Istituto Zooprofilattico Sperimentale
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Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia – Romagna "Bruno Ubertini"
Reparto Tecnologie Biologiche Applicate – Laboratorio Batteriologia Specializzata
Email: mario.dincau@izsler.it, crn.leptospirosi@izsler.it
Telefoni: 030 2290268, 030 2290323

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Widiastuti D., Paramita D.K., Murwanti R., Kusrini I., Wijayanti N., Haryanto A.

Evaluation of synthetic-gene recombinant LipL32 antigen for IgM ELISA detection of *Leptospira* infection

(2025) Indonesian Journal of Biotechnology, 30 (4), pp. 226 - 235

DOI: 10.22146/ijbiotech.111102

ABSTRACT: Leptospirosis presents with nonspecific clinical features and requires time-consuming laboratory tests for gold standard diagnosis. This study aims to design and characterize the recombinant LipL32 from synthetic gene and assess its performance as an antigen for detecting leptospirosis. The antigen was developed by cloning the LipL32 gene conserved portion of Leptospira interrogans serovar Icterohaemorrhagiae strain Langkawi. The immunoinformatic was used to characterize the developed rLipL32. Western blot results using anti-histidine revealed a band of rLipL32 protein at ~40 kDa. Subsequently, it was used to examine the IgM antibody on human sera by using ELISA. The IgM-LipL32 ELISA was evaluated using 67-positive and 25-negative sera and compared with a commercial ELISA. With a cut-off value of 0.8, it showed 85.7% sensitivity, 83.3% specificity, a 48% positive prediction value (PPV), and 97% negative prediction value (NPV), indicating modest performance compared to existing commercial kits. The rLipL32 is a potential antigen for detecting IgM using ELISA; however, for use in low incidence areas, a confirmation test is crucial.

LANGUAGE OF ORIGINAL DOCUMENT: English

Didkowska A., Brodard I., Zalewski A., Filip-Hutsch K., Kuhnert P.

Serological and molecular evidence of *Leptospira spp*. in martens from Poland

(2026) BMC Veterinary Research, 22 (1), art. no. 131

DOI: 10.1186/s12917-026-05317-x

ABSTRACT: Background: Leptospirosis is a globally-distributed zoonotic disease caused by pathogenic Leptospira spp., affecting humans, domestic animals, and wildlife. Despite its importance, little is known about the ecological and epidemiological aspects of Leptospira spp. infection in wild carnivores, particularly martens. This study investigated the presence of Leptospira spp. in stone martens (Martes foina) and pine martens (Martes martes) in northern Poland using serological (MAT) and molecular (real-time PCR and MLST) methods. Results: Samples from 129 martens collected between 2012 and 2022 revealed an 18% seroprevalence and a 13% PCR-positivity rate. Seroreactivity against six Leptospira spp. serovars was identified, all associated with rodent transmission cycles. Molecular analysis confirmed the presence of sequence types ST117 and ST110, previously reported in small mammals in Central Europe. Conclusions: Martens are susceptible hosts for Leptospira spp. Given their adaptability and overlapping habitats with livestock and humans, they also represent valuable targets for integrated surveillance within the One Health framework. This study provides the first evidence of Leptospira spp. sequence types and serological diversity in martens in Poland, and offers valuable insights into the epidemiology of wildlife leptospirosis.

LANGUAGE OF ORIGINAL DOCUMENT: English

Schick L.A., Kovacs K.M., Lydersen C., Rohner S., Prenger-Berninghoff E., Heydel C., Ewers C., Postel A., Gremmel N., Becher P., Strube C., Siebert U.

Sharing is caring? pathogens and pathogen-specific antibodies in arctic endemic seal species and the newly sympatric harbor seals in Kongsfjorden, Svalbard

(2026) Marine Mammal Science, 42 (2), art. no. e70143

DOI: 10.1111/mms.70143

ABSTRACT: Climate change associated transformations of Arctic marine ecosystems are having detrimental impacts on Arctic endemic marine mammals. However, warming conditions are providing new habitats for temperate marine mammals, some of which are expanding into Arctic regions, posing a threat of novel pathogen introduction and disease transmission. We analyzed swab samples for Influenza A, morbilli- (Phocine distemper virus, PDV), and herpesvirus nucleic acid and performed microbiological screenings and serological analyses for antibodies for the same viral pathogens, the bacterial agents Brucella spp. and Leptospira spp. and the protozoan parasite Toxoplasma (T.) gondii from ringed (Pusa hispida), bearded (Erignathus barbatus), and the newly established harbor seals (Phoca vitulina) in Kongsfjorden, Svalbard. Antibodies against Phocine Herpesvirus-1 or antigenetically related phocine herpesviruses (PhHV) were detected in all species. Antibodies against Influenza A were only found in one ringed seal and antibodies against PDV were found in two harbor seals. Twelve harbor seals and two ringed seals tested positive for Herpesvirus DNA by PCR. Brucella spp. and Leptospira spp. antibodies were detected in multiple harbor seals and a single bearded seal. Three harbor, two ringed, and one bearded seal had antibodies against T. gondii. Our results indicate an overlap and possible transmission of pathogens between all investigated seal species. The introduction of new pathogens to the Arctic through temperate species' range expansions could have fatal consequences for immunologically naive Arctic seal populations and should be further investigated.
LANGUAGE OF ORIGINAL DOCUMENT: English

Rajaonarivelo J.A., Kauffman K.M., Randriamoria T.M., Herrera J.P., Wickenkamp N., Turpin M., Baudino F., Young H.S., Soarimalala V., Goodman S.M., Nunn C.L., Tortosa P.

***Leptospira* prevalence and lineages vary across land-use types due to shifts in small mammal communities**

(2026) Applied and Environmental Microbiology, 92 (2)
DOI: 10.1128/aem.02061-25

ABSTRACT: Human-induced land-use change can affect the composition of small mammal communities and the ecology of their zoonotic pathogens — yet questions remain on the direction and generality of these changes, which can have opposite effects on disease prevalence depending on the ecological context and pathogen involved. These contrasting patterns highlight the need to investigate how specific host-pathogen assemblages respond to local anthropogenic land-use mosaics. To address this need, we studied terrestrial and bat species composition, Leptospira infection prevalence, and Leptospira species composition across a mosaic of land-use types in northeastern Madagascar. We found differences in host communities between forested, agricultural, and village land-use types for both bat (n = 400) and terrestrial (n = 2,053) small mammal communities. Leptospira infection prevalence was higher in bats (37.7%) than in terrestrial small mammals (13.8%), and bats were infected with Leptospira strains that were molecularly distinct from those shed by terrestrial small mammals. Non-native mice and rats were almost exclusively infected with cosmopolitan L. kirschneri and L. interrogans, respectively, while some native terrestrial small mammals sheltered L. mayottensis, and bats hosted a more diverse set of Leptospira species. Leptospira prevalence across land-use types varied in terrestrial small mammals, but not in bats. Altogether, the highest prevalence occurred in mice in flooded rice fields. Our data show that land use predominantly impacts Leptospira infecting terrestrial mammals, likely due to habitat disturbance favoring replacement of endemic hosts and pathogens with Muridae rodents and their associated pathogens, many of which are zoonotic.
LANGUAGE OF ORIGINAL DOCUMENT: English

Xu C., Pang Y., Liao M., Shen J., Liu Z.

A stochastic approach to leptospirosis disease in human and vector populations: analysis, dynamics and validation with worldwide real data

(2026) Journal of Biological Systems

DOI: 10.1142/S0218339026500142

ABSTRACT: Leptospirosis is a bacterial infection transmitted through contact with water contaminated by the urine of infected animals, often affecting both humans and animals, particularly in tropical and subtropical regions. This paper illustrates a stochastic model for the transmission dynamics of leptospirosis infections in both human and vector populations. The model enhances key factors such as rainfall impact, vector behavior, and human interactions to capture the transmission of the disease. Through a detailed mathematical investigation, the paper explains the criteria required for the existence and uniqueness of a global solution for the stochastic model. Nonlinear analysis notions are utilized to investigate the ergodic aspects of the stochastic model. To validate the model's effectiveness, numerical simulations are conducted, and the results are compared with deterministic behavior. The comparison highlights the importance of considering stochasticity in accurately capturing the dynamics of leptospirosis. The paper also illustrates the relevance of the proposed system by comparing the model's dynamics with real-world leptospirosis cases globally. This validation displays the model's ability to capture the epidemiological characteristics and trends observed in different geographical regions. Moreover, the impact of the rate of transmission of leptospirosis from an infected vector to a susceptible human on the evolution of infected individuals within the population is visualized, delivering insightful information. Major outputs of the study include the identification of critical parameters influencing disease spread and the demonstration of the stochastic model's superior accuracy over deterministic approaches in reflecting real-world scenarios.

LANGUAGE OF ORIGINAL DOCUMENT: English

Tian H., Tao X., Hu N., Liu Y., Li Y., Zhou L., Zeng L.

***Leptospira interrogans* HtrA protease is a potent inducer of multifaceted cellular responses**

(2026) Antonie van Leeuwenhoek, International Journal of General and Molecular Microbiology, 119 (3), art. no. 57

DOI: 10.1007/s10482-026-02270-5

ABSTRACT: Leptospirosis, a bacterial zoonosis caused by select pathogenic spirochetes belonging to the genus Leptospira, can trigger a systemic inflammatory response syndrome due to a cytokine storm that can occur during infection. However, the molecular mechanisms underlying the extensive inflammatory responses during leptospiral infection remain poorly understood. In this study, we characterized a high temperature requirement protein A (HtrA) homologue encoded by the L. interrogans gene locus LIC12812, referred herein as LepHtrA. We used AlphaFold 3 to predict the structure of this protein. And we show that LepHtrA is located on the surface of L. interrogans, and its expression is upregulated by increased temperature. An in vitro enzyme assay using purified LepHtrA provides direct evidence of its serine protease activity. We demonstrate that LepHtrA induces a robust pro-inflammatory response in RAW264.7 cells, a mouse macrophage cell line, by promoting their differentiation into pro-inflammatory M1 macrophages. This differentiation leads to an increased production of pro-inflammatory cytokines and the generation of reactive oxygen species, ultimately inducing cellular apoptosis via modulation of Bcl-2/Bax expression. Collectively,

our study suggests that LepHtrA is a temperature-induced and surface-exposed antigen that can contribute to cellular inflammation, stress, and apoptosis, potentially influencing the pathogenesis of leptospirosis.
LANGUAGE OF ORIGINAL DOCUMENT: English

Baimova R., Karmokov I., Riabiko E., Lyzenko I., Grechishkina D., Ramsay E., Ostankova Y., Tokarevich N., Loan H.K., Tung L.T., Trung P.C.
Molecular detection and genotyping of pathogenic *Leptospira* in small mammals from Southern Vietnam
(2026) Microorganisms, 14 (2), art. no. 465
DOI: 10.3390/microorganisms14020465
ABSTRACT: Leptospirosis is a major zoonosis, yet genetic data on Leptospira strains in animal reservoirs in Southern Vietnam are limited. This study aimed to detect and genotype pathogenic Leptospira in synanthropic small mammals. From 2016 to 2020, 856 animals were captured in three regions. Kidneys were screened by qPCR targeting pathogenic Leptospira 16S rRNA, and positive samples were genotyped via secY gene sequencing. The overall prevalence was 7.8%. Rattus norvegicus was the primary host (12.4% infected). Leptospira interrogans predominated (77.6%), followed by L. borgpetersenii (22.4%). Infection risk was significantly associated with the following factors: larger host body size (increased body mass and hindfoot length); capture in Ho Chi Minh City; and the rainy season. The study confirms the stable circulation of highly virulent L. interrogans in urban R. norvegicus populations. The identified risk factors provide a basis for targeted interventions to mitigate human health risks.
LANGUAGE OF ORIGINAL DOCUMENT: English

Ferrari Salviano de Almeida A., Merighi Davi G.S., Visnardi Biazola A., Silva Roberto G., Gonçalves Cauê A.B., Sanchez-Limache D.E., Ogusku Cardoso B.S., Silva de Souza A., de Souza R.F., Guzzo Rodrigues C.
Discovery of novel c-di-GMP-related genes in *Leptospira interrogans*
(2026) Pathogens, 15 (2), art. no. 151
DOI: 10.3390/pathogens15020151
ABSTRACT: Cyclic di-GMP (bis-(3′→5′) cyclic dimeric guanosine monophosphate) is a ubiquitous bacterial second messenger that regulates a wide range of cellular processes, including biofilm formation, motility, virulence, and environmental adaptation. Its intracellular levels are dynamically controlled by diguanylate cyclases (DGCs), which synthesize c-di-GMP from GTP, and phosphodiesterases (PDEs), which degrade it into linear pGpG or GMP. The functional effects of cytoplasmic c-di-GMP are mediated through diverse effector proteins, including PilZ domain-containing receptors, transcription factors, and riboswitches. In Leptospira interrogans, a major pathogenic species responsible for leptospirosis, the regulatory roles of c-di-GMP remain poorly understood. Here, we performed a comprehensive bioinformatics and structural analysis of all predicted c-di-GMP related proteins in L. interrogans serovar Copenhageni strain Fiocruz L1-130, a serovar generally associated with severe manifestations of leptospirosis in humans. Our analysis identified seventeen proteins containing GGDEF domain, five proteins containing both GGDEF and EAL domains, four proteins containing EAL domain, five proteins containing HD-GYP domain, twelve proteins containing PilZ domain, and one protein containing an MshEN domain. Comparative analysis with well-characterized bacterial homologs suggests that L. interrogans possess a complex c-di-GMP signaling network, likely involved in modulating biofilm formation, host–pathogen interactions, and environmental survival. These findings provide new insights into the c-di-GMP

regulatory network and on signal transduction in Leptospira and lay the foundation for future functional studies aimed at understanding its roles in physiology, virulence, and persistence.
LANGUAGE OF ORIGINAL DOCUMENT: English

Birlutiu V., Birlutiu R.-M.

Leptospirosis in Central Romania: a 17-year single-center cohort study of hospitalized adults

(2026) Microorganisms, 14 (2), art. no. 298

DOI: 10.3390/microorganisms14020298

ABSTRACT: Leptospirosis is an important zoonosis that can present as a self-limited influenza-like illness or progress to severe, including life-threatening multiorgan dysfunction. We report the epidemiology, clinical profile, and correlates of severity among adults hospitalized patients with leptospirosis diagnosed in central Romania over a period of 17 years. We conducted a retrospective, single-center cohort study of adults admitted between 1 January 2008 and 1 December 2025 with laboratory-confirmed leptospirosis. Confirmation was based on positive anti-Leptospira IgM serology, with repeat testing when the initial result was equivocal and confirmation with a microscopic agglutination test. We extracted demographic, exposure, clinical, laboratory, treatment, and outcome data from medical records. The modified Faine score was also calculated using admission data. Sixty-four patients were included in this analysis, of which 53 (82.8%) were male patients. Admissions peaked in 2023–2025 (34/64, 53.1%) and in the August–September months. Reported exposures were predominantly peri-domestic (46.9%), followed by rural/animal-related occupations (20.3%) and freshwater contact (17.2%). Severe disease occurred in 26/64 (40.6%), was more frequent in men ($p = 0.021$), and was more common pre-pandemic than during/after the pandemic ($p < 0.001$). Severe cases were associated with oliguria/anuria, hematuria, and jaundice, alongside higher urea/creatinine and bilirubin, lower hemoglobin and lymphocyte percentages, and a longer hospitalization period. One in-hospital death occurred (1.6%). Serogroup identification was available for 10 patients (15.6%) (pre-pandemic only). The mean modified Faine score was 27.5 ± 6.0. In this temperate-region cohort study, hospitalized leptospirosis showed a marked male predominance, a late-summer peak, and a substantial burden of severe disease. Early renal and hepatobiliary manifestations with concordant laboratory abnormalities may support timely risk stratification and escalation of care, while expanded molecular diagnostics and systematic typing are needed to clarify temporal trends and guide prevention.
LANGUAGE OF ORIGINAL DOCUMENT: English

Bance-Anicama D.I., Diaz-Orihuela M.M., Diaz-Orihuela L.M., Morales-García W.C.

Factors associated with the prevalence of dengue–leptospirosis coinfection in patients hospitalized for febrile syndrome

(2026) Tropical Medicine and Infectious Disease, 11 (2), art. no. 50

DOI: 10.3390/tropicalmed11020050

ABSTRACT: Background: In tropical regions, dengue and leptospirosis coexist and share a nonspecific clinical onset that hinders timely diagnosis. Coinfection may worsen the clinical course and increase mortality. Objective: To estimate the prevalence of dengue, leptospirosis, and coinfection among patients with febrile syndrome in Madre de Dios (Peru) and to identify associated clinical factors. Methods: Observational, analytical, cross-sectional, retrospective study conducted at a primary-level health facility. Clinical and laboratory records of patients with febrile syndrome seen in 2024 were analyzed. Categorical variables were

summarized as frequencies (%) and numeric variables as mean ± SD or median [IQR]. Comparisons used chi-square or Fisher's exact test, Student's t test, or the Mann–Whitney U test, as appropriate. Associations were estimated using Poisson regression models with robust variance, adjusted for sex, reporting prevalence ratios (PRs) and 95% CIs. Analyses were performed in R 4.0.2. Results: A total of 226 patients were included. Positivity was 19.0% for dengue (43/226), 66.8% for leptospirosis (151/226), and 5.8% for coinfection (13/226). In the bivariate analysis, dengue was associated with higher temperature ($p < 0.001$), lower mean arterial pressure ($p = 0.007$), mucosal bleeding/ecchymosis ($p = 0.049$), and lower fluid intake ($p = 0.021$); temperature was also higher in coinfection ($p = 0.021$). In Poisson models, dengue was associated with tachycardia (PR = 5.69; 95% CI: 1.95–13.07; $p < 0.001$), temperature (PR = 1.61 per °C; 1.23–2.12; $p = 0.001$), bilateral polyarthralgia (PR = 2.55; 1.14–5.04; $p = 0.012$), and mucosal bleeding/ecchymosis (PR = 3.31; 0.94–8.37; $p = 0.027$). Leptospirosis was associated with male sex (PR = 0.78 vs. female; 0.65–0.94; $p = 0.010$) and fever (PR = 2.38; 1.17–6.03; $p = 0.035$). Leptospira–dengue coinfection was related to higher temperature (PR = 1.75 per °C; 1.05–3.01; $p = 0.036$). Conclusions: Simple clinical signs such as fever/elevated temperature, tachycardia, bilateral polyarthralgia, and mucosal bleeding can help prioritize suspicion of dengue, leptospirosis, or coinfection; guide requests for dual testing (dengue–Leptospira), early hydration in dengue, and timely initiation of antibiotic therapy in leptospirosis. These findings support the development of integrated triage algorithms and strengthening access to molecular diagnostics in high-burden febrile syndrome settings.
LANGUAGE OF ORIGINAL DOCUMENT: English

Matiz-González J.M., Silva-Ramos C.R., Agudelo-Flórez P., Wunder E.A., Jr., Hidalgo M.

Phylogenetic evidence of possible zoonotic circulation of Leptospira species between human febrile patients and bats within a same interface

(2026) One Health, 22, art. no. 101382

DOI: 10.1016/j.onehlt.2026.101382

ABSTRACT: Leptospirosis is a widespread zoonotic disease caused by pathogenic Leptospira spp., maintained by a wide range of animal reservoirs. In Colombia, it remains a major cause of acute undifferentiated febrile illness, yet the role of wildlife, particularly bats, in its transmission cycle is poorly understood. To investigate the relationship between Leptospira infecting humans and bats in Villeta, Colombia, thirty partial available leptospiral 16S rRNA sequences from febrile patients (n = 13) and bats (n = 17) were analyzed. Hierarchical clustering identified twelve groups (A–L), two (C and G) containing sequences from both hosts, showing 99–100% identity. Phylogenetic analysis placed these clusters within the P1 clade, forming distinct monophyletic groups separate from known species, suggesting Leptospira lineages shared between bats and febrile patients. These findings provide molecular evidence suggesting a genetic relationship between Leptospira species identified from febrile patients and bats within a shared ecological interface in Colombia.
LANGUAGE OF ORIGINAL DOCUMENT: English

Romero V.A., Lucero-Prisno D.E., III, Romero E.T., Cabansag J.N., Vidad M.I., Garcia R.D., Daet A.A., Ignacio M.D.

Reassessing leptospirosis: the need for proactive public health strategies

(2026) Ethics, Medicine and Public Health, 34, art. no. 101257

DOI: 10.1016/j.jemep.2026.101257

LANGUAGE OF ORIGINAL DOCUMENT: English

Schuler E.J.A., Patel D.T., Moylan A.D., Miller D.P., Marconi R.T.

AUTHOR FULL NAMES: Schuler, Edward J.A. (57218607098); Patel, Dhara T. (57661531300); Moylan, Aidan D. (58922965700); Miller, Daniel P. (55494848200); Marconi, Richard T. (7007019632)

57218607098; 57661531300; 58922965700; 55494848200; 7007019632

The *Leptospira interrogans* CdaA protein is a functional diadenylate cyclase

(2026) Infection and Immunity, 94 (3)

DOI: 10.1128/iai.00716-25

ABSTRACT: Leptospirosis is a zoonotic disease that affects humans, companion animals, livestock, and wildlife. There are over 60 species that are established pathogens. Leptospires must rapidly adapt to changing environmental conditions as they pass between the environment and vertebrates. Bioinformatic analyses have identified a putative CdaA-type diadenylate cyclase (DAC) in Leptospira interrogans Fiocruz L1-130 (lic10844). DACs catalyze the synthesis of cyclic di-adenosine monophosphate (c-di-AMP) from two ATP molecules. The potential regulatory roles and effector mechanisms of c-di-AMP among pathogenic Leptospira species have not been explored. Here, we demonstrate that lic10844 encodes a functional DAC (henceforth referred to as CdaA). Cellular localization analyses, size exclusion chromatography, and DAC assays revealed that CdaA is an inner membrane-associated protein that functions biologically as a homodimer, utilizing cobalt or manganese for enzymatic activity. Transcription of cdaA is responsive to and elevated by potassium levels. Individual amino acid residues that directly or indirectly mediate the DAC activity of CdaA were identified using site-directed mutagenesis. This report represents an important initial step in elucidating the biological function of CdaA, and by extension, c-di-AMP, in the biology and pathogenesis of Leptospira species.

LANGUAGE OF ORIGINAL DOCUMENT: English

Skinner V.J., Ward M.P., Griebsch C.

Risk of infection in dogs in contact with clinical canine leptospirosis cases

(2026) Australian Veterinary Journal

DOI: 10.1111/avj.70069

ABSTRACT: Background and aim: Canine leptospirosis cases have been increasing since the disease emerged in urban Sydney in 2017. Clinical infection is associated with a high case fatality rate and might pose public health risks. This study was conducted to determine whether Leptospira spp. exposure of healthy dogs in contact with clinical cases is a risk for leptospirosis infection. Methods: In-contact (exposed) dogs were identified from clinical leptospirosis cases and prospectively enrolled. In-contact dogs underwent leptospirosis testing by polymerase chain reaction (PCR) and microscopic agglutination test (MAT). An historical comparison population of dogs unexposed to clinical leptospirosis cases was selected from a previous seroprevalence study, from which exposure status and MAT titres were available. Dogs were excluded from analysis if they had a prior history of leptospirosis vaccination or did not have MAT performed. An ordinary logistic regression model was used to estimate the prevalence odds ratio of infection given exposure. Potential confounding by age, sex and neuter status was assessed. Results: Exposure to a dog with clinical leptospirosis was significantly associated with an increased risk of infection ($P < 0.05$). The odds of becoming infected with canine leptospirosis were five times greater for dogs exposed to clinical cases than for dogs not known to have been exposed (OR 5.0, 95% CI: 1.3–20.0). This association was not confounded by age, sex or neuter status. Conclusion: These findings support the prophylactic use of antimicrobials in dogs that have been in contact with dogs with clinical leptospirosis.

LANGUAGE OF ORIGINAL DOCUMENT: English

Perera T., Schwarz F., Muzeniek T., Siriwardana S., Becker-Ziaja B., Perera I., Handunnetti S., Weerasena J., Premawansa G., Premawansa S., Yapa W., Kohl C., Nitsche A.

First report of pathogenic *Leptospira* in Sri Lankan bats: a potential reservoir risk?

(2026) PLoS neglected tropical diseases, 20 (3), pp. e0012576

DOI: 10.1371/journal.pntd.0012576

ABSTRACT: BACKGROUND: The genus Leptospira, classified under the phylum Spirochaetes, includes saprophytic, intermediate, and pathogenic species. Pathogenic Leptospira spp. are the causative agents of leptospirosis, a widespread and often neglected zoonotic disease that causes severe illness in humans, particularly in tropical and subtropical regions. In Sri Lanka, leptospirosis causes annual outbreaks, especially during the monsoon seasons. While rodents are recognized as primary reservoirs, bats have also been identified as potential reservoir hosts. This study aimed to detect and characterize Leptospira species in bats roosting in Wavulgalge cave, Sri Lanka. METHODOLOGY/PRINCIPAL FINDINGS: Urine samples (n = 148) were collected during natural urination from four bat species: Miniopterus fuliginosus (n = 117), Hipposideros speoris (n = 8), Rousettus leschenaultii (n = 10), and Rhinolophus rouxii (n = 13). DNA was extracted and screened for Leptospira using real-time PCR targeting the lipL32 gene. Sixteen samples tested positive, including 14 from M. fuliginosus, one from H. speoris, and one from R. leschenaultii. Positive samples were further analyzed by amplifying additional loci (flaB, secY, and rrs2) for Sanger sequencing and phylogenetic analysis. Sequences were obtained from 12 samples. Leptospira borgpetersenii was identified in M. fuliginosus, while the sequence from R. leschenaultii represented a genetically distinct Leptospira species. Phylogenetic analysis showed clustering with sequences from the same bat host genera reported in other countries, and one L. borgpetersenii sequence clustered with strains previously detected in Sri Lankan hosts, including humans. CONCLUSIONS/SIGNIFICANCE: This study provides the first molecular evidence of Leptospira in Sri Lankan bats and highlights their potential role as reservoirs contributing to the environmental circulation of pathogenic Leptospira.

LANGUAGE OF ORIGINAL DOCUMENT: English

Rojas Morales H.R., Rivas Zambrano A.G.

Leptospirosis with neurological complications in pediatrics [Leptospirosis con complicaciones neurológicas en pediatría]

(2025) Revista Cubana de Investigaciones Biomedicas, 44, art. no. e3867

ABSTRACT: Leptospirosis is a zoonosis of global relevance, whose clinical presentation is highly variable and may include atypical neurological complications, especially in endemic areas. The objective of this study was to describe a clinical case of leptospirosis with neurological complications in a 10-year-old male patient living in a rural area of Ecuador. A prospective case report was conducted, systematically collecting clinical, paraclinical, and imaging data to characterize the progression of the condition and the response to antibiotic treatment. The results show that, despite the absence of severe hepatic or renal involvement, the patient presented significant muscle weakness and difficulty walking, with laboratory findings confirming an active inflammatory process and a positive serology for Leptospira. Early intervention with Ceftriaxone was associated with a rapid recovery of motor function, highlighting the importance of timely diagnosis and individualized management in the context of leptospirosis with neurological manifestations. The conclusions of this study emphasize the need to consider leptospirosis in the differential diagnosis of atypical neurological

conditions in pediatric populations and reinforce the effectiveness of early antibiotic treatment in reversing clinical progression, providing valuable evidence for clinical practice in endemic areas.
LANGUAGE OF ORIGINAL DOCUMENT: Spanish

Giraud-Gatineau A., Haustant G., Monot M., Picardeau M., Benaroudj N.

In vivo dual RNA-Seq uncovers key effectors of epithelial barrier disruption by an extracellular pathogen

(2026) Nature communications, 17 (1)

DOI: 10.1038/s41467-026-69033-8

ABSTRACT: Disruption of host cell barriers is a fundamental strategy enabling pathogens to establish a paracellular infection. Here, using dual RNA-Seq, we determine the in vivo host-pathogen transcriptomic landscape upon infection by the extracellular pathogen Leptospira interrogans and uncover a mechanism of cell-cell junction disruption. We demonstrate that, upon infection, an increase in intracellular calcium triggers tight junction destabilization, by activating the calmodulin and myosin light chain kinase signalization. We identify two bacterial effectors of the Virulence-Modifying (VM) proteins family, structurally related to toxin-like proteins, that promote modulation of calcium homeostasis and disruption of cell-cell junctions, thereby allowing Leptospira translocation across epithelium barriers, tissue colonization and pathogenicity. Furthermore, we demonstrate that at least one of these VM proteins is secreted and associates with host cells. Altogether, these findings reveal a unique strategy by which an extracellular pathogen secretes toxin-like proteins to exploit host calcium signaling for breaching epithelial barriers.
LANGUAGE OF ORIGINAL DOCUMENT: English

Costa G.M., Gaspar J.P., Teixeira A.F., Nascimento A.L.T.O.

Functional validation of the proteome-identified LIC_13056 putative lipoprotein of *Leptospira interrogans* and the potential role in pathogenesis

(2026) International Journal of Molecular Sciences, 27 (5), art. no. 2086

DOI: 10.3390/ijms27052086

ABSTRACT: Leptospirosis is a widespread zoonosis of human and veterinary concern. The etiological agent of the disease is the pathogenic bacteria of the genus Leptospira. Transmission typically occurs through mucosal contact and/or injured skin with the urine of infected animals or contaminated environmental sources. Understanding the biology and pathogenesis of leptospires is the main focus of our study. In this work, we characterized a novel protein encoded by the LIC_13056 gene from L. interrogans serovar Copenhageni, having an OmpA-like domain. We show that this coding sequence (CDS), previously assigned as a hypothetical protein with an unknown function, is capable of binding to the cellular receptor α8 integrin subunit, potentially contributing to kidney colonization. Additionally, the protein bound to both purified and normal human serum (NHS) plasminogen (PLG). In both conditions, PLG bound to protein was able to generate plasmin (PLA). Furthermore, rLIC_13056 interacted with the complement system components C4b, C4BP, C8 and C9. The interaction of recombinant protein to the C9 had a negative impact on C9 polymerization. Taken together, the protein LIC_13056, having an OmpA-like domain, appears to be involved in leptospiral pathogenesis via different stages of the infection process; PLA generation together with the inhibition of the membrane attack complex (MAC) may contribute to the immune evasion mechanism of Leptospira, thus facilitating the infection.
LANGUAGE OF ORIGINAL DOCUMENT: English

De Souza Costa Lima M., Nepomuceno R., Santos Moreira C., Abe Mari C., Barbosa Silva A.

***Leptospira* glyceraldehyde-3-phosphate dehydrogenase (LiGAPDH): a cell-surface plasminogen binding protein**

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ABSTRACT: Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) is classically recognized as a glycolytic enzyme that catalyzes the conversion of glyceraldehyde 3-phosphate into D-glyceryl 1,3-bisphosphate. However, it also exhibits "moonlighting"functions, serving roles unrelated to metabolism. Notably, this multifunctional protein, which lacks a conventional membrane anchor, is present on the surface of many prokaryotic and eukaryotic cells. In this study, we demonstrate that Leptospira interrogans GAPDH (LiGAPDH) is surface-exposed and interacts with plasminogen. In the presence of the exogenous activator uPA, plasminogen is converted into its active form, plasmin. The LiGAPDH-plasmin complex can degrade fibrinogen (α and β chains) and the 75-kDa form of vitronectin over time. Interestingly, plasmin, when bound to LiGAPDH, completely degrades the C5 α-chain but does not affect C3b. The functional characterization of moonlighting proteins and the identification of host molecules they interact with may offer insights for understanding the mechanisms of invasion, dissemination, and immune evasion employed by pathogenic leptospires.

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Rathnayake N., Takabe K., Muthusinghe D., Vijeyakumaran R., Senarathne P., Dissanayake N., Urata S., Yoshimatsu K., Akeda Y., Gamage C., Koizumi N.

Molecular epidemiology of rodent-borne *Leptospira spp*. in Sri Lanka: identification of novel sequence types and previously unrecognized reservoir animals

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ABSTRACT: Introduction. Leptospirosis is an important zoonotic disease globally, which is most prevalent in tropical regions. This disease is endemic in Sri Lanka, where the complex ecology of Leptospira spp., reservoir animals and environmental and occupational factors has resulted in a public health problem. Gap Statement. Although genomic analysis of Leptospira isolates has recently revealed the diversity of Leptospira spp. in Sri Lanka, the genetic relationship between human patients and reservoir animals remains unclear. Aim. This study investigated the genetic diversity of Leptospira spp. circulating in rodent populations in three districts of Sri Lanka: Kurunegala, Anuradhapura and Badulla. Methodology. Leptospira DNA was detected from rodent kidney tissue samples by real-time PCR, from which positive samples were subjected to flaB sequencing and multilocus sequencing typing (MLST). Results. Pathogenic Leptospira DNA was detected by real-time PCR in 33 of 257 kidney tissue samples (12.8%) from 4 rodent species: Bandicota bengalensis, Mus booduga, Rattus rattus and Vandeleuria sp. MLST and partial flaB sequencing of real-time PCR-positive samples identified Leptospira borgpetersenii, Leptospira interrogans, Leptospira kirschneri and Leptospira licerasiae in the rodent population. Five sequence types (STs), including two novel STs, ST389 and ST392, were identified. The novel STs of L. interrogans and L. kirschneri were genetically distinct from other STs detected in Sri Lanka. R. rattus and M. booduga were newly identified as the source of L. interrogans ST49 and of L. borgpetersenii ST144 and L. licerasiae infections in humans, respectively. Conclusion. This study identified the genetic diversity of Leptospira spp. in rodent populations and reservoir animals for human infections in Sri Lanka.

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