp., primarily transmitted through the urine of infected rodents. The objective of this research is to analyze the spatial distribution of rat populations and to detect the presence of Leptospira spp within these populations in Pitue Village, South Sulawesi. A descriptive observational approach was used to determine rat density and detect Leptospira sp. in captured rodent kidney samples. A total of 200 live traps were set in residential areas, both indoors and outdoors, over three consecutive days using roasted coconut as bait. Polymerase Chain Reaction (PCR) testing was conducted on rat kidney samples at Hasanuddin University Medical Research Center (HUM-RC). Geospatial mapping using Quantum GIS (QGIS) was employed to visualize rat density and Leptospira sp. distribution. The study found a trap success rate of 18.5%, with 37 rats captured, exceeding the national standard of less than 1%. Suncus murinus (62%) was the most frequently trapped species, followed by Rattus tanezumi (16%), Rattus norvegicus (12%), and Rattus argentiventer (5.4%). PCR testing confirmed Leptospira sp. in three rat kidney samples. Spatial analysis revealed clustering of rat presence within a 60-meter buffer zone, indicating high-risk areas for leptospirosis transmission. By identifying areas with high rat density and the occurrence of Leptospira infection, the study seeks to evaluate the potential public health risks posed by leptospirosis, a zoonotic disease transmitted through environmental exposure to contaminated urine from infected rodents. Future research should explore predictive modeling and environmental factors influencing leptospirosis transmission.
LANGUAGE OF ORIGINAL DOCUMENT: English

Imani F., Fattahi E., Khoshbakht R., Fattahi S., Asouri M.

Isolation, molecular detection, and sequence analysis of pathogenic *Leptospira spp*. in paddy field water samples in Amol, Northern Iran

(2025) Avicenna Journal of Clinical Microbiology and Infection, 12 (4), pp. 188 - 194
DOI: 10.34172/ajcmi.3712

ABSTRACT: Background: Leptospirosis constitutes a zoonotic affliction prevalent in tropical and subtropical locales, instigated by the pathogenic strains of Leptospira. The objective of the present study was to isolate and detect Leptospira from water samples sourced from paddy fields located in Amol, northern Iran. Methods: A total of 108 samples were procured from rice fields during the spring and summer of 2023. Cultivation, microscopy, and molecular analyses were employed to accurately identify L. interrogans. Both conventional and real-time polymerase chain reactions (RT-PCR) targeting the lipL32 gene were executed for the detection of L. interrogans. In addition, the sequence analysis of the sucA and gluM genes was performed after PCR. Results: The findings revealed that 6/108 (5.55%) of the samples were culture-positive, with all cases corroborated through both RT-PCR and traditional PCR methods. A simple PCR assay showed positive results for 17/108 (15.74%) water samples. RT-PCR successfully identified 17/108 (15.74%) samples as positive for L. interrogans. The sequence analysis of the sucA gene from the water sample demonstrated high similarity to Leptospira weilii. Eventually, the sequence analysis of the gluM gene from two water samples displayed high similarity to Leptospira borgpetersenii. Conclusion: This investigation highlights the efficacy of synergizing molecular techniques with traditional culture methodologies for the surveillance of Leptospira in areas characterized by an elevated risk. The current research serves as the inaugural report, delineating the emergence of leptospires from rice field samples, alongside the characterization of isolates obtained from culture.
LANGUAGE OF ORIGINAL DOCUMENT: English

Saputra Y.A., Armawan L.V.A., Lisa M., Muharramah D.H., Pratiwi L.D.

The role of hydrometeorological factors in leptospirosis transmission in Central Java, Indonesia

(2025) Journal of Preventive Medicine and Public Health, 58 (6), pp. 553 - 562
DOI: 10.3961/jpmph.25.114
ABSTRACT: Objectives: This study investigates the relationship between hydrometeorological factors and leptospirosis cases in Central Java to elucidate disease spread patterns. Methods: An ecological study design was utilized, incorporating spatial elements by integrating geographic information systems (GIS) with statistical techniques. The analysis included data on temperature, humidity, rainfall, solar radiation, flooding, and monthly leptospirosis cases recorded from 2018 to 2022. Data sources comprised the Ministry of Health of the Republic of Indonesia, the Meteorology, Climatology, and Geophysics Agency, and the Central Java Provincial Water Resources Management Center. The study employed correlation tests, multiple linear regression, and spatial data visualization. Results: Correlation analysis indicated that monthly leptospirosis cases were significantly and positively correlated with minimum temperature (r=0.423; p=0.001), humidity (r=0.589; p<0.001), and rainfall (r=0.413; p=0.001). In contrast, maximum temperature (r=-0.355; p=0.005) and solar radiation (r=-0.431; p=0.001) showed significant negative correlations. Subsequent multiple linear regression showed that higher monthly leptospirosis was associated with higher humidity. Conclusions: The findings offer essential insights for developing a comprehensive, science-based leptospirosis management strategy. A recommended approach is to establish a spatial monitoring system aimed at identifying high-risk areas, especially those with increased humidity and frequent flooding.
LANGUAGE OF ORIGINAL DOCUMENT: English

Sarma A., Phukan H., Devasahayam Arokia Balaya R., Thoduvayil S., Dhandapani G., Christie S.A.D., Prasad, T.S.K., Madanan M.G.

Exoproteome profiling reveals increased secretion of adhesins and proteases by *Leptospira interrogans* to facilitate host colonization and immune modulation

(2025) ACS Omega, 10 (30), pp. 32728 - 32743

DOI: 10.1021/acsomega.4c10983

ABSTRACT: Leptospirosis, a re-emerging zoonotic disease, is challenging human and animal health due to the lack of early and rapid diagnostic tools and effective vaccines. The exoproteome of the pathogen Leptospira interrogans expressed under pathogenic conditions possesses a rational diagnostic significance due to its consistent presence in body fluids. L. interrogans were challenged to conditions simulating infection using physiological temperatures and osmolarity. Using state-of-the-art extraction techniques, efficient enrichment of nonabundant proteins, and high-resolution LC-MS/MS, we identified 1575 exoproteins from both the pathogen surface and culture supernatant. The results indicate a significant upregulation of 155 exoproteins, of which 41 were predicted to have moonlighting properties, 35 were identified as adhesins, and several proteins were components of the type 2 secretion system (T2SS). Additionally, 10 proteins showed extracellular matrix (ECM) binding properties, out of which 4 orthologs were found using the T2SS. The overall characteristics of upregulated proteins show that they can help Leptospira establish infection, invasion, and protection from the host defense, thereby providing new insights into the pathogen to confront the host via an increased energy level, secretion system, and host ECM binding molecules. Furthermore, the study suggests potential candidates for efficient antileptospiral countermeasures.

LANGUAGE OF ORIGINAL DOCUMENT: English

Vargas A.C.S., González N.L., de la Peña-Moctezuma A., Barbosa A.S., Isaac L., Sahagún-Ruiz A.

Culture-attenuated pathogenic *Leptospira* lose the ability to survive complement lytic activity due to decreased C4BP uptake

(2025) Microbes and Infection, art. no. 105589

ABSTRACT: Pathogenic Leptospira spp. evade the complement system by capturing soluble regulators of the alternative, classical, and lectin pathways - such as factor H, C4BP, and vitronectin - via proteins on their surface. By capturing these regulators, Leptospira can disrupt the complement activation cascade, thereby preventing opsonization by C3b/iC3b and lysis by the membrane attack complex (MAC). The ability of low-passage pathogenic Leptospira strains - LOCaS46 (L. interrogans sv Canicola), LOVe30 (L. interrogans sv Icterohaemorrhagiae), and MOCA45 (L. santarosai sv Tarassovi) - to bind C4BP was evaluated and compared to their corresponding culture-attenuated (LOCaS46, LOVe30, and MOCA45) and to the saprophytic Patoc I strain of Leptospira biflexa sv Patoc. Binding to C4BP was assessed by ELISA and confirmed by Western blot, the expression level of the genes for C4BP-binding proteins was evaluated by RT-qPCR, and the survival of the Leptospira spp. strains in normal human serum (NHS) was estimated to assess complement resistance. Results showed that culture attenuated (CA) strains had a lower capacity for binding to C4BP, and surviving to NHS as compared to low-passage (LP) strains. Also, transcription level of the genes for the C4BP-binding proteins LigA, LigB, LcpA, enolase and Lsa23, was lower in the CA strains than in their corresponding LP strains. This suggest that reduction of the ability to capture C4BP in culture attenuated (CA) strains is due at least in part to lower expression of C4BP-binding proteins, affecting the evasion of classical and lectin pathways of the complement system and therefore the capability of survival in NHS.

LANGUAGE OF ORIGINAL DOCUMENT: English

Cukoski S., Brehm T.T., Büttner S., Van Praet J., Dolff S., Eberwei, L., Falces I., Cornely O.A., Wanken M., Müller R.-U., Burst V., Koehler F.C.

Design and set-up of the leptospirosis registry LeptoScope for epidemiology, outbreaks and clinical studies on human leptospirosis

(2025) Frontiers in Public Health, 13, art. no. 1687249

DOI: 10.3389/fpubh.2025.1687249

ABSTRACT: Objective: Human leptospirosis is a widespread zoonosis with endemic appearance in different parts of the world. Despite causing more than 1 million cases, nearly 60.000 deaths and 3 million disability-adjusted life-years per year, leptospirosis remains an underrecognized and neglected disease calling for multinational surveillance and international collaboration. Methods: The leptospirosis registry LeptoScope is a novel project enabling both international and multi-disciplinary research on Leptospira-caused diseases. LeptoScope has an electronic case report form and can be assessed on the General Data Protection Regulation compliant platform clinicalsurveys.net. Due to its modular structure, LeptoScope depicts or hides items according to the documented case (e.g., patients treated in outpatient setting versus patient admitted to the intensive care unit). This ensures rapid, but standardized enrolment of patients even in epidemics. Results: Information collected in LeptoScope include demographics, pre-existing diseases, clinical presentation and measures in addition to outcome. A multinational research team from Germany, Belgium and Spain contributed a pilot cohort of 78 cases with Leptospira-associated diseases to confirm LeptoScope's functionality and practicality. Conclusion: LeptoScope is to our knowledge the first worldwide research platform on public health and clinical studies concerning Leptospira-associated diseases. LeptoScope promotes the needed collaboration at the cross-roads of public health, microbiology, infectious diseases and nephrology for an underrecognized and often neglected disease. Ensuring controlled or uncontrolled level II evidence LeptoScope may improve patient care and may provide evidence for robust treatment recommendations in future.

LANGUAGE OF ORIGINAL DOCUMENT: English

Pereira Dos Santos P.V., Cupello A.P., Correia L.F., Lilenbaum W., Souza-Fabjan, J.M.G.

First detection of *Leptospira spp.* in cumulus-oocyte complexes from naturally infected cows

(2026) Animal Reproduction Science, 285, art. no. 108088

DOI: 10.1016/j.anireprosci.2025.108088

ABSTRACT: Although a few studies have reported Leptospira spp. in cumulus-oocyte complexes (COCs) from experimentally infected cows, it remains unclear whether this bacterium can penetrate COCs in naturally infected animals. This study aimed to detect the presence of Leptospira spp. in COCs from naturally infected cows. Ovaries and uterine body fragments were collected from 40 cows after slaughter. Follicular fluid (FF) and uterine fragments (UF) were screened using conventional PCR (cPCR), and negative results were confirmed by quantitative PCR (qPCR). COCs were immunolabeled using a monoclonal anti-LipL41 antibody, followed by an Alexa Fluor 488-conjugated secondary antibody, and counterstained with propidium iodide. Detection of Leptospira spp. was performed by epifluorescence microscopy. Cows were then classified as positive (POS-FF, POS-UF, or both) or negative (NEG). In POS-FF animals (n = 8), 9.1 COCs/female were recovered, with 51.1 ± 12.7 % showing Leptospira presence (not significant; n.s.). In POS-UF cows (n = 12), 6.6 COCs/female were obtained, and 81.0 ± 5.5 % showed bacterial presence (n.s.). In animals positive for both FF and UF (n = 10), 5.4 COCs/female were collected, with 63.7 ± 12.9 % testing positive (n.s.). In NEG

animals (n = 10), which were both cPCR- and qPCR-negative, 69.3 ± 9.7 % of COCs exhibited bacterial labeling, suggesting a low bacterial load (n.s.). These cows yielded 9.7 ± 3.7 COCs/female (n.s.). Although no difference was observed between the groups, this is the first report demonstrating the presence of Leptospira spp. in COCs from naturally infected cows, highlighting a mechanism contributing to reproductive failure in cattle.
LANGUAGE OF ORIGINAL DOCUMENT: English

Stubbe S.P., Kramer E.M., Büchner S., Jelinek C., Mehl C., Ryll R., Heuser E., Richter D., Hoffmann D., Vasiliunaite E., Buck C.B., Kučinskaite-Kodze I., Gedvilaite A., König P., Haring V.C., Schulze V., Holtfreter S., Kohler C., Eisenberg T., Apfel M.C., Drewes S., Jeske K., Raileanu C., Meinig H., Obiegala A., Pfeffer M., Raafat D., Pöhle D., Ulber C., Silaghi C., Ulrich R.G., Lier, M., Lan, J.

Pathogens in the garden dormouse *Eliomys quercinus*

(2026) European Journal of Wildlife Research, 72 (1), art. no. 4
DOI: 10.1007/s10344-025-02008-0
ABSTRACT: Wild rodents are important reservoirs and vectors of various pathogens, and play a crucial role in the spread of zoonotic pathogens. The garden dormouse (Eliomys quercinus), an arboreal nocturnal rodent species native to Europe, has declined throughout much of its natural range in recent decades. The reason for this ongoing decline is not yet fully understood, but infectious diseases may play a role. This study aimed to review the diversity of pathogens associated with the garden dormouse. For this purpose, a comprehensive review of the existing literature on garden dormouse-associated viruses, bacteria and protozoa was conducted. In parallel, we analysed samples from 294 garden dormice, that were found dead in Germany, for rodent-associated and zoonotic pathogens. The scientific literature currently, comprising 53 references, covers 73 years and primarily addresses Borrelia spp. and Eimeria myoxi. In the literature, a total of eight pathogens have been detected in garden dormice. In our own investigations, we were able to detect four different pathogens as well as antibodies against hepatitis E virus. The most prevalent pathogen found in our study was Staphylococcus aureus (29%, n = 58). Borrelia spielmanii and B. afzelii were found in 5.6% of garden dormice (n = 143) and 22% of the ticks attached to garden dormice (n = 32). This study reports the first documentation of Leptospira spp. in garden dormice, with L. borgpetersenii, serogroup Sejroe, sequence type 197 detected in 2 of 176 animals. Beside these zoonotic pathogens metagenomic sequencing of selected samples revealed representatives of multiple DNA-virus families, including Parvoviridae and Polyomaviridae, most likely without zoonotic potential. There is currently no evidence, either from the literature or from our own investigations, that pathogens play a significant role in the decline of the garden dormouse in Germany.
LANGUAGE OF ORIGINAL DOCUMENT: English

de Oliveira Rodrigues N., Andrade Colares M., Kremer Schmitt F., Moreira Da Luz A., Santos Campos Da Motta B., Kunde San Martins G., Gerber Lehmkuhl A., Vasconcelos Ribeiro A.T., Pizani Cavalcanti M.A., Arancibia Morales P.C., Bohn Oliveira T.L., Dellagostin, O.A.

Whole-genome sequencing as a regulatory tool for quality control of *Leptospira* strains for vaccines and diagnostics

(2026) Vaccine, 71, art. no. 128110
DOI: 10.1016/j.vaccine.2025.128110

ABSTRACT: The maintenance of well-characterized Leptospira seed strains is critical for vaccine production and diagnostic applications. Conventional methods such as the cross-agglutinin absorption test (CAAT), multilocus variable-number tandem repeat analysis (MLVA), and multilocus sequence typing (MLST) have provided useful information but remain limited in resolution and are not routinely applicable in industrial settings. In this study, 25 Leptospira strains from vaccine manufacturers and diagnostic laboratories were characterized using MLVA and whole-genome sequencing (WGS). MLVA achieved partial typing (72 %), whereas MLST from WGS data resolved 88 % of the strains. MLVA was precise for confirming the identity of strains with an expected genetic profile but lacked the resolution to identify strains that had been misidentified. Complete classification (100 %) was only achieved by WGS through average nucleotide identity (ANI), MLST, and analysis of the lic12008 gene INDEL to differentiate the Copenhageni and Icterohaemorrhagiae serovars. Importantly, eight strains (32 %) showed discrepancies relative to company records, revealing misclassification and possible cross-contamination in industrial collections. These findings demonstrate the superior accuracy of WGS for Leptospira strain typing and highlight its value as a routine quality control tool. We propose that WGS be incorporated as a regulatory requirement for strain authentication in vaccine production and diagnostic applications, to ensure genetic purity, enhance biosafety, and improving the reliability of leptospirosis prevention and control.
LANGUAGE OF ORIGINAL DOCUMENT: English

Moura Midon L., DuarteNeto A.N., Gonçalves da Silva A.M., Heinemann M.B., Kundu S., Gomes-Solecki M., Isaac L.

Complement C3 deficiency enhances renal leptospiral load and inflammation while impairing T cell differentiation during chronic *Leptospira interrogans* infection

(2025) Infection and Immunity, 93 (12), pp. e0039825
DOI: 10.1128/iai.00398-25

ABSTRACT: Leptospirosis is a neglected disease caused by pathogenic Leptospira spp., affecting an estimated 1 million people annually and resulting in approximately 60,000 deaths. The disease can lead to hepatic, renal, and pulmonary dysfunctions and may contribute to the development of chronic kidney disease. The Complement System plays an important role in eliminating bacteria by lysis, generating opsonins and anaphylatoxins, which degranulate mastocytes and basophils, and attracting immune cells to the site of infection, among other important functions. We aimed to investigate the role of C3 during chronic infection by L. interrogans strain FIOCRUZ L1-130 (LIC) in C57BL/6 wild-type (WT) and C3 knockout (C3KO) mice, monitored for 15, 30, 60, 90, or 180 days post-infection (d.p.i.). LIC-infected C3KO mice exhibited significantly higher leptospiral loads in the kidneys compared to WT counterparts. While both groups showed local inflammation at 15 and 30 d.p.i., LIC-infected C3KO showed a higher number of Leptospira DNA copies at 30 d.p.i. At this same time point, C3KO LIC-infected mice developed a larger fibrotic area than WT mice. Additionally, levels of specific IgG2b and IgG3 antibodies were significantly higher in LIC-infected C3KO mice compared to WT mice. The number of naïve T lymphocytes (both CD4+ and CD8+) was also increased in LIC-infected C3KO mice. This study demonstrates that during LIC infection, the absence of C3 does not impact mouse survival but results in increased renal leptospiral load and fibrosis. It also highlights the role of C3 in promoting the maturation and differentiation of T lymphocytes into pre-effector cells.
LANGUAGE OF ORIGINAL DOCUMENT: English

Baimova R.R., Karmokov I.A., Riabiko E.G., Khalilov E.S., Blinova O.V., Tokarevich N.K., Boumbaly S., Camara A., Soropogui B., Camara J., Bérété, F.

Leptospirosis in the Republic of Guinea

(2025) Russian Journal of Infection and Immunity, 15 (5), pp. 977 - 982

DOI: 10.15789/2220-7619-LIT-17937

ABSTRACT: Leptospirosis is an acute zoonotic infection caused by pathogenic bacteria from the genus Leptospira. Leptospirosis creates significant though underdiagnosed public health problems in Africa. The Republic of Guinea (Guinea) is a country in West Africa, its capital is Conakry. The study objective was to assess the prevalence of the leptospirosis in febrile patients in the Republic of Guinea. We analyzed 827 blood serum samples obtained from febrile patients who applied to municipal health services, in the period from 2020 to 2024. RT-PCR was used to test 627 blood serum samples for the presence of genetic material of pathogenic Leptospira spp. Genotyping of positive samples was performed with the help of primers selected for a fragment of the secY gene. As a result of our study, IgG antibodies to Leptospira spp. were detected in 202 blood serum samples, which amounted to 24.4%.154 blood serum samples (18.6%) were positive for IgM to Leptospira spp. In 80 of the 276 positive samples both antibodies (IgG and IgM) were detected, 122 samples contained only IgG, while 74 only IgM. Leptospira spp. DNA was detected in 5 (0.8%) of 657 serum samples tested for the presence genetic markers of pathogenic leptospira. Sanger sequencing was applied to all 5 samples, and for three samples it resulted in successful leptospira genotyping, but it failed for two other samples may be due to insufficient amount of DNA or its degradation. When analyzed according to the BLAST algorithm, the obtained sequences revealed 100% similarity to those of L. kirschneri that was further confirmed by clustering when constructing the phylogenetic tree. Our study revealed high level of antibodies to leptospirosis in febrile patients, which bear witness to the wide spread of this pathogen in the Republic of Guinea. Joint research with international organizations can provide valuable information on the epidemiology of leptospirosis and improve control and prevention of the disease.

LANGUAGE OF ORIGINAL DOCUMENT: English

Davignon G., Thibeaux R.

A modular workflow for quantitative, structural and functional analysis of Leptospira biofilms

(2025) Journal of Visualized Experiments, 2025-December (226), art. no. e69511

DOI: 10.3791/69511

ABSTRACT: Here, we present an integrated suite of protocols for the cultivation, quantitative monitoring, structural and functional characterization of Leptospira spp. biofilms over time. This workflow combines crystal violet microtiter assays to measure biofilm biomass at multiple time points, with a time-resolved fractionation approach that distinguishes attached (biofilm) and non-attached (liquid-phase) bacterial populations, time-lapse phase-contrast imaging for non-destructive kinetic observation, confocal laser-scanning microscopy to generate full 3D reconstructions with matrix-probe readouts, and membrane-supported scanning electron microscopy for ultrastructural analysis. In parallel, we detail a standardized procedure for harvesting intact biofilm aggregates and preparing them for intraperitoneal injection into the susceptible golden Syrian hamster model, enabling direct assessment of biofilm-associated virulence in vivo alongside matched planktonic controls. Optimized for the pathogenic strain Leptospira interrogans Manilae L495, each module is readily transferable to other Leptospira species and mutant libraries to compare biofilm-forming capacity. Together,

these coordinated modules provide a robust foundation for screening anti-biofilm strategies, probing genetic determinants, and clarifying the contribution of biofilms to Leptospira persistence and pathogenesis.
LANGUAGE OF ORIGINAL DOCUMENT: English

Chaurasia R., Zeiss C.J., Holter M., Walsh C.A., Vinetz J.M.

Potential for early diagnosis of leptospirosis in experimentally infected rhesus macaques based on detection of leptospiral virulence-modifying protein exotoxin antigen and antibody

(2025) American Journal of Tropical Medicine and Hygiene, 113 (6), pp. 1331 - 1340
DOI: 10.4269/ajtmh.25-0262
ABSTRACT: Molecular and cellular mechanisms of leptospirosis pathogenesis remain poorly understood. Recent genomic, in vitro, and animal model data indicate that the novel PF07598 gene family encodes the so-called virulence-modifying proteins (VMPs), secreted exotoxins that are hypothesized to mediate the clinical manifestations of leptospirosis. Key to understanding the mechanistic role of VMPs in disease pathogenesis is testing the hypothesis that VMPs are produced during infection. Rhesus macaques were experimentally inoculated at multiple sites with low-passage Leptospira interrogans serovar Copenhageni strain Fiocruz L1-130. Microscopic agglutination test and polymerase chain reaction confirmed infection, but animals did not develop observable illness. An ELISA using recombinant VMPs demonstrated anti-VMP IgM and IgG antibodies on days 4 and 8, respectively, indicating that the infectious strain produced VMPs expectedly after infection. An antigen-capture ELISA detected VMP antigen in infected monkey urine and blood. Liver, kidneys, and lungs demonstrated mild histopathological abnormalities, demonstrating that target organs were subclinically involved in non-severe leptospirosis. Elevated serum levels of multiple cytokines (TNFa, IL-15, IL-8, sCD40L, MCP-1, and MIPb) showed systemic host inflammatory responses. This study addresses key gaps in understanding leptospirosis pathogenesis in nonhuman primates, aiming to develop VMP-based biomarkers for improved diagnosis and prognosis.
LANGUAGE OF ORIGINAL DOCUMENT: English

Sonam A., Hameed A., Stothard P.M., Grant J.R., Bhagwath A.B.

Draft genome sequence of Leptospira sp. SA-E8, isolated from a farmland soil

(2025) Microbiology Resource Announcements, 14 (12)
DOI: 10.1128/mra.00929-25
ABSTRACT: We report the draft genome sequence of Leptospira sp. SA-E8, isolated from a farmland soil in India. SA-E8 shared 88.8% OrthoANI and 36.2% dDDH scores with L. andrefontaineae PZF11-2T, indicating distinct taxonomic placement of the isolate. In silico analysis predicted potential drug resistance and hemolytic traits in SA-E8.
LANGUAGE OF ORIGINAL DOCUMENT: English

Fauzi N.A., Mohamad M., Mat Ruzlin A.N., Mazlan A., Mahir H.M.A., Shamsudin N., Chen X.W.

Leptospirosis in Perak State for the year 2024: hospitalisation rate and its associated factors

(2025) Medical Journal of Malaysia, 80 (6), pp. 770 - 779
ABSTRACT: Introduction: Leptospirosis remains a public health concern in Malaysia, particularly in high-burden states like Perak. Understanding the hospitalisation rate and its associated factors is important for informing early intervention strategies and optimising disease management; however, local data on these

aspects remain scarce. This study seeks to address this gap by determining the hospitalisation rate and identifying the risk factors associated with hospitalisation among probable and confirmed leptospirosis cases in Perak. Materials and Methods: This is a retrospective cohort study using secondary data from two data sources obtained from the e-Notifikasi system database and laboratory reports of all registered leptospirosis cases in Perak from January to December 2024. The outcome variable, which was hospitalisation status, was determined by the treating team based on clinical manifestation and disease severity. Multiple logistic regression was applied to identify factors associated with hospitalisation cases. Data was analysed using SPSS version 29. Results: A total of 764 registered leptospirosis cases were included in the study, with 75.5% (n=577) required hospital admission (95% CI: 72%,79%). The average age of patients was 32 years (SD: 20.5), with two-thirds (67.8%) being male. Kinta district reported the highest proportion of cases (30.4%). Factors significantly associated with hospitalisation included: presence of complications (aOR: 8.06, 95% CI: 1.57,41.48), vomiting (aOR: 11.00, 95% CI: 6.63,18.25), headache (aOR: 4.44, 95% CI: 2.70,7.32), onset-to-diagnosis (aOR: 1.37, 95% CI: 1.23,1.52), histories of recreational activity exposure (aOR: 3.41, 95% CI: 2.07,5.62), soil exposure (aOR: 2.60, 95% CI: 1.11,6.07) and types of occupation; student (aOR: 2.79, 95% CI: 1.58,4.93), agriculture (aOR: 5.06, 95% CI: 2.20,11.63), military personnel (aOR: 4.87, 95% CI: 1.08,21.92) and pensioners (aOR: 5.96, 95% CI: 3.31,10.74). Conclusion: This study adds to the existing knowledge on the hospitalisation rate and its associated factors among registered leptospirosis cases in Perak. These findings highlight the importance of targeted health education, enhanced clinical vigilance and risk-based interventions tailored to local exposure patterns. While the study's strengths include comprehensive case capture and validated data, limitations include the absence of meteorological, socioeconomic status and health literacy data. These limitations emphasise the need for future longitudinal and behavioural studies. © 2025, Malaysian Medical Association. All rights reserved.

LANGUAGE OF ORIGINAL DOCUMENT: English