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Gunathilaka N., Jayakody D., Erathna S.

Spatiotemporal patterns and climate influences on leptospirosis in Sri Lanka from 2009 to 2024

(2026) BMC Infectious Diseases, 26 (1), art. no. 159

DOI: 10.1186/s12879-026-12533-1

ABSTRACT: Background: Leptospirosis remains a major public health concern in Sri Lanka, a country with a tropical climate conducive to transmission. Despite ongoing surveillance, there is limited evidence on the spatial and climatic determinants driving long-term disease dynamics. This study aimed to investigate the spatiotemporal distribution and climatic sensitivity of leptospirosis from 2009 to 2024 using advanced statistical modelling. Methods: District-level monthly leptospirosis case data for the period 2009–2024 were obtained from the Epidemiology Unit of the Ministry of Health, Sri Lanka. Corresponding monthly district-level climatic variables, including total rainfall, mean temperature, minimum temperature, maximum temperature, and mean relative humidity, were retrieved from the NASA POWER satellite dataset. Associations between climatic variables and leptospirosis incidence, as well as spatial heterogeneity in case distribution, were assessed using a Generalized Additive Model for Location, Scale, and Shape with a Zero-Adjusted Gamma distribution, while spatial clustering and autocorrelation were examined using Moran’s I. Results: A total of 81,629 confirmed cases of leptospirosis were recorded during the study period. The ZAGA-GAMLSS model identified several climatic, spatial, and temporal predictors that were significantly associated with district-level incidence. Relative humidity and maximum temperature showed immediate negative associations with incidence, while humidity, mean temperature, and rainfall demonstrated positive lag-dependent effects at 1–3 months. In contrast, maximum and minimum temperatures exhibited predominantly negative association at 3-month lag. Spatial heterogeneity was evident in both incidence rates and zero-inflation, and temporal dependence was detected at 1 and 12-month lags. Higher relative humidity three months earlier was linked to more stable leptospirosis incidence rates across districts. Spatial analysis further revealed significant clustering, with hotspots identified in the districts of Ratnapura, Galle, Matara, and Hambantota, while Colombo was identified as a spatial outlier. Conclusions: Leptospirosis in Sri Lanka exhibits distinct spatiotemporal patterns influenced by climatic variability, with elevated risk following monsoon rains in the south-western part of the country. Climate-sensitive modelling, as demonstrated in this study, supports the integration of meteorological surveillance into early warning and response systems to enhance leptospirosis control, particularly in identified hotspot regions.

LANGUAGE OF ORIGINAL DOCUMENT: English

Basurto-Hurtado M.R., Becerra-Sepúlveda L.O., García-Pérez A.P., Granados-Molina E.A.

Secondary hemophagocytic lymphohistiocytosis in a patient with severe leptospirosis: a case report

(2026) Journal of Medical Case Reports, 20 (1), art. no. 46

DOI: 10.1186/s13256-025-05561-z

ABSTRACT: Background: Hemophagocytic lymphohistiocytosis is a rare but life-threatening hyperinflammatory syndrome that can be triggered by infections, malignancies, and autoimmune diseases. Case presentation: We present a case of hemophagocytic lymphohistiocytosis secondary to severe leptospirosis in a 59-year-old Latin American male with no medical history of relevance, which is rarely reported in the literature. One week prior to admission, the patient presented with frontal headache, fever, hyporexia, choluria, jaundice, and hepatomegaly. Sepsis was initially suspected. After antibiotic therapy, his condition deteriorated, leading to acute kidney injury and respiratory failure. Serology and dark-field microscopy in urine and blood were requested and reported positive for Leptospira. Bone marrow aspiration confirmed hemophagocytic lymphohistiocytosis. Treatment with corticosteroids led to clinical and laboratory improvement. Conclusion: This case highlights the need for early recognition of hemophagocytic lymphohistiocytosis in patients with sepsis-like syndromes unresponsive to standard therapy.

LANGUAGE OF ORIGINAL DOCUMENT: English

Clemente B., Ghoraishizadeh P., Saimuang K., Limsampan S., Suwannin P., Manahan E.P., Jangpatarapongsa, K.

Evaluating the diagnostic accuracy of clinical judgement and rapid tests for leptospirosis in the Philippines: implications for public health management

(2026) Infectious Diseases of Poverty, 15 (1), art. no. 14

DOI: 10.1186/s40249-026-01413-0

ABSTRACT: Background: Leptospirosis is endemic in the Philippines; however, its diagnosis remains challenging because of the lack of rapid and accurate diagnostic tools for detecting infection. Physicians must therefore resort to diagnosing leptospirosis through their clinical judgement, and this often results in under- or overestimation of cases. This study aimed to assess and compare the diagnostic accuracy of physicians' clinical judgement and commercially available rapid test kits for leptospirosis against reference methods such as the microscopic agglutination test (MAT) and real-time polymerase chain reaction (qPCR) in the Philippines. Methods: A total of 127 serum samples were collected from patients suspected to have leptospirosis at three hospitals in the Philippines from August to December 2024. Rapid test kit results and final diagnoses were retrieved from the patients' charts. MAT was performed on all the samples as a confirmatory method. Moreover, qPCR was performed on 30 randomly selected samples to increase the sensitivity of the reference standard. Sensitivity, specificity, positive and negative predictive values, and 95% confidence intervals were computed to determine the accuracy of both clinical judgement and rapid tests. Results: Among the 75 MAT-confirmed leptospirosis cases, approximately 24.0% were misdiagnosed as other febrile illnesses, such as dengue and typhoid fever, on the basis of clinical judgement, whereas 67.3% of the 52 MAT-negative patients were falsely diagnosed with leptospirosis. Overall, clinical judgement demonstrated high sensitivity (76.0%) but low specificity (33.7%), indicating possible overdiagnosis. The rapid test kits used in the laboratory exhibited significantly lower sensitivity (42.7%) but higher specificity (82.7%), suggesting a high probability of false-negative results. When qPCR was used in conjunction with these methods, relatively similar results were obtained. Conclusions: These findings highlight the diagnostic limitations in detecting leptospirosis in the Philippines, where laboratory testing options remain limited and inaccurate, resulting in physicians often relying on their clinical judgement. Misdiagnosis, whether through clinical judgement or rapid testing, could lead to inappropriate patient management, increased morbidity, and underestimation of leptospirosis incidence.

LANGUAGE OF ORIGINAL DOCUMENT: English

Limothai U., Srisawat N., Haake D.A.

Early diagnosis and treatment of leptospirosis: optimizing clinical outcomes

(2026) Journal of Infection, 92 (2), art. no. 106675

DOI: 10.1016/j.jinf.2025.106675

ABSTRACT: Leptospirosis is a globally prevalent zoonotic infection causing more than one million cases and nearly 60,000 deaths annually yet is often diagnosed late after organ dysfunction and other complications have

arisen. Delayed diagnosis leads to late initiation of antibiotics and other therapeutic interventions, at which point complications such as renal failure, jaundice, or pulmonary hemorrhage are more common and therapy is less effective. This review highlights the critical importance of early recognition and intervention, emphasizing the therapeutic window during the leptospiremic phase when antibiotics are most effective. We examine the limitations of current clinical and laboratory diagnostic methods, the evolving role of molecular and biomarker-based platforms, and the potential of integrated scoring systems for frontline triage. Evidence supporting early antibiotic therapy, supportive care strategies, and severity prediction tools is summarized. We propose a paradigm shift toward field-adaptable, point-of-care diagnostics and integrated care pathways to ensure earlier treatment, improved outcomes, and reduced global disease burden.
LANGUAGE OF ORIGINAL DOCUMENT: English

Torres Higuera L.D., Rojas-Tapias D.F., Jiménez-Velásquez S., Renjifo-Ibáñez, C.

Comprehensive genotyping and taxonomic analysis uncovers extensive distribution of intermediate Leptospira species in Colombia

(2026) World Journal of Microbiology and Biotechnology, 42 (2), art. no. 57

DOI: 10.1007/s11274-025-04670-7

ABSTRACT: Leptospirosis, a globally prevalent zoonosis caused by pathogenic and intermediate Leptospira species, poses significant threats to public health and livestock industries. Despite its substantial impact, knowledge gaps persist regarding the prevalence and genetic diversity of Leptospira strains in many regions, including South America. This study aimed to characterize a diverse collection of Leptospira strains isolated from various sources in Colombia to enhance our understanding of the genetic diversity within this genus. Using a tiered approach combining conventional and genomic methods, we genotyped 55 isolates from various sources using 16S rRNA and rpoB gene sequencing, DNA ribotyping, and Multiple-Locus Variable-Number Tandem Repeat Analysis (MLVA). Most isolates were classified into phylogenetic groups containing pathogenic and intermediate strains of L. interrogans and L. wolffii, respectively, which was corroborated by ribotyping and MLVA. Whole-genome sequencing of selected strains revealed distinct genomic characteristics compared to related strains. Pan-genome analysis identified strain-specific genes, primarily hypothetical, while virulence factor analysis distinguished species-specific patterns. Furthermore, CRISPR-Cas system analysis uncovered genetic variations among the isolates. This study provides a framework for understanding Leptospira genetic diversity in Colombia and its potential implications on human and animal health. Our findings highlight the need for improved diagnostic methods and surveillance strategies that encompass both pathogenic and intermediate Leptospira species, which could significantly impact public health policies and veterinary practices in the region.
LANGUAGE OF ORIGINAL DOCUMENT: English

Jayasinghe M.S., Warnasekara J.N., Gunarathne S.P., Wickramasinghe N.D., Agampodi, S.

Direct, indirect and intangible costs incurred by leptospirosis patients: the magnitude, aspects and methods of assessing the costs - a systematic review and meta-analysis protocol

(2026) BMJ open, 16 (1), pp. e106730

DOI: 10.1136/bmjopen-2025-106730

ABSTRACT: INTRODUCTION: Leptospirosis is a significant public health concern worldwide, as it imposes a substantial economic burden on the global economy. Despite a comprehensive search of the relevant

literature, few studies evaluating the economic burden experienced by leptospirosis patients were identified. In particular, very few studies thoroughly examined the cost components, including direct, indirect and intangible costs. This paucity of evidence further motivates the need to conduct a more focused search using a systematic review approach. Thus, this study aims to systematically review the global literature on the magnitude and aspects of the direct, indirect and intangible costs incurred by leptospirosis patients and the methods available for assessing these costs. METHODS AND ANALYSIS: This review will follow the Preferred Reporting Items for Systematic Reviews and Meta-Analyses Protocols 2015 guidelines. The Population, Intervention, Comparison, Outcomes, Study Design framework was used to develop the review questions. The search strategy will comprise two key term blocks: 'Leptospirosis' and 'Economic cost'. A comprehensive literature search will be conducted in PubMed, Web of Science, Scopus, MEDLINE, CINAHL, the Cochrane Library, EconStor and IDEAS to collect publications from inception to July 2025. The search will be limited only to English-language and peer-reviewed publications. The Mixed Methods Appraisal Tool will be used to assess the quality of eligible studies. Extracted cost data will be categorised into direct, indirect and intangible costs. A meta-analysis will be conducted to quantify the magnitude of these costs if sufficient methodological and contextual homogeneity exists. Moreover, a narrative synthesis will be performed to analyse the qualitative data related to intangible costs. ETHICS AND DISSEMINATION: As this study will use secondary data, ethical approval is not required. The systematic review's findings will be published in a scientific journal and presented at relevant conferences to address the knowledge gap regarding the economic burden (including direct, indirect and intangible costs) faced by leptospirosis patients. The results of this systematic review will guide policies for prioritising prevention, improving surveillance and efficiently allocating resources to control leptospirosis.
LANGUAGE OF ORIGINAL DOCUMENT: English

Looijaard S.M.L.M., Jolink H., Delfos, N.M., Lauw F.N.
Severe neurological complications of leptospirosis, presentation of two cases
(2026) IDCases, 43, art. no. e02505
DOI: 10.1016/j.idcr.2026.e02505
ABSTRACT: We discuss two cases of severe leptospirosis, in which the most concerning symptoms affected the nervous system. These cases illustrate the wide range of neurological symptoms that can be seen in patients with leptospirosis, which can affect both the central and peripheral nervous system. These symptoms are thought to be caused by an inflammatory reaction to Leptospira, rather than by the infection itself. Both patients experienced a variety of neurological symptoms that prolonged and altered their course of treatment. The first patient developed radicular pain secondary to polyradiculitis, which was confirmed by spinal MRI. He was treated with antibiotics but continued to experience bilateral leg pain following treatment. He was referred to a rehabilitation clinic to help him deal with his persisting complaints. The second patient was admitted to the intensive care unit and failed to regain consciousness after sedation was discontinued. Neuroimaging revealed multiple intracranial microhemorrhages. He was treated with antibiotics in combination with corticosteroids. Following extensive rehabilitation, he recovered without residual neurological deficits.
LANGUAGE OF ORIGINAL DOCUMENT: English

Ibrahim A., Wannasingha Humphries U.W., Kiss G., Hlaing P.T., Attahir, Z.A.

Beyond conventional routes: an approach to understanding leptospirosis transmission dynamics through mathematical modeling with real data from Thailand

(2026) Journal of Biological Systems, pp. 1 - 42

DOI: 10.1142/S0218339026500129

ABSTRACT: Leptospirosis is a zoonotic disease caused by Leptospira bacteria, that occurs mainly in tropical regions such as Thailand. This study presents a mathematical model that captures the dynamics of Leptospira transmission. The model incorporates direct and environmental transmission pathways and notably includes an exposed human compartment, an often-neglected element in existing leptospirosis models. We combined several control interventions, including environmental management, reservoir control, and human treatment to explore strategies for mitigating disease spread. The equilibrium points of the system are identified, and their stability properties are analyzed. Using real data from Thailand, we estimate key parameters and perform a global sensitivity analysis to identify the dominant factors driving leptospirosis transmission. Finally, we evaluate optimal control theory and conduct a comparative cost-effectiveness analysis of the proposed interventions. Our findings suggest that environmental management is the most effective and potentially cost-effective strategy to reduce leptospirosis transmission.

LANGUAGE OF ORIGINAL DOCUMENT: English

Murag S., Rathnamma D.D., Koppad S., Choudapur M.K., Suresh, K.P., Balamurugan V., Patil S.S.

Seroprevalence and determination of serogroup-specific antibodies of *Leptospira* in cattle and buffaloes in Karnataka, India

(2025) Indian Journal of Animal Sciences, 95 (7), pp. 580 - 587

DOI: 10.56093/ijans.v95i7.146618

ABSTRACT: This study sought to evaluate seroprevalence and distribution of Leptospira serovars among bovines experiencing reproductive disorders across four revenue divisions in the state of Karnataka, India. A total of 582 serum samples, consisting of 314 cows and 268 buffaloes, were randomly collected from Bengaluru, Belgaum, Gulbarga, and Mysore divisions of Karnataka. Microscopic Agglutination Test (MAT) was employed to assess these samples against the reference panel of serovars comprising of eight pathogenic Leptospira namely Hardjo, Pomona, Canicola, Icterohaemorrhagie, Hebdomadis, Grippotyphosa, Pyrogenes, and Autumnalis. The findings indicated an overall seroprevalence rate of 28% (163/582), with specific antibodies against the employed serovars: Hardjo (34.35%), Pomona (16.56%), Canicola (11.66%), Icterohaemorrhagie (10.43%), Hebdomadis (10.43%), and Autumnalis (9.81%). No specific positive reactions were observed for Grippotyphosa and Pyrogenes serovars. Further, buffaloes exhibited a higher seropositivity (29%) as compared to cattle (27%). Serovar Hebdomadis was most prevalent in both cattle and buffaloes. Furthermore, among the 163 MAT reactive positive samples, the majority (62.58%) were linked to a history of abortion, followed by repeat breeding (28.22%), while the remaining cases (9.2%) were associated with other reproductive disorders. Bengaluru, Mysore, and Belgaum divisions displayed higher seropositivity and a greater diversity of serovars, potentially due to increased risk factors in these regions compared to Gulbarga division of Karnataka. These results underscore the necessity for enhanced surveillance and diagnostic efforts, particularly in animals with a history of abortion, to address leptospirosis in bovines. Furthermore, identifying prevalent serovars may be useful for targeted interventions in particular geographical areas, and may be of use in the reference panels of antigens in the MAT in disease diagnostic laboratories which pay the way for

more accurate, efficient, and timely diagnosis of leptospirosis, and ultimately contribute to the management of ‘One Health’ concerns.
LANGUAGE OF ORIGINAL DOCUMENT: English

Mathew T., Karau B.
Neuroleptospirosis
(2025) Encyclopedia of the Neurological Sciences, pp. V1 - 210
DOI: 10.1016/B978-0-323-95702-1.00453-X
ABSTRACT: Leptospirosis is a zoonotic disease prevalent worldwide, particularly in tropical and warm-climate countries. Transmission of Leptospira occurs through exposure to urine from infected animals, such as rodents and cattle. The disease has diverse clinical manifestations, ranging from a non-specific febrile illness to severe, multi-organ involvement, particularly affecting the kidneys and liver. Most cases follow a subclinical or asymptomatic course. Neurological manifestations are observed in approximately 10%–15% of cases, affecting both the central and peripheral nervous systems. Common presentations include headache, meningitis, and meningoencephalitis. Since early diagnosis and management are crucial, physicians should maintain a high index of suspicion and possess comprehensive knowledge of the various presentations of leptospirosis, particularly neuroleptospirosis. This article covers the epidemiology, microbiology, clinical manifestations, diagnostic approach, and management of neuroleptospirosis.
LANGUAGE OF ORIGINAL DOCUMENT: English

Pereira Dos Santos P.V., Cupello Da Silva A.P., Correia Lucas F.L., Lilenbaum W., Souza-Fabjan, J.M.G.
Finding the hiding spots: uneven distribution of pathogenic *Leptospira* spp. in the bovine genital tract
(2025) Frontiers in public health, 13, pp. 1735321
DOI: 10.3389/fpubh.2025.1735321
ABSTRACT: Background: Bovine genital leptospirosis (BGL) is a chronic reproductive disease caused by pathogenic Leptospira spp., whose uneven distribution in the genital tract may compromise diagnosis. Objective: This study evaluated the presence of pathogenic Leptospira spp. in different regions of the bovine reproductive tract of naturally infected cows to identify the most reliable anatomical site for molecular detection. Methods: Oviducts (OVID) and uterine fragments from the uterine body (UB), base of the uterine horn (BUH), and apex of the uterine horns (AUH) were collected post-mortem from 40 cows. Results: Pathogenic Leptospira spp. DNA was detected by lipL32 PCR in at least one anatomical site in 55% (22/40) of animals. The highest positivity rate was observed in UB (20/40; 50%), whereas AUH (7.5%), BUH (0%), and OVID (2.5%) showed no or minimal detection. Conclusion: The findings demonstrate that pathogenic Leptospira spp. are unevenly distributed within the bovine reproductive tract, with a clear preference for the uterine body. This anatomical site provides the greatest diagnostic accuracy and should be prioritized for molecular testing to minimize false-negative results and improve BGL surveillance.
LANGUAGE OF ORIGINAL DOCUMENT: English

Kakita T., Takabe K., Morita M., Okano S., Taira K., Kudeken T., Taira H., Kyan H., Shinya S., Murata R., Akeda Y., Ohnishi M., Koizumi N.
Genomic comparison of *Leptospira interrogans* isolated from humans, dogs, and wild and feral animals in Japan

(2026) International Journal of Medical Microbiology, 322, art. no. 151702

DOI: 10.1016/j.ijmm.2026.151702

ABSTRACT: Leptospirosis, caused by pathogenic Leptospira spp., is one of the most prevalent zoonotic diseases worldwide. While whole genome sequencing (WGS) has revealed global genetic diversity of Leptospira spp., large-scale genomic comparisons between human and animal isolates remain limited, and their epidemiological relationships are not fully understood. In this study, we performed WGS on 204 Leptospira isolates obtained from humans, dogs, and wild or feral animals in Japan between 1989 and 2021. Among these, 146 isolates of L. interrogans—the most frequently isolated Leptospira species with epidemiological relevance—were analyzed using Bayesian analysis of population structure (BAPS) and core genome multilocus sequence typing (cgMLST). These strains were classified into 30 clonal groups (CGs), including 26 novel CGs. Each CG consistently corresponded to a single serogroup, highlighting the potential of cgMLST for serogroup prediction. BAPS analysis revealed that serogroup Hebdomadis—particularly clades Li20 and Li13—predominated among human infections on islands of Okinawa Prefecture. Li20/CG486 strains were also isolated from mongooses and Ryukyu mouse, suggesting that these animals may serve as reservoirs. Li3/CG6 strains of serogroup Icterohaemorrhagiae were detected in both humans and brown rats in urban areas, underscoring the role of rats in transmission. Several canine isolates shared CGs with wildlife: Li20/CG481 with mongooses, Li20/CG486 with raccoons, Li6/CG485 with brown rats, and Li20/CG470 with large Japanese field mice, supporting environmental exposure as a likely route of canine infection. These findings demonstrate the utility of cgMLST and BAPS for high-resolution genotyping and emphasize the need for monitoring native and introduced wildlife to better understand and control leptospirosis in Japan.

LANGUAGE OF ORIGINAL DOCUMENT: English

Motta D., Aymée L., Roussouliéres I., Di Azevedo Nogueira M.I., Jacob Ferraz J.C., Lilenbaum, W.

Diagnosis of Equine Genital Leptospirosis (EGL) in mares with poor reproductive performance

(2026) Veterinary Microbiology, 315, art. no. 110924

DOI: 10.1016/j.vetmic.2026.110924

ABSTRACT: Leptospirosis is a zoonotic disease caused by spirochetes of the genus Leptospira . Equine genital leptospirosis (EGL) has been described as a chronic and silent syndrome, presenting reproductive alterations such as abortion, stillbirth, placentitis, embryonic loss, repeat breeding syndrome, and subfertility. This study aimed to investigate the genital Leptospira infection in naturally infected mares with poor reproductive performance, as well as to genetically characterize the agents. A total of 41 mares with a history of poor reproductive performance were selected. Sera were collected for serology by Microscopic Agglutination Test (MAT), while urine, uterine mucus, and uterine fragment samples were collected for a lipL 32-PCR screening. Samples positive at lipL32 -PCR were submitted to secY gene sequencing. Considering MAT, 17/41 mares were seroreactive (41.5 %). The most frequent serogroup was Australis, detected in 13 animals (76.5 % of the reactive). Out of the 41 mares, 25 (61.0 %) were positive in lipL 32-PCR and, of these, 21 (84.0 %) showed positive in at least one genital sample. Regarding secY nested-PCR, only six samples, all from the uterine fragment, were amplified, and all were characterized as Leptospira interrogans with ≥ 99 % of similarity with isolates of serovar Bratislava, from the Australis serogroup. Our results confirmed the diagnosis of EGL and highlighted the high detection rate of Leptospira DNA in genital samples of mares with poor reproductive performance.

LANGUAGE OF ORIGINAL DOCUMENT: English

Almazar C.A., Montala Y.B., Rivera W.L.

Leptospirosis in Southeast Asia: investigating seroprevalence, transmission patterns, and diagnostic challenges

(2026) Tropical Medicine and Infectious Disease, 11 (1), art. no. 18

DOI: 10.3390/tropicalmed11010018

ABSTRACT: Leptospirosis remains a significant public health and economic burden in Southeast Asia, particularly in low- and middle-income countries where environmental, occupational, and socioeconomic factors contribute to its endemicity. Transmission is driven by close interactions between humans and infected animal reservoirs, alongside climatic conditions such as heavy rainfall and flooding. The region's high but variable seroprevalence reflects inconsistencies in diagnostic methodologies and surveillance systems, complicating disease burden estimation. Major gaps persist in diagnostic capabilities, with current tools often unsuitable for resource-limited settings, leading to underdiagnosis and delayed treatment. Environmental modeling and spatial epidemiology are underutilized due to limited interdisciplinary data integration and predictive capacity. Addressing these challenges requires a One Health approach that integrates human, animal, and environmental health sectors. Key policy recommendations include harmonized surveillance, standardized and validated diagnostics, expanded vaccination programs, improved animal husbandry, and targeted public education. Urban infrastructure improvements and early warning systems are also critical, particularly in disaster-prone areas. Strengthened governance, cross-sectoral collaboration, and investment in research and innovation are essential for sustainable leptospirosis control. Implementing these measures will enhance preparedness, reduce disease transmission, and contribute to improved public health outcomes in all sectors across the region.

LANGUAGE OF ORIGINAL DOCUMENT: English

Cardoso Laner T., Wozeak Rodriguero D., Pereira Ladeira I., da Silva Ribeiro Dias L., Rodrigues Rogério R., Hartwig Drawanz D.

Advances in ELISA-based detection of equine leptospirosis

(2026) Brazilian Journal of Microbiology, 57 (1), art. no. 52

DOI: 10.1007/s42770-025-01854-z

ABSTRACT: Leptospirosis is a globally distributed zoonosis that affects both humans and animals, with Leptospira interrogans being the main causative agent. In horses, the disease is associated with considerable economic losses. The Microscopic Agglutination Test (MAT) is the reference test for diagnosis but has limitations, emphasizing the need for effective diagnostic alternatives. In this study, was evaluated the use of a recombinant chimera, composed of ErpY-like and LemA proteins, as an antigen for ELISA-based detection of equine leptospirosis. The chimera was successfully expressed, purified and tested on 915 horse serum samples previously analyzed by MAT. The ELISA correctly identified all positive samples, with no false negative observed. The ROC curve analysis, considering different hypothetical prevalence values, reached up to 0.92. The assay demonstrated sensitivity ranging from 98.8% to 100%, specificity from 77.6% to 84%, positive predictive value between 68.6% and 77.2%, and negative predictive value between 92% and 100%. The Kappa coefficient was 0.7432, indicating good agreement with MAT. When samples were categorized by titers, those with a 1:400 dilution achieved the highest accuracy (99%), while those with a 1:100 dilution showed slightly lower accuracy (94.8%), demonstrating that higher antibody titers resulted in a more effective assay. The major serovars that cause infection in horses, such as Bratislava, Icterohaemorrhagiae, Sejroe, Pomona,

and Copenhageni, react with rErpY-lemA. These results suggest that the ErpY-LemA chimera is a promising screening tool for equine leptospirosis, offering a valuable alternative for the rapid and accurate detection of different serovars and titers.
LANGUAGE OF ORIGINAL DOCUMENT: English

Ruwanpathirana P., Rambukwella R., Perera, N., Priyankara, D.
Severe leptospirosis in the intensive care unit: single centre prospective cohort study from Sri Lanka
(2026) BMC Infectious Diseases, 26 (1), art. no. 265
DOI: 10.1186/s12879-025-12477-y
ABSTRACT: Background: Severe leptospirosis often requires intensive care unit (ICU) treatment. The clinical phenotypes and outcomes of severe leptospirosis remain poorly characterised. We aimed to characterise the phenotypes and outcomes of patients with severe leptospirosis treated in the ICU. Methods: We conducted a prospective cohort study at the Medical ICU of the National Hospital of Sri Lanka between January 2019 and January 2022 on adult patients with serologically or microbiologically confirmed leptospirosis. Clinical and laboratory data were recorded prospectively. Unsupervised two-step cluster analysis using six variables selected a priori (acute kidney injury, pulmonary haemorrhage, myocarditis, mechanical ventilation, renal replacement therapy, and hospital-acquired infections) was used to identify clinical phenotypes and to generate phenotypically distinct clusters of patients. Laboratory and biochemical parameters were compared across clusters. Kaplan–Meier survival analysis was used to compare mortality. The primary outcome was in-hospital mortality. Results: One hundred and sixteen patients were included (mean age 43.9 years; males n = 103, 88.8%). Among them, 99.1% (n = 115) developed acute kidney injury, 62.1% (n = 72) developed pulmonary haemorrhage, and 75.9% (n = 88) developed myocarditis. Mechanical ventilation and dialysis were required in 56.9% (n = 66) and 75% (n = 87), respectively. Mortality rate was 17.2% (n = 20). Cluster analysis identified four phenotypes: (1) multi-organ failure (n = 43) (mortality of 25.6%, n = 11), (2) predominant respiratory failure (n = 20) (mortality of 35.0%, n = 7), (3) predominant renal failure (n = 26) (mortality of 7.7%, n = 2), and (4) intermediate severity (n = 27) (No mortality). Clusters with multi-organ and respiratory failure had higher hospital-acquired infection rates ($p < 0.001$) and a longer ICU stay ($p < 0.001$). Conclusions: Critically ill patients with leptospirosis exhibit distinct clinical phenotypes with variable outcomes. Isolated pulmonary haemorrhage and multi-organ failure are associated with high mortality. These findings support the need for phenotype-based risk stratification, prognostication, and treatment. Clinical trial registration: Not applicable.
LANGUAGE OF ORIGINAL DOCUMENT: English

Thumar R., Shekh S.L., Chauhan A., Kapoor K., Joshi A., Gajjar D., Sriram S., Jhala D., Joshi C.G., Patel, A.
Immunoinformatics design and in vivo evaluation of a multiepitope vaccine targeting OMPL1, Lipl32, Lipl41, and Lipl46 for leptospirosis in a male ICR mouse model
(2026) Vaccine, 76, art. no. 128331
DOI: 10.1016/j.vaccine.2026.128331
ABSTRACT: Leptospirosis is the most widespread and under-recognized zoonotic disease with around 1.03 million cases and ~ 60,000 reported fatalities occurring each year. It is a threat to humans as well as animals and can only be avoided by appropriate immunization. In this study, epitopes from proteins present on the exterior membrane of selected pathogenic Leptospira species were used as immunogens viz. OMPL1, LipL32,

LipL41 and LipL46. Conserved epitopes from each of the proteins across 8 species of Leptospira were screened and used to generate a multi-epitope vaccine that activates B cells, CD4+ and CD8+ cells. Six vaccine constructs were analyzed employing various immunoinformatics tools for physicochemical properties, structure prediction followed by validation, docking with immune receptors and molecular dynamics simulation. The vaccine construct 4 (LH) was found to comply with all the desired parameters to further consider for in vivo efficacy evaluation. For in vivo validation, gene for LH was cloned in a pVAX1 vector to be used as a DNA vaccine and in pET30a vector to express protein vaccine. DNA and protein vaccines were administered intramuscularly in ICR male mice along with adjuvant alhydrogel. Both types of vaccines elicited strong immune response evidenced from significantly increased serum IgG level evaluated by ELISA post the duration of 14 to 42 days. IFN-γ cytokine producing T cells were significantly stimulated in protein vaccine as revealed by flow cytometry suggesting the priming of CD4+ and CD8+ T cells by vaccine. The neutralizing antibody response to Leptospira serovars was confirmed with microscopic agglutination test. In summary, this study illustrates the prospective of multi-epitope DNA and protein vaccines incorporating epitopes from four outer membrane proteins to generate a strong immune response, paving the way forward for protection during challenge study against virulent Leptospira pathogens in animal model.

LANGUAGE OF ORIGINAL DOCUMENT: English

Narthanareeswaran M., Nagarajan H., Subramaniyan S., Narthanareeswaran B., Ranganathan S., Jeyakanthan J.

Probing the conserved catalytic mechanism of ThiL protein in pathogenic Leptospira species: an *in silico* strategy for inhibitor discovery to combat leptospirosis

(2026) Computers in Biology and Medicine, 204, art. no. 111540

DOI: 10.1016/j.compbiomed.2026.111540

ABSTRACT: Leptospirosis is a zoonotic bacterial disease caused by Leptospira spirochetes , with limited therapeutic options, symptoms ranging from mild flu-like illness to severe organ failure and death. It presents a broad clinical spectrum, complicating diagnosis and treatment. This study targets Leptospira thiamine monophosphate kinase (ThiL), an essential enzyme conserved across the pathogenic species of Leptospira that is crucial for bacterial survival, with no known human homolog, making it a promising and selective therapeutic candidate for drug development. This study aims to discover effective inhibitors of Leptospira ThiL using Structure-Based Virtual Screening (SBVS). Potential hits were evaluated for drug-like properties, followed by Density Functional Theory (DFT) calculations to assess electronic structure properties. Further molecular dynamics simulations and binding free energy calculations were performed using the MM/PBSA approach to confirm the stability and affinity of the inhibitor. High-throughput Virtual Screening (HTVS) of phytochemicals revealed five promising candidates, namely, IMPHY004345, IMPHY005869, IMPHY006284, IMPHY002964, and IMPHY005688, exhibiting better docking scores (−12.36 to −10.54 kcal/mol) and strong MM/GBSA binding energies (−47.26 to −40.72 kcal/mol), along with optimal pharmacokinetic profiles. DFT analysis assessed the electronic properties of these compounds, providing insights into their chemical reactivity. MD simulations demonstrated stable binding and persistent hydrogen-bond interactions in the ThiL-ligand complexes. The conformational stability was monitored through MD-based distance plot analysis, revealing sustained interactions with catalytically significant residues (Glu9, Gln23, Asp39, Arg140, Thr209 Lys218) across all pathogenic Leptospira species, underscoring ThiL's evolutionary and functional importance. MM/PBSA calculations also support the high-affinity binding, with key residues emerging as crucial for

maintaining complex stability and contributing to energy. This study establishes ThiL as a structurally stable, evolutionarily conserved, and highly druggable target in Leptospira . The identified leads, IMPHY006284 and IMPHY004345, emerged as the most potent broad-spectrum ThiL inhibitors, exhibiting multi-target inhibition across pathogenic species. This offers a promising strategy to overcome strain-specific variability and deliver broad-spectrum therapeutics for leptospirosis management.

LANGUAGE OF ORIGINAL DOCUMENT: English

Libera K.C., Parmley E.J., Clow K.M., Grant L.E., Weese J.S., Jardine C.M.

Bridging the gap: Multi-sector perspectives on human, domestic animal, and wildlife leptospirosis in Ontario, Canada

(2026) PLOS ONE, 21 (2 February), art. no. e0340404

DOI: 10.1371/journal.pone.0340404

ABSTRACT: Although leptospirosis is one of the most common zoonotic diseases worldwide, limited surveillance and poor coordination between human and animal health sectors have resulted in scarce and disparate data on its occurrence. Strengthening integrated surveillance requires cross-sector collaboration, beginning with the engagement of key organizations. The aims of this study were to 1) determine key health experts' awareness and risk perceptions of leptospirosis and of zoonotic disease surveillance in Ontario, Canada, and 2) examine key components of engagement, such as perceived value and interest, during the initial stages of developing an integrated leptospirosis surveillance framework. A web-based survey was sent to 543 experts in human, animal, and environmental health in Ontario, and analyzed using a mixed-methods approach to identify key factors influencing perceptions of leptospirosis, including views on Leptospira distribution, the impact of human behavior, and the influence of environmental conditions. Leptospirosis was recognized as a health threat in Ontario by 90% (74/82) of respondents, and 91% (70/77) indicated that current surveillance efforts are inadequate. A higher proportion of animal health sector respondents identified leptospirosis as a threat to human (93%, 37/40) and animal health (90%, 44/49) compared to public health sector respondents (76%, 25/33 and 83%, 25/30, respectively). All participants (81/81) acknowledged the benefits of integrated surveillance over the current siloed approach. Our findings highlight that key public and animal health experts perceive leptospirosis as a health threat in Ontario and support more integrated disease surveillance to better respond to this emerging zoonotic pathogen.

LANGUAGE OF ORIGINAL DOCUMENT: English

Epps J., Massey P.D., Ranmuthugala G., Colvin A., Usher, K., Heal C., Hall, L., Guppy, M.

A One Health approach to leptospirosis: current serosurveillance practices and climate change leave Australia at increasing risk

(2026) Australian and New Zealand Journal of Public Health, 50 (1), art. no. 100297

DOI: 10.1016/j.anzjph.2025.100297

LANGUAGE OF ORIGINAL DOCUMENT: English

Thongdee M., Chaiwattanarungruengpaisan S., Paungpin W., Sungpradit S., Jiemtaweeboon S., Tiyanun E., Ruchisereekul K., Suwanpakdee S., Thaipadungpanit J.

Pathogenic Leptospira species identified in dogs and cats during neutering in Thailand

(2026) PLoS neglected tropical diseases, 20 (2), pp. e0013421

DOI: 10.1371/journal.pntd.0013421

ABSTRACT: Pathogenic species of the genus Leptospira cause an underdiagnosed zoonosis in humans and animals called leptospirosis. Animal reservoirs often remain asymptomatic yet shed the active spirochete in urine, making the control of leptospirosis transmission to humans more challenging. Asymptomatic leptospirosis in human companions, such as dogs and cats, resulting in unrecognised infections, has been demonstrated in a few countries. Crucially, the current lack of molecular epidemiology data on Leptospira among companion animals in Thailand underscores the urgent need to investigate transmission dynamics for effective regional control. We investigated the prevalence of Leptospira infection in cats and dogs during neutering in seven provinces across Thailand. The urine samples were screened for Leptospira DNA by PCR targeting the rrs gene and further speciation using the Sanger Sequencing Analysis. The 56/567 (9.9%) animals were positive for Leptospira in the Pathogen clade, including 34/303 (11.2%) dogs and 22/264 (8.3%) cats. The partial rrs gene analysis identified L. interrogans, L. weilii, and L. borgpetersenii (4.4%) as well as Pathogen subclade 2 species (1.4%). Notably, this study reports the first molecular detection of L. yasudae (1.0%) in companion animals in Thailand. The identification of these three key pathogenic Leptospira species, common causes of human leptospirosis in Southeast Asia, in clinically healthy owned and free-roaming dogs and cats, suggests the risk of human leptospirosis in the areas investigated. These companion animals, often living in close contact with human, may contribute to daily risks. Therefore, enhanced surveillance and vaccination programs for dogs and cats, coupled with targeted public awareness campaigns, are critical for mitigating the risk of human infections.

LANGUAGE OF ORIGINAL DOCUMENT: English

Kannan E.P., Venkatachalam P., Gopal J., Hasan N., Muthu M.

Investigating the existing analytical methods deployed for leptospirosis detection and diagnostics

(2026) Analyst

DOI: 10.1039/d6an00005c

ABSTRACT: The morbidity and mortality of Leptospirosis have been rapidly increasing each year, currently reaching up to 1.03 million and 58 900, respectively, even though it is not yet popularly recognised as a pathogenic disease. The zoonotic property of leptospirosis further escalates concerns regarding human health and the implementation of the One Health framework. Hence, early and specific detection becomes exceedingly imperative for the prompt initiation of treatment. In this review article, various conventional and molecular methods, including microscopic agglutination test (MAT), enzyme-linked immunosorbent assay (ELISA), polymerase chain reaction (PCR), loop-mediated isothermal amplification (LAMP), mass spectrometry (MS) and rapid diagnostic tests, have been comprehensively and critically reviewed for the detection of leptospirosis based on the available literature. This review is the first of its kind, focusing on consolidating the mass spectrometric methods that have been employed and highlighting the limitations and achievements of these sophistications. The review disclosed that the available analytical expertise has not been fully utilized for Leptospirosis detection. Future directions and recommendations have been put forth for the rapid, simple, sensitive, accurate and early detection of Leptospirosis.

LANGUAGE OF ORIGINAL DOCUMENT: English

Heine J., Selbertinger B., Binder B., Theissen N., Schmid S., Mester P., Müller-Schilling M., Pavel V.

Ictero-hemorrhagic leptospirosis - Weil's disease

(2026) IDCases, 43, art. no. e02515

DOI: 10.1016/j.idcr.2026.e02515

LANGUAGE OF ORIGINAL DOCUMENT: English

Rodrigues da Silva L., Carneiro Carvalho M., Lorga Mikejevs A.C., Barbosa Rodrigues dos Santos L., Moura Midon L., Nunes Duarte Neto A., Akemi Amamura, T., Isaac L.

Leptospirosis-associated pulmonary hemorrhagic syndrome: immune mechanisms, clinical manifestations, and experimental models

(2026) Revista do Instituto de Medicina Tropical de Sao Paulo, 68, pp. e9

DOI: 10.1590/S1678-9946202668009

ABSTRACT: Leptospirosis is a neglected zoonotic disease caused by bacteria of the genus Leptospira, mainly acquired via direct contact with water and soil contaminated by the urine of infected animals. This is most observed in tropical and subtropical regions, and it is strongly associated with urban population growth in areas lacking adequate sanitation conditions. Leptospira infection can lead to several clinical manifestations in humans, ranging from a nonspecific febrile illness to severe complications such as jaundice, renal failure, and life-threatening pulmonary disease. One of the most severe forms is leptospirosis-associated pulmonary hemorrhagic syndrome (LPHS), characterized by coughing, chest pain, dyspnea, and massive pulmonary hemorrhage. The mortality rate of LPHS is approximately 50%, with death generally occurring within 72 hours after symptom onset. The etiopathogenesis of LPHS remains poorly understood. Some studies suggest that Leptospira spp. may directly damage blood capillaries and alter vascular permeability. Additionally, the host immune response, via the cytokine release, high expression of adhesion molecules, and activation of the Complement System, may further disrupt endothelial integrity, promoting vascular leakage and the systemic dissemination of leptospires. Animal models are essential for a better understanding of Leptospira transmission, colonization, and pathogenesis. This review aims to consolidate current understanding of LPHS, with emphasis on its pathogenesis, immune mechanisms, clinical manifestations, virulence factors, and experimental models.

LANGUAGE OF ORIGINAL DOCUMENT: English

Anderson P.N., Hahn B.L., Thao G., Johnson M.S., Giraud-Gatineau A., Gao Y., Picardeau M., Coburn J., Surdel M.C.

In vitro and in vivo endothelial interactions of Leptospira species are markers of virulence

(2026) PLoS neglected tropical diseases, 20 (1), pp. e0013939

DOI: 10.1371/journal.pntd.0013939

ABSTRACT: Leptospirosis is a global zoonotic disease caused by pathogenic species of the genus Leptospira. Leptospira species are classified into two major clades (pathogenic, P, and saprophytic, S), and four subclades (P1, P2, S1, and S2), with the P1 subclade further divided into high virulence (P1+) and low virulence (P1-) groups. While previous studies have associated P1 + species to greater virulence in the host, phenotypic characterization across clades, particularly regarding dissemination and cell barrier disruption, remains limited. In this study, sixteen strains of pathogenic and saprophytic Leptospira representing subclades P1 + , P1-, P2, and S1 were evaluated in vitro to assess association with human endothelial cells, disruption of host VE-cadherin localization in adherens junctions, and immune response as measured by cytokine and chemokine release. Our findings indicate that VE-cadherin disruption correlates with P1 + species and the presence of

virulence-associated genes. Additionally, bacterial association with host cells correlates with the loss of VE-cadherin localization in adherens junctions. In vitro Leptospira interaction with endothelial cells induced production of chemokine and cytokines, most prominent in the P1 + clade and correlating with the presence of virulence-associated genes. Using an in vivo murine model of hematogenous dissemination to assess tissue tropism, live Leptospira were cultured from relevant tissues of animals inoculated with most of the strains tested and bacterial burdens were quantified to measure adhesion to tissues. Four of the six P1 + strains exhibited significantly higher tissue burdens in kidney, liver, and bladder at one hour post-inoculation compared to other Leptospira species. Together, these results suggest that endothelial cell interactions may be a key phenotypic marker for virulence classification in Leptospira. Further defining these interactions may therefore provide insights into interventions to combat this potentially fatal disease.
LANGUAGE OF ORIGINAL DOCUMENT: English

Raj D.P., Jena S., Dash S., Sailesh K., Gollapalli P.K., Baral, P.

Investigation of outbreak of leptospirosis in a village in Koraput, Odisha, 2024

(2026) Indian Journal of Public Health, 70, pp. S35 - S38

DOI: 10.4103/ijph.ijph_656_25

ABSTRACT: Background: Leptospirosis outbreaks have risen in India over the past three decades, especially in coastal regions. On September 9, 2022, a cluster of fever with myalgia and diarrhoea was reported in Village X, Koraput district, Odisha. A rapid response team confirmed the outbreak, and an investigation was initiated on September 11. Objectives: Our objective was to describe the event in terms of time, place, and person, and to identify potential sources. Materials and Methods: On confirmation of the outbreak, we diagnosed leptospirosis in seven cases by immunoglobulin M (IgM) enzyme-linked immunosorbent assay (ELISA). We initiated the investigation on September 11 to describe the outbreak and identify its source. We defined a probable case as an individual who reported at least one listed symptom on or after August 9, 2022, and conducted an active surveillance by door-to-door survey. We conducted a descriptive analysis of the reported cases by plotting an epidemiological curve and calculating the attack rate by place and person. Results: We identified 26 cases from September 3 to 17, 2022. The epi-curve indicated a continuous source outbreak. Higher attack rates were observed in low-lying areas, especially Majhi and Harijan Sahi. Adults aged 45–60 years and males were more affected. Most cases reported close contact with livestock and walking barefoot. All seven samples tested were positive for leptospirosis by IgM ELISA. Conclusion: Heavy rainfall and subsequent flooding likely increased rodent infestation, which may have led to the outbreak. Chemoprophylaxis for contacts reduced cases, and chlorination of drinking water was recommended to prevent further outbreaks.
LANGUAGE OF ORIGINAL DOCUMENT: English

Kumar K.V., Bokade P.P., Lakshman R., Deenadayalan O., Sowjanyakumari S., Nayak A. Pal, A., Swathi M., Arun Y.P., Suresh K.P., Dharmashekar C., Shivamallu C., Balamurugan V.

Meta-analysis of bovine leptospirosis prevalence in India

(2025) Archives of Razi Institute, 80 (6), pp. 1353 - 1368

DOI: 10.32598/ARI.80.6.3504

ABSTRACT: Leptospirosis is a globally significant and neglected zoonotic disease caused by pathogenic Leptospira spp., affecting a wide range of mammalian hosts including humans, cattle, and buffaloes. In

livestock, it leads to considerable economic losses through abortions, stillbirths, reduced fertility, and decreased milk production, especially in tropical and subtropical regions where environmental conditions favor bacterial persistence and transmission. Despite its severity, bovine leptospirosis remains under reported in endemic regions such as India. This meta-analysis synthesized data from 46 studies (2001–2021) to estimate the pooled prevalence, epidemiology, and diagnostic challenges of bovine leptospirosis in India. The pooled prevalence was 29% in cattle and 32% in buffaloes. Seropositivity ranged from 50– 70% in animals with reproductive disorders to 15–20% in healthy bovines. Coastal states such as Gujarat, Andhra Pradesh, Maharashtra, Tamil Nadu, Kerala, and the Andaman Islands showed the highest prevalence, influenced by favorable ecological conditions. Twenty pathogenic Leptospira serogroups were identified, with dominant serogroups (Sejroe, Icterohaemorrhagiae, Hebdomadis, Pomona, etc.) and evidence of temporal shifts in the prevalent serogroups. Significant diagnostic challenges included variability in sample sizes, heterogeneity among studies, and the limited sensitivity of enzyme-linked immunosorbent assay (ELISA) compared to the gold-standard microscopic agglutination test (MAT). These findings underscore the urgent need for enhanced surveillance, incorporation of diverse serogroups into diagnostic panels, and region-specific vaccination strategies. Strengthening molecular diagnostic tools, improving seroepidemiological studies, and implementing targeted control measures are essential for reducing the impact of leptospirosis on livestock productivity and public health in India. This work offers critical insights that can inform policy decisions and intervention strategies for effective disease management.

LANGUAGE OF ORIGINAL DOCUMENT: English

Zambrano A., Trilleras J.E., Arana Rengifo V.A., Lima Kassio M.G., Neves Menezes A.C., Morais C.L.M., Figueira Câmara A.B., García-Alzate R.J., Piñeres-Ariza, I.E., Romero-Vivas C.M.E., Falconar A.K.I., Cuello-Pérez M., Carmona-Patiño C.A.

Combined biospectroscopy with multivariate analysis for the differential diagnosis of leptospirosis disease: a pilot study

(2026) ACS Omega, 11 (4), pp. 5622 - 5631

DOI: 10.1021/acsomega.5c09285

ABSTRACT: Currently, reported estimates indicate that there are 1.03 million annual cases of leptospirosis, with 58,900 deaths worldwide. The Pan American Health Organization (PAHO) in 2022 indicates that the febrile symptoms of leptospirosis are similar to other diseases such as influenza and dengue, among other diseases. Therefore, an early and accurate diagnosis of leptospirosis is essential for adequate and rapid treatment. In this study, attenuated total reflection Fourier transform infrared (ATR-FTIR) spectroscopy combined with multivariate analysis techniques was employed to classify between healthy controls and leptospirosis positive samples. Spectra from 113 dried blood plasma samples from patients (n = 43 leptospirosis, and n = 80 controls) were analyzed by linear discriminant analysis (LDA), quadratic discriminant analysis (QDA), and support vector machine (SVM), combined with genetic algorithm (GA), successive projections algorithm (SPA), and principal component analysis (PCA) for feature selection/extraction. The GA-LDA model showed good sensitivity at 85.71% and specificity at 100% to discriminate both classes. Cross-validation was also performed, with the Venetian blinds method, showing the GA-LDA-CV model with better results in percentage sensitivity (76%), specificity (91%), precision (83%) and acurracy (86%), F-score (0.828), and AUC (0.835), when compared with the results of the preliminary GA-LDA model, and it is possible to rule out the possibility of overfitting of the preliminary GA-LDA model. Suggesting that combined ATR-FTIR

spectroscopy with multivariate analysis has great potential to detect biochemical variations produced by the Leptospira pathogen in the blood of infected patients. These findings emerge as a new potential tool for improving leptospirosis diagnosis in the future using a rapid, low-cost, and minimally invasive methodology.
LANGUAGE OF ORIGINAL DOCUMENT: English

Jost H.E., Henriksen De Linde M., Hawley J., Lappin M.R.

Evaluation of Leptospira species as a cause of endogenous uveitis in cats: a pilot study

(2026) Journal of feline medicine and surgery, 28 (2), pp. 1098612 - X251409537

DOI: 10.1177/1098612X251409537

ABSTRACT: Objectives: Although Leptospira species infections can be associated with intraocular inflammation in dogs and horses, there is limited information regarding the role these agents play in feline uveitis. The primary objective of this study was to report the prevalence of antibodies to Leptospira species and the presence of Leptospira species DNA in samples from cats with endogenous uveitis. The secondary objective was to assess for coinfections with Bartonella species, Toxoplasma gondii and eubacteria. Methods: Serum and aqueous humor (AH) samples from 37 cats diagnosed with endogenous uveitis that had been stored at -80°C were selected for this study based on sample availability. PCR assays for Leptospira species, T gondii, Bartonella species and 16S eubacterial rDNA were performed on AH. Sera were evaluated for antibodies to Leptospira species (microscopic agglutination test [MAT]), Bartonella species (IgG ELISA) and T gondii (IgM and IgG ELISA). Results: lthough sera from 2/37 (5.4%) cats were positive for antibodies to Leptospira interrogans serovar Pomona by MAT (1:100 titers), all AH samples were negative for DNA of Leptospira species. One AH sample was positive for DNA of a Streptococcus species but all were negative for DNA of T gondii and Bartonella species. Serum antibodies to Bartonella species (21/37, 56.8%), T gondii (7/37, 18.9%) or multiple agents (5/37, 13.5%) were common.Conclusions and relevanceAlthough the results of this study cannot be used to prove or refute Leptospira species as a cause of endogenous uveitis in cats, the detection of specific antibodies to Leptospira Pomona in the sera of two cats suggests that a larger cohort of cats should be tested to further evaluate the hypothesis. The AH of one cat was positive for the DNA of a Streptococcus species and future studies should investigate if post-streptococcal uveitis syndrome can also be found in cats. Evaluation of Leptospira species as a cause of intraocular inflammation (uveitis) in cats: a pilot study.A research team from Colorado State University College of Veterinary Medicine and Biomedical Sciences investigated the possibility of Leptospira species causing intraocular inflammation (known as uveitis) in cats. Leptospira species is a bacterium that lives in our surroundings, such as lake and river water, as well as in areas with rats, swine and deer. Leptospira-associated uveitis is a well-known eye disease in horses, dogs and humans but has never been investigated as a possible underlying cause for uveitis in cats. The research team looked at intraocular fluid (aqueous humor) samples from 37 cats from all over the USA and found only two samples that were positive for Leptospira species. They also found only one sample that was positive for Streptococcus species DNA. The Streptococcus bacterium has been associated with uveitis in humans after systemic Streptococcus infection and is known in humans as post-streptococcal uveitis syndrome. Although results of this study cannot be used to prove or refute Leptospira species as a cause of uveitis in cats, the detection of specific antibodies to Leptospira interrogans serovar Pomona in two cats suggests that a larger cohort of cats should be tested to further evaluate the hypothesis. In addition, continued work to determine if post-streptococcal uveitis syndrome occurs in cats should be considered.
LANGUAGE OF ORIGINAL DOCUMENT: English

Zhang S., Ma L., Cao Q., Zhang M., Yan G., Jiang W., Xie X., Zhang W., Cao Y.

Effect of a gut commensal *Lactobacillus* strain *Limosilactobacillus caviae* JL20 on leptospiral whole-cell inactivated vaccine in hamsters

(2026) PLoS neglected tropical diseases, 20 (2), pp. e0013951

DOI: 10.1371/journal.pntd.0013951

ABSTRACT: Leptospirosis is a global zoonotic threat caused by pathogenic Leptospira, and it remains challenging to combat because of persistent bottlenecks in vaccine development. The lack of well-defined protective antigens across Leptospira serovars continues to necessitate reliance on whole-cell inactivated vaccines, despite their recognized limitations: suboptimal efficacy and the absence of cross-serovar protection. In this study, we presented a Limosilactobacillus caviae (L. caviae) JL20 that significantly potentiated leptospiral vaccine efficacy through adjuvant-like effects. Survival assessment of hamsters demonstrated that JL20 enhances both vaccine efficacy and cross-protection. Oral JL20 significantly increased vaccine-induced cross-reactive binding antibody titers and total IgG antibody responses. In addition, JL20 exerted a priming effect in splenic macrophages, augmenting the expression of IL-1β and IL-6 in response to leptospiral vaccine stimulation, with a parallel enhancement in glycolytic activity. In vivo experiments demonstrated that JL20 significantly upregulated the expression of surface molecules CD38, CD69, and CD25 on T cells, as well as the production of the cytokine IL-2. JL20 enhanced the surface expression of key markers-including CD40, CD80, CD86, and MHC-II-on B cells. These effects indicate that JL20 enhances both cellular and humoral immune responses of leptospiral vaccine. ©: © 2026 Zhang et al. This is an open access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

LANGUAGE OF ORIGINAL DOCUMENT: English

Onafruo D.K., Klein J., Kostoulas P., Erume J., Kokas I., Jubara A.S., Sánchez Romano J., Odoch T., Kitale E., Marin P.M., Sabbath E., Kankya C.

Bayesian estimation of true prevalence and associated risk factors for Leptospira spp. among slaughterhouse workers and slaughtered cattle in the Bahr el Ghazal region of South Sudan

(2026) Zoonoses and Public Health

DOI: 10.1111/zph.70039

ABSTRACT: Introduction: Leptospirosis is a major but under-reported zoonotic disease, and epidemiological data from South Sudan remain limited. This study estimated the true prevalence of Leptospira spp. exposure and identified associated risk factors among slaughterhouse workers and slaughtered cattle in Western Bahr El Ghazal. Methods: A cross-sectional study was conducted in major slaughterhouses. Serum samples from workers and cattle were tested using the microscopic agglutination test (MAT). Bayesian hierarchical models were used to adjust for diagnostic test imperfections and to estimate true prevalence. Structured questionnaires captured occupational and animal-level risk factors for analysis within the Bayesian framework. Results: The estimated true prevalence was 10% in slaughterhouse workers and 85% in slaughtered cattle, indicating a high zoonotic exposure risk. Among workers, flaying, inconsistent use of protective equipment, and handling higher numbers of carcasses per day were significantly associated with seropositivity. In slaughtered cattle, exposure varied by breed, age, and sex. The model further indicated a 78% probability that a randomly selected slaughterhouse was affected and a 65% probability that infection levels among workers remained below 5%. Conclusions: This study provides the first Bayesian-based estimates of leptospiral

exposure in slaughterhouse settings in Western Bahr El Ghazal. The findings underscore the need to improve occupational safety, strengthen surveillance, and apply One Health approaches to reduce zoonotic transmission. Despite limitations, including lack of environmental data, the Bayesian framework proved effective for generating robust prevalence estimates in a resource-limited setting. Expanded geographic coverage and incorporation of environmental assessments are recommended to inform targeted leptospirosis control strategies.
LANGUAGE OF ORIGINAL DOCUMENT: English

Sethi G., Sahoo S., Han S.-C., Shin D., Hwang J.H.

Computational identification of natural inhibitors targeting GroEL in *Leptospira interrogans*: an integrative virtual screening and molecular dynamics approach

(2026) Frontiers in Cellular and Infection Microbiology, 15, art. no. 1733096

DOI: 10.3389/fcimb.2025.1733096

ABSTRACT: Introduction: Leptospirosis is a zoonotic disease caused by Leptospira interrogans and represents a major public health and veterinary concern. The persistence of the pathogen is closely associated with biofilm formation, yet targeted therapeutics are currently unavailable. The GroEL chaperonin, a conserved protein involved in biofilm formation and immunogenicity, was investigated as a potential therapeutic target. Methods: A structure-based virtual screening approach was performed using a library of 543,503 natural compounds from the Life Chemicals database. Top-ranked ligands were evaluated using molecular docking and physicochemical and pharmacokinetic property analyses. Density functional theory calculations were performed to assess electronic stability, followed by molecular dynamics simulations to evaluate ligand–protein complex stability. Principal component analysis and MM-PBSA binding free energy calculations were subsequently applied to characterize conformational dynamics and binding affinity. Results: Five compounds (F3385-2019, F1243-0200, F3139-0927, F2801-0179, and F1864-0208) exhibited strong binding affinities toward GroEL, with docking energies ranging from −10.34 to −8.26 kcal/mol. All shortlisted compounds complied with Lipinski’s Rule of Five and demonstrated favorable pharmacokinetic properties. Molecular dynamics simulations and MM-PBSA analyses indicated stable ligand–protein interactions. Among the candidates, F1864–0208 and F1243–0200 emerged as the most stable and promising leads, whereas the remaining compounds showed moderate inhibition. Discussion: This study provides computational evidence supporting GroEL as a viable drug target in L. interrogans. The identified natural compounds may represent promising scaffolds for the development of novel anti-leptospiral agents. Further in vitro and in vivo studies are required to validate their therapeutic efficacy and safety.
LANGUAGE OF ORIGINAL DOCUMENT: English

Ruiz C., Rodríguez-Pastor R., Escolar Rodríguez C., Alonso H., Millán J.

Artificial irrigation impacts the seasonal occurrence of pathogenic *Leptospira* in its wild reservoirs in a Mediterranean environment

(2026) Zoonoses and Public Health

DOI: 10.1111/zph.70043

ABSTRACT: Background: Human activities play a significant role in the emergence of infectious diseases. We aimed to test whether artificial irrigation affects the occurrence of a zoonotic bacteria sensitive to desiccation, pathogenic Leptospira species (pathoLep), in micromammals inhabiting Mediterranean ecosystems. Methods:

A total of 361 individuals, including 217 Algerian mice (Mus spretus), 79 wood mice (Apodemus sylvaticus), and 65 greater white-toothed shrews (Crocidura russula), were captured during the four seasons of 2022 in six sites along a riparian forest close to a large city in north-eastern Spain and the surrounding agricultural fields, which are irrigated by flooding. A piece of kidney from each individual was analysed by means of two real-time PCR protocols targeting the lipL32 gene, which is exclusively found in pathoLep. Generalised Linear Models were used to study the factors that may be related to the presence of pathoLep. Results: DNA of pathoLep was detected in 28% of the individuals, a relatively high occurrence compared to similar studies. The best model for the general micromammal population included four significant factors: season, age, species, and habitat. Prevalence was significantly lower during the dry seasons; in juveniles than in adult individuals; in the wood mouse than in the Algerian mouse and the shrew; and in natural than in agricultural habitats. Prevalence was consistently higher in agricultural habitats during all the seasons, reaching over 55% prevalence in these areas during spring. For the core species, the Algerian mouse, the best model included two factors (seasons and habitat), in the same sense as the general population model. Conclusions: This study shows that pathoLep are widespread among micromammals in the Middle Ebro Valley and that their occurrence is shaped by intrinsic and extrinsic factors. We identified a human activity (artificial irrigation) as an important driver favouring leptospiral survival in rural environments.
LANGUAGE OF ORIGINAL DOCUMENT: English

Wekalao J., A. Elsayed H.A., Solouma E.M., Mehaney A., A., Kabarokole P., Bin-Jumah M.N.
High-sensitivity multilayer SPR biosensor based on ZnO/Graphene/Ag/MXene architecture for simultaneous detection of leptospirosis, malaria, and glucose imbalance
(2026) Journal of Electromagnetic Waves and Applications
DOI: 10.1080/09205071.2025.2612568
ABSTRACT: Infectious diseases and metabolic disorders remain major global health challenges, especially in areas with limited diagnostic infrastructure. Conventional diagnostic methods are often costly, complex, and restricted to detecting a single analyte. This study presents a multilayer surface plasmon resonance (SPR) biosensor composed of zinc oxide (ZnO), graphene, silver (Ag), and MXene layers for simultaneous, label-free detection of leptospirosis, malaria, and glucose imbalance. The combined material system improves plasmonic field confinement, increases surface electron density, and strengthens biomolecular interaction sensitivity. The sensor uses a Kretschmann configuration with p-polarized light excitation and is analyzed through the transfer matrix method. Systematic optimization of layer thickness and refractive index variation improves optical performance across several biomarkers. Numerical simulations show that the sensor achieves 1240°/RIU sensitivity with a 1.5° resonance shift for polyuria detection, 2° angular tuning for oliguria, a 2.5° resonance shift for glucose detection, and a 10° shift with 271.43°/RIU sensitivity for malaria biomarkers. Quality factors range from 19.76 to 24.03, and detection limits vary between 0.006 and 0.134 RIU across analytes. Regression-based machine learning analysis verifies the model's predictive accuracy, with R^2 values above 0.995 for refractive index variation.
LANGUAGE OF ORIGINAL DOCUMENT: English

Sagar T., Patwardhan V., Rathi A., Bordoloi T., Verma, N.
Leptospirosis: unveiling the hidden threat in a non-endemic region of India
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ABSTRACT: Introduction: Leptospirosis is a globally significant yet often overlooked zoonotic disease caused by pathogenic Leptospira bacteria. The disease manifests with a wide range of non-specific symptoms, making clinical diagnosis challenging. It remains underreported especially in non-endemic settings possibly due to lack of awareness, clinical features overlapping with other common diseases and non-availability of suitable microbiological diagnostics. This study assessed the seroprevalence of leptospirosis in clinically suspected cases in a tertiary care hospital of New Delhi and it also evaluated the PCR test results obtained from urine and plasma specimens in anti-Leptospira IgM positive patients. Methods: A retrospective observational single centre study was conducted between January 2023 and December 2024. A total of 2181 patients, clinically suspected of leptospirosis, were serologically tested using anti-Leptospira IgM ELISA kit (Panbio, Australia). Urine and whole blood specimens from sero-positive patients were further analysed using an in-house standardised PCR assay. Results: Among the 2181, 448 (20.6%) tested positive for anti-Leptospira IgM by ELISA. PCR testing was performed in a total of 350 out of 448 ELISA-positive patients, of which 98 (28%) patients were found to be positive either from urine/whole blood or both the specimens. A total of 140/448 (31.3%) of the seropositive cases were categorised as possible leptospirosis, while 245/448 (54.7%) were classified as presumptive leptospirosis based on modified Faine's criteria. Conclusion: This study highlights a significant seropositivity rate of leptospirosis among clinically suspected cases in a tertiary care setting in New Delhi, underscoring its clinical relevance even in non-endemic regions. The combined use of serological testing and targeted PCR analysis provided complementary diagnostic value, aiding in more accurate case classification. These findings emphasise the need for heightened clinical awareness, improved diagnostic access and early detection strategies to better manage and control leptospirosis in urban healthcare settings.
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Genetic diversity of pathogenic Leptospira spp. in small mammals of the Northwestern Federal District of Russia

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ABSTRACT: Introduction. Leptospirosis is a dangerous zoonotic disease maintained by small mammal reservoirs. Studying the pathogen’s genetic diversity in animal populations is crucial for epidemiological surveillance. Aim — detection and molecular genetic characterization of leptospirosis pathogens in small mammals (rodents, insectivores, bats) in the Northwestern Federal District (NWFD) of Russia to assess their species diversity and potential epidemiological significance. Materials and methods. From 2023 to 2025, 88 bat urine samples and organ specimens from 773 rodents and insectivores trapped in the Arkhangelsk, Leningrad, and Pskov regions, the Republic of Karelia, and Saint Petersburg were collected. DNA of pathogenic leptospires was detected by real-time PCR. Genotyping of positive samples was performed by Sanger sequencing the secY gene fragment followed by phylogenetic analysis. Results. Genetic markers of Leptospira spp. were found in 11.4% of bat urine samples and in 2.5% of organ samples from rodents and insectivores. The highest infection rates were noted in Saint Petersburg (3.2%) and the Republic of Karelia (3.0%). Phylogenetic analysis revealed the circulation of three species of pathogenic leptospires: L. kirschneri (the dominant species), L. interrogans and L. borgpetersenii. Genetically distinct variants were found in bats, and one isolate (PV807621) showed only 95% similarity to reference strains of L. interrogans, suggesting the

possible discovery of a new bat-adapted genetic variant. Conclusion. This study is the first to demonstrate that small mammal populations in the NWFD are a reservoir for a wide range of pathogenic leptospires. The detection of potentially novel genetic variants in bats underscores their important role in the maintenance and evolution of Leptospira pathogens and highlights the need to consider this factor in epidemiological risk assessment.

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