Istituto Zooprofilattico Sperimentale
della Lombardia e dell’Emilia – Romagna “Bruno Ubertini”
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BOLLETTINO BIBLIOGRAFICO

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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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Aponso T., Wanninayake W.M.D.A.S., Wijesinghe I.P., Jayasekara N., Iddamalgoda W., Wanasinghe W.M.M.A.

Secondary sclerosing cholangitis: an unusual presentation of leptospirosis

(2025) Tropical Medicine and Health, 53 (1), art. no. 20

DOI: 10.1186/s41182-025-00700-0

ABSTRACT: Sclerosing cholangitis is a rare progressive cholestatic disease that is classified as secondary sclerosing cholangitis when it is caused by an identifiable cause. Sclerosing cholangitis has been linked to infections like COVID-19 and parasitic infections like Clonorchis sinensis and Ascaris lumbricoides. However, leptospirosis has not been linked to sclerosing cholangitis in the medical literature. In this article, we report a 37-year-old gentleman who was diagnosed with leptospirosis, worsened by painless cholestasis, while he was improving from leptospirosis. Magnetic resonance cholangiopancreatography revealed multiple short-segment biliary strictures, segmental dilatation, and mural irregularities in both intrahepatic ducts confirming the diagnosis of sclerosing cholangitis. After ruling out other potential causes and considering the initial presentation during a leptospirosis infection, we concluded that leptospirosis caused secondary sclerosing cholangitis. We report this as the first case of secondary sclerosing cholangitis in a leptospirosis patient without renal, respiratory, or cardiac complications, emphasizing the importance of ruling out this cause in a leptospirosis patient with persistent cholestasis.

LANGUAGE OF ORIGINAL DOCUMENT: English

Oliveira M.D.D., Barnabé N.N.D.C., Roberto J.P.D.L., Silva M.L.C.R., Azevedo S.S.D., Limeira C.H., Alves C.J.

Molecular detection of Leptospira spp. in goat's milk produced in a semiarid region

(2025) Research in Veterinary Science, 187, art. no. 105584

DOI: 10.1016/j.rvsc.2025.105584

https://www.scopus.com/inward/record.uri?eid=2-s2.0-

ABSTRACT: Brazil has a large flock of goats, and in the Northeast, there are around 94.5 % of the total flock, highlighting the states of Bahia, Ceará, Pernambuco, Piauí and Paraíba. Dairy goat farming based on the development of alternative models instigates the generation of income, the creation and strengthening of rural micro-enterprises linked to credit programs, aiming to reach quality in the products for the regional consumer market. Infectious diseases, such as leptospirosis, highlights regarding the drop in productivity, and, for detection of this agent, PCR (Polymerase Chain Reaction) is used as a direct diagnosis method. In the present work, molecular tests were carried out in 189 goat milk samples, collected in the dry period of 2019, from flocks of four municipalities in the backlands of Paraíba state, Brazil, five samples of collective cooling tank milk and four pasteurized milk samples. The primers LipL32-45F and LipL32-286R were used to amplify the gene LipL32, specific to pathogenic leptospires. The PCR technique detected the agent's DNA in 146 (77.24 %) goat milk samples; from collective tank, all five samples (100 %) showed Leptospira spp. DNA, so like the four pasteurized milk samples. The presence of leptospires in the mammary gland in lactating females is associated with the bacteremia phase of the infection, leading to a potential zoonotic risk in the consumption of raw milk by humans. Therefore, the goat milk production chain must consolidate efforts to improve milk quality, through the implementation of more effective health control measures and hygienic milking for flocks, including the use of monitoring and control tools, such as Hazard Analysis and Critical Control Point (HACCP), at all stages of goat milk production.

LANGUAGE OF ORIGINAL DOCUMENT: English

Gurung S., Tewari D., Sherpa U., Chhophel T.P., Siddique A.I., Sarmah N., Borkakoty B.

Fatal case of Leptospira wolffii infection in Sikkim, India: an autochthonous case from a new geographical region

(2025) Indian Journal of Medical Microbiology, 54, art. no. 100813

DOI: 10.1016/j.ijmmb.2025.100813

ABSTRACT: This case report describes the first documented fatal case of Leptospira wolffii in Sikkim, India, marking a novel geographic occurrence of leptospirosis in the Himalayan state. A 40-year-old female presented with fever, sepsis, and acute kidney injury, succumbing despite intensive care and antibiotic treatment. Targeted 16S rRNA sequencing confirmed a 100 % identity with L. wolffii. Phylogenetic analysis showed close relatedness to strains from Thailand, Bangladesh, and Assam. Environmental investigations revealed rodent infestation and livestock proximity as potential sources. This study underscores the need for awareness of leptospirosis in non-endemic regions, rapid diagnostics, and a one health approach to mitigate such outbreaks.

LANGUAGE OF ORIGINAL DOCUMENT: English

Restrepo-López N., Silva-Ramos C.R., Rodas J.D., Arboleda M., Fernández D., Uribe-Restrepo P., Agudelo-Flórez P., Tobón-Castaño A., Hidalgo M., Melby P.C., Aguilar P.V., Cabada M.M., Díaz F.J.

Malaria, dengue fever, and leptospirosis in the Urabá Antioqueño Region, Colombia: etiological and molecular characterization among patients with acute undifferentiated febrile illness

(2025) The American journal of tropical medicine and hygiene, 112 (2), pp. 403 - 413

DOI: 10.4269/ajtmh.24-0490

ABSTRACT: Acute undifferentiated febrile illness (AUFI) is the main cause of medical attention in the tropics worldwide. Malaria, arboviral diseases, and leptospirosis are the most important etiologies. These are highly endemic in the Urabá antioqueño, Colombia, being the main causes of fever in several municipalities in this region. However, up-to-date data regarding the infecting species and serotypes are lacking. Thus, we characterized the etiology of AUFI, focusing on malaria, arboviruses, and leptospirosis in this region and the circulating infecting species. An active surveillance was conducted between January and April 2022, and July and October 2023 in two local hospitals in the Urabá antioqueño. Febrile patients were enrolled voluntarily. Malaria, arboviral diseases, and leptospirosis were screened through direct, serological, molecular, and rapid diagnostic methods. Amplicons obtained for dengue virus (DENV) and Leptospira spp. were analyzed through phylogenetic analysis. A total of 184 febrile patients were enrolled. A confirmed etiology was detected in 43.4% of patients from Apartadó and 61.2% from Turbo. Malaria was the most frequent cause in both municipalities, which was caused mainly by Plasmodium falciparum in Apartadó and Plasmodium vivax in Turbo. Dengue virus serotype 1 genotype V, DENV genotype Asian-American, and DENV genotype Cosmopolitan were identified, as well as pathogenic Leptospira species closely related to Leptospira santarosai and Leptospira noguchii. The present study confirms the importance of malaria, dengue fever, and leptospirosis in the Urabá antioqueño. Plasmodium falciparum and P. vivax were identified, as well as two DENV serotypes and three DENV genotypes and two different Leptospira species.

LANGUAGE OF ORIGINAL DOCUMENT: English

Kositanont U., Thawornkuno C., Sitthipunya A., Dachavichitlead W., Tribuddharat C., Brameld S., Doungchawee G., Lertanantawong B., Srisawat C.

Production of recombinant electron transfer flavoprotein beta subunit protein and its application in a lateral flow assay for early diagnosis of leptospirosis

(2025) Medical Microbiology and Immunology, 214 (1), art. no. 12

DOI: 10.1007/s00430-025-00822-6

ABSTRACT: Leptospirosis is a major cause of acute febrile illness, often presenting with non-specific symptoms that can lead to misdiagnosis. Early laboratory diagnosis is essential for confirmation to avoid misdiagnosis and ensure appropriate management. This study aimed to identify and produce a recombinant protein, approximately 25 kDa, with high antigenicity for diagnostic applications. The 25 kDa protein from Leptospira interrogans was identified as electron transfer flavoprotein beta subunits (Etfβ) and exhibited 98% nucleotide and 99% amino acid homology to the reference strain. Lateral flow assays (LFAs) using recombinant Etfβ (rEtfβ) as antigens were developed to detect specific antibodies, namely rEtfβ-IgM and rEtfβ-IgG, and evaluated their performance against the standard microscopic agglutination test (MAT). Testing 33 paired serum samples from confirmed leptospirosis cases and 24 controls revealed sensitivities of 69.7% for IgM and 57.6% for IgG. However, the combined assays yielded enhanced diagnostic accuracy, achieving a sensitivity of 94.0%, specificity of 95.8%, positive predictive value of 96.9%, negative predictive value of 92.0%, and percent agreement of 94.7% (kappa value of 0.89). Also, the combined LFAs demonstrated 66.7% in initial serum samples whose MAT results were negative, enhancing the capacity for early diagnosis. In conclusion, the developed rapid tests demonstrated strong diagnostic capability, particularly in early-phase leptospirosis, distinguishing between initial and recurrent infections. Importantly, rEtfβ-IgG identified a subset of patients lacking detectable IgM. Thus, integrating rEtfβ-IgM and rEtfβ-IgG is recommended to improve sensitivity and accuracy in endemic populations. The rEtfβ is a promising target for future antigen-based diagnostic strategies for leptospirosis. The rEtfβ antigen shows promise as a target for future development of antigen-based diagnostic strategies for leptospirosis.

LANGUAGE OF ORIGINAL DOCUMENT: English

Dwivedi J.S., Shah D.R., Desai G.S., Mali K.A., Mayadeo N.M.

Maternal and foetal outcomes of leptospirosis in pregnancy: an observational descriptive study at a tertiary care centre in Western India

(2025) Journal of Obstetrics and Gynecology of India

DOI: 10.1007/s13224-024-02080-7

ABSTRACT: Background: Leptospirosis is one of the most prevalent zoonoses worldwide. Its presentation is varied in severity and non-specific mimicking other infectious diseases and pregnancy conditions such as HELLP or AFLP. Aims and Objectives: This study aims to evaluate the maternal and foetal outcomes of leptospirosis and estimate its prevalence in pregnancy at a tertiary care centre. Methods: This is an observational descriptive study conducted at a tertiary care teaching hospital in Western India over a duration of 5 years. All pregnant patients diagnosed as leptospirosis via IgM ELISA were included. Results: A total of 37 patients were enrolled. Majority presented in the first trimester and belonged to the low socio-economic strata. Fever was the most persistent symptom. Five patients had a spontaneous abortion, two underwent MTP, eight had a preterm delivery, whereas 22 patients carried up till term (of which 18 delivered vaginally and four underwent a LSCS). Majority had leucocytosis and were anaemic. Twelve cases had

hyperbilirubinaemia, six had deranged transaminases, three had raised serum creatinine values and two had thrombocytopenia. Four patients required management in the ICU out of which two progressed to Weil's disease and one succumbed to death. The research team at our centre yielded an estimated 9.06% prevalence of leptospirosis. Conclusion: Leptospirosis is often underdiagnosed and hence under-reported. Being a re-emerging infectious disease, an early clinical suspicion and sound understanding of the disease process in pregnant women is required.
LANGUAGE OF ORIGINAL DOCUMENT: English

Saraullo V., Hamer M., Esteban M., Sanchez C., Brihuega B., Martinez M.
Evaluation of LigB polymerase chain reaction as a complementary tool to microscopic agglutination test for the detection of bovine leptospirosis in serum samples
(2025) Research in Veterinary Science, 187, art. no. 105602
DOI: 10.1016/j.rvsc.2025.105602
ABSTRACT: Leptospirosis is a significant infectious disease affecting livestock. Microscopic agglutination test (MAT) is used as the gold standard; however, the inclusion of molecular tools (PCR) could improve the accuracy of diagnosis. We evaluated the combination of MAT and a LigB-PCR in bovine serum to detect positive cases in animals clinically suspected of leptospirosis. 127 samples were classified by MAT (cut-off 1:100). Of 45 negative samples negative by MAT, 42.2 % were positive by PCR. In addition, the number of confirmed cases of bovine leptospirosis based on clinical suspicion and MAT and/or PCR increased the diagnostic rate to 79.5 %. LigB-PCR can detect traces of leptospiral DNA in serum with negative or low antibody titers and could be used as a complementary tool to MAT.
LANGUAGE OF ORIGINAL DOCUMENT: English

Chong-Guzmán L.A., Aréchiga-Ceballos N., Ballados-Gonzáles G.G., Miranda-Caballero C.I., Grostieta E., Aguilar-Domínguez M., Romero-Salas D., Hernández-Herrera R.I., San Martín-del Ángel P., Lammoglia-Villagómez M.A., Becker I., Colunga-Salas P., Cruz-Romero A., Sanchez-Montes S.
Leptospira interrogans associated with the common vampire bat (Desmodus rotundus) from the neotropical region of Mexico
(2025) Microbiology Research, 16 (2), art. no. 43
DOI: 10.3390/microbiolres16020043
ABSTRACT: The genus Leptospira includes at least 69 Gram-negative, aerobic spirochetes, of which 25 are pathogenic and associated with a diverse range of mammals, including members of the order Chiroptera. On the American continent, there are six confirmed Leptospira species. Among these, the common vampire bat (Desmodus rotundus), which ranges widely from northern Mexico to northern Argentina, has been reported to harbor four pathogenic taxa: Leptospira borgpetersenii, Leptospira interrogans, Leptospira weilii, and Leptospira cf. noguchii. All these species are frequently isolated from beef and dairy cattle, suggesting that contact with urine from infected cattle could serve as a potential source of infection for bats. However, previous studies have been limited by small sample sizes and low geographical representation among the countries where they were conducted. For this reason, the aim of this study was to identify the species of Leptospira associated with D. rotundus populations in five states within the Neotropical region of Mexico. Between 2015 and 2021, 54 bats were collected across five Mexican states. Our analysis identified the exclusive presence

of L. interrogans in 13 specimens. The findings are discussed within the framework of a One Health perspective, emphasizing their relevance to understanding interspecies transmission dynamics.
LANGUAGE OF ORIGINAL DOCUMENT: English

Di Bella S., Giacchino I., Blanda V., Gucciardi F., Scibetta S., La Russa F., Lastra A., Purpari G., Grasso R., Spena M.T., Orlandella B.M., Vicari N., Olivieri E., Grippi F., Guercio A.

Zoonotic bacteria and vector-borne protozoa in Troglophilus bat colonies in Sicily (Southern Italy): a biomolecular survey

(2025) Animals, 15 (4), art. no. 488

DOI: 10.3390/ani15040488

ABSTRACT: Bats, as members of the order Chiroptera, are vital to ecosystems and serve as reservoirs for numerous microorganisms, some of which can cause zoonotic diseases. Human interactions with bats are increasing due to habitat alterations, making it essential to understand their microbiota, particularly potential pathogens. This study aimed to evaluate the excretion of zoonotic bacteria and protozoa in insectivorous bats from four caves in the provinces of Ragusa, Catania, and Syracuse (Sicily, Southern Italy) using molecular biology tests for zoonotic agents, including Bartonella henselae, Borrelia, Coxiella burnetii, Leptospira, Chlamydia, Rickettsia, Anaplasma, and Piroplasmids. From December 2020 to April 2023, urine, fecal swabs, ocular conjunctival swabs, and oropharyngeal swabs were collected from 149 bats of six species, along with guano samples from the caves. Bartonella henselae DNA was detected in 3 of the 149 tested bats, one ocular conjunctival swab and two oropharyngeal swabs. Chlamydia spp. DNA was detected in a sample of guano, in feces, ocular conjunctival and oropharyngeal swabs of a bat, and in four urine samples. Piroplasmid DNA was detected in 10 of 149 fecal swabs and in 5 of 16 bat ectoparasites. No samples were positive for Leptospira spp., Borrelia spp., Coxiella burnetii, Rickettsia spp., or Anaplasma spp. These findings underscore the importance of multiple sample types in assessing bats as reservoirs for zoonotic pathogens, particularly highlighting their role in transmitting pathogens through various body habitats, including saliva, urine, and ocular excretions. This study highlights the relevance of monitoring bat populations and studying their microbiota to enhance protections for both human and animal health.
LANGUAGE OF ORIGINAL DOCUMENT: English

Lynch M.J., Kurniyati K., Deshpande M., Charon N.W., Li C., Crane B.R.

Inhibitors of lysinoalanine cross-linking in the flagella hook as antimicrobials against Spirochetes

(2025) ACS Chemical Biology

DOI: 10.1021/acschembio.4c00749

ABSTRACT: Spirochetes are especially invasive bacteria that are responsible for several human diseases, including Lyme disease, periodontal disease, syphilis, and leptospirosis. Spirochetes rely on an unusual form of motility based on periplasmic flagella (PFs) to infect hosts and evade the immune system. The flexible hook of these PFs contains a post-translational modification in the form of a lysinoalanine (Lal) cross-link between adjacent subunits of FlgE, which primarily comprise the hook. Lal cross-linking has since been found in key species across the phylum and involves residues that are highly conserved. The requirement of the Lal cross-link for motility of the pathogens Treponema denticola (Td) and Borreliella burgdorferi (Bb) establish Lal as a potential therapeutic target for the development of antimicrobials. Herein, we present the design, development, and application of a NanoLuc-based high-throughput screen that was used to successfully identify two

structurally related Lal cross-link inhibitors (hexachlorophene and triclosan) from a library of clinically approved small molecules. A structure-activity relationship study further expanded the inhibitor set to a third compound (dichlorophene), and each inhibitor was demonstrated to biochemically block autocatalytic cross-linking of FlgE from several pathogenic spirochetes with varied mechanisms and degrees of specificity. The most potent inhibitor, hexachlorophene, alters Lal cross-linking in cultured cells of Td and reduces bacterial motility in swimming plate assays. Overall, these results provide a proof-of-concept for the discovery and development of Lal-cross-link inhibitors to combat spirochete-derived illnesses.
LANGUAGE OF ORIGINAL DOCUMENT: English

Darlan D.M., Mayasari E., Hutagalung S.V., Kurniawan A., Sinaga L.A., Pinem A., Ambarita B.
Molecular and serological detection of Leptospira interrogans among wild rats in flood-prone residential areas of Indonesia
(2025) Open Veterinary Journal, 15 (1), pp. 437 - 445
DOI: 10.5455/OVJ.2025.v15.i1.39
ABSTRACT: Background: Indonesia is a tropical country with heavy rainfall, mostly in low-lying areas. Floods are one of the most common natural disasters in Indonesia, with climate change causing continuous flooding in some regions. The spread of human pathogens as a severe consequence of flooding, such as Leptospira, which may cause Weil’s disease, is a concern for public health. Aim: In this cross-sectional study, we compared DNA from the rat kidney to serum samples to identify pathogenic Leptospira using polymerase chain reaction (PCR) amplification to promote a less invasive method of collecting samples from the rat vectors. Methods: Fifty-nine rodents inhabiting highly populated, flood-prone suburban regions were captured inside and outside houses. Following DNA extractions, we analyzed the quantity and quality of DNA concentration from the kidney and serum specimens using a nanophotometer. The lipL32 gene was amplified to detect the pathogenic Leptospira. Results: The mean value of kidney DNA was 151.67 ng/µl with an average A260/A280 value of 1.836, whereas the mean value of serum DNA was 22.08 ng/µl with an average A260/A280 value of 1.233. Twenty (33.9%) kidney DNA and 10 (16.9%) serum DNA samples showed the target DNA (lipl32). The multiple sequence alignment analysis revealed the lipL32 sequences homology to Leptospira interrogans ser. Copenhageni. Conclusion: Rat kidneys exhibited higher DNA amount and purity than the serum. Moreover, the PCR detection of lipl32 revealed higher positive results in kidney DNA than serum DNA samples, with high similarity to L. interrogans lipl32 sequences. Therefore, the kidney remains a better DNA source than serum for the molecular analysis of Leptospira in rats.
LANGUAGE OF ORIGINAL DOCUMENT: English

Lynch-Dawson H.M., Lubbers C., Deakin H., Bella A.D.
Diagnosis and clinical management of leptospirosis in three canine puppies
(2025) Veterinary Record Case Reports
DOI: 10.1002/vrc2.70016
ABSTRACT: Leptospirosis is a significant bacterial disease in veterinary medicine. This report describes the diagnosis and treatment of three puppies with an acute infection of leptospirosis: a 10-week-old, female, entire labrador retriever; an 11-week-old, male, entire, standard wire-haired dachshund; and a 14-week-old, female, entire Staffordshire bull terrier. Two dogs recovered from the disease and were clinically well at the time of the case series submission. One dog did not recover from the disease and was euthanased due to poor response

to treatment. This case series aims to raise awareness of leptospirosis in puppies and discuss the risk factors that may have contributed to their disease.
LANGUAGE OF ORIGINAL DOCUMENT: English

Kamaruzaman I.N.A., Ong S.Z., Jafri I.N.S., Pengiran-Isa D.U.A., Abdul-Rahman M.S., Reduan M.F.H., Nisansala T., Goh S.H., Mamat S.N.H., Zalati S.C.W., AbuBakar S., Loong S.K.

Histopathological and molecular analyses of Leptospira borgpetersenii and Leptospira interrogans in bovine kidneys in Kota Bharu, Kelantan, Malaysia

(2025) Pakistan Journal of Zoology, 57 (2), pp. 727 - 736

DOI: 10.17582/journal.pjz/20230420000426

ABSTRACT: Leptospirosis is a zoonotic bacterial disease affecting both humans and animals. This is the first study aiming to detect the Leptospira spp. in bovine kidneys collected from selected wet markets in Kota Bharu, Kelantan and subsequently determine the predominant Leptospira species. Additionally, the pathological alterations to the bovine kidneys as a result of leptospirosis were also analyzed. A total of fifty bovine kidney samples (n=50) were collected from four wet markets within Kota Bharu town and the samples were tested using a polymerase chain reaction (PCR) assay. From the results, thirteen samples (n=13; 26%) were found to be positive for the 16S rRNA gene. DNA sequencing of the positive samples revealed the presence of Leptospira borgpetersenii (n=11) and Leptospira interrogans (n=1), which are known to be pathogenic Leptospira species in cattle and humans. One sample cannot be sequenced due to poor yield and quality. Furthermore, the kidneys that were PCR-positive showed significant histopathological lesions of bovine leptospirosis, consisting of interstitial nephritis, glomerular atrophy and tubular necrosis. In conclusion, the present study demonstrated the presence of L. borgpetersenii and L. interrogans in local cattle and this is an indisputable public health risk to the public considering that the samples were obtained from the local wet markets.
LANGUAGE OF ORIGINAL DOCUMENT: English

Villanueva S., Brundage C.

Evaluating a response to a canine leptospirosis outbreak in dogs using an owner survey

(2025) Veterinary Sciences, 12 (2), art. no. 119

DOI: 10.3390/vetsci12020119

ABSTRACT: Leptospirosis is a bacterial zoonotic disease that spreads through contaminated soil and water or directly from infected animals through urine. Although animal-to-human transmission is low, humans are most susceptible to contracting leptospirosis from these contaminated sources. This makes leptospirosis a public health concern, and therefore it is important to control these bacteria from spreading into the environment. A survey targeting Los Angeles County communities, in which a 2021 leptospirosis outbreak occurred, was sent out via groups on the online platforms Instagram and Facebook to gather dog and owner demographics. With 92 (90.2%) respondents having a primary veterinarian, it could not be determined what caused certain owners to have a greater vaccination rate than those who did not (n = 10; 9.8%). Overall, 69 respondents (68%), regardless of whether they had a primary veterinarian or not, reported not knowing of canine leptospirosis and 79 (77%) not knowing the signs to look for or that it is zoonotic. These data help provide a basis in terms of the status of dog owners' knowledge of leptospirosis and how to begin to inform dog owners better about preventatives for this disease.
LANGUAGE OF ORIGINAL DOCUMENT: English

Chauhan A., Jhala D., Thumar R., Kapoor K., Joshi A., Gajjar D., Seshadri S., Shekh S., Joshi C., Patel A.

Design and evaluation of potent multiepitope broad spectrum DNA and protein vaccine candidates against leptospirosis

(2025) Microbial Pathogenesis, 202, art. no. 107418

DOI: 10.1016/j.micpath.2025.107418

ABSTRACT: Leptospirosis is a widespread zoonotic disease that causes severe health complications with no approved vaccine which provide broad range protection. In this study, we have focused on LruC protein from the outer membrane of Leptospira spp. LruC protein has been considered as promising target for vaccine due to its immunogenicity and conservancy. We have identified total 13 conserved B-cell, CTL, and HTL epitopes from 22 different pathogenic Leptospira species and serovars, which were linked with 4 linkers and 3 adjuvants (HBHA, CTB, TLR4) to design 36 multiepitope vaccine constructs to study the effect of different components on vaccine effectiveness. The antigenicity, immunogenicity, and non-allergenicity of the constructs were confirmed through computational analyses. Physico-chemical properties, secondary structure, and tertiary models of the vaccine constructs were predicted and validated. Molecular docking studies were conducted with Toll-like receptors (TLR2, TLR4) to assess binding affinity, identifying three top vaccine candidates (HBHA-construct 6, CTB-construct 9, and TLR4-construct 12) for further investigation. Further, these candidates were successfully cloned into pVAX1 and pET30a vectors to prepare DNA and protein vaccines, respectively. Moreover, these multiepitope vaccines were tested in mice models to assess its immunogenicity. ELISA performed with antisera against vaccine antigen, as well as crude extract of pathogenic Leptospira species showed significant IgG responses, particularly in protein vaccines. Flow cytometry revealed increased IFN-γ producing CD4+ and CD8+ T cells, especially in the TLR4-adjuvanted vaccine groups. The microscopic agglutination test further confirmed the specificity of the antibody response to Leptospira serovars. Overall, this study demonstrates the potential of these multiepitope vaccine constructs in eliciting a robust immune response, laying the foundation for future challenge study and preclinical evaluation.

LANGUAGE OF ORIGINAL DOCUMENT: English

Ferson M.J., Flanigan S., Westman M.E., Pastrana Velez A.M., Knobel B., Cains T., Martinello M.

Rare urban-acquired human leptospirosis and environmental health investigation in Sydney, Australia

(2025) Communicable diseases intelligence (2018), 49

DOI: 10.33321/cdi.2025.49.011

ABSTRACT: Abstract: Leptospirosis is a zoonosis caused by exposure to Leptospira excreted into the environment by rodents or other mammals. A notification of a case of leptospirosis in an adult male with no history of travel or exposure to livestock or rodents triggered an environmental health investigation of his workplace, a local golf course. We hypothesised that a water splash in the eye from a creek running through the golf course, which occurred after a period of heavy rainfall, had led to Leptospira exposure, likely on the basis of contamination of the creek water by rodent urine. Testing of environmental water samples detected pathogenic Leptospira DNA in ten of eleven samples, although cultures were negative. However, we had difficulty interpreting this finding as we found Leptospira DNA in ten of 14 environmental samples in inner and eastern Sydney remote from the workplace, and these were not associated with notified human cases. When we reviewed the 53 human leptospirosis cases notified over the twenty-year period 2003-2022 in residents of metropolitan Sydney, of the 49 cases with Leptospira exposure information, 46 had recognised sources of exposure: travel overseas (27) or to tropical northern Australia (5); rural exposure often to livestock and/or

rodents (12); work in an abattoir (1); and involvement in a raspberry farm outbreak (1). Only three, including the case described, acquired infection in suburban Sydney. Acquisition of human leptospirosis is a rare event in suburban Sydney; true cases without a travel or occupational exposure history may be under-recognised by clinicians. However, with increasing biodiversity loss and where climate change results in heavier rainfall and more frequent floods, it is likely that human leptospirosis will become more common in urban as well as endemic settings.

LANGUAGE OF ORIGINAL DOCUMENT: English

Katsafourou E., Nikolaidou F., Nikolaou E., Gaitanis N., Karakasidis E., Potolidis E.

Leptospirosis outbreak in Magnesia, Central Greece linked to catastrophic floods

(2024) Hippokratia, 28 (3), pp. 129 - 133

ABSTRACT: Background: Leptospirosis, a widespread zoonotic bacterial disease, is transmitted to humans through direct contact with infected animals-primarily rodents-or exposure to contaminated standing water. Its incidence is higher in tropical climates and areas prone to heavy rainfall or flooding. After the severe floods in Magnesia, Central Greece, in the fall of 2023, we observed a significant increase in leptospirosis cases. Case Description: We present three cases of previously healthy young adults who contracted leptospirosis and required medical attention. These cases highlight the variability in clinical presentations, the challenges of differential diagnosis, and the different treatment approaches used for each patient. Conclusions: Extreme weather events, such as flooding, are associated with increased incidence of leptospirosis in areas where the disease was uncommon in the past. Early suspicion, comprehensive investigation, and accurate diagnosis are critical to improving patient outcomes.

LANGUAGE OF ORIGINAL DOCUMENT: English

Dias C.S., Pinna M.H.

Leptospira biofilms: implications for survival, transmission, and disease management

(2025) Applied and Environmental Microbiology, 91 (2), art. no. e01914-24

DOI: 10.1128/aem.01914-24

ABSTRACT: Leptospirosis is a zoonotic disease caused by Leptospira bacteria, affecting humans and a broad range of wild and domestic animals in diverse epidemiological settings (rural, urban, and wild). The disease’s pathogenesis and epidemiology are complex networks not fully elucidated. Epidemiology reflects the One Health integrated approach of environment–animal–human interaction, causing severe illness in humans and animals, with consequent public health burdens. Saprophytic and pathogenic leptospires have been shown to form biofilms in vivo, in vitro, and in environmental samples. Biofilms are characterized by a polymeric matrix that confers protection against hostile environments (both inside and outside of the host), favoring bacterial survival and dissemination. Despite its significance, the role of this bacterial growth mode in leptospiral survival, transmission, and decreased antibiotic susceptibility remains poorly understood and underexplored. Even so, the literature indicates that biofilms might be correlated with lower antimicrobial susceptibility and chronicity in leptospirosis. In this minireview, we discuss the aspects of biofilm formation by Leptospira and their significance for epidemiology and therapeutic management. Understanding the current scenario provides insight into the future prospects for biofilm diagnosis, prevention, and treatment of leptospirosis.

LANGUAGE OF ORIGINAL DOCUMENT: English

Wang Z., Li K., Liu Y., Ward M.P., Chen Y., Li S., Zhang J., Zhao Y., Wang N., Qiu H., Lian Y., Zhang C., Zhang Z., Kan B.

Changing epidemiology of leptospirosis in China from 1955 to 2022

(2025) Infectious Diseases of Poverty, 14 (1), art. no. 17

DOI: 10.1186/s40249-025-01284-x

ABSTRACT: Background: Leptospirosis, a zoonotic disease caused by pathogenic species of the genus Leptospira, is an important public health concern globally. Leptospirosis has been notifiable under statute in China since 1955, and its epidemiological characteristics have evolved during near 70 years. This study aimed to describe the spatial and temporal patterns and demographic characteristics of leptospirosis from 1955 to 2022 in China, and explore the possible factors that influence leptospirosis transmission risk. Methods: Wavelet time series analysis, global Moran's I coefficients, space–time scanning statistics, and so on were used to analyze temporal, seasonal, geographic, and demographic trends in leptospirosis using reported national surveillance data from Chinese mainland from 1955 to 2022. Additionally, a Bayesian spatiotemporal model was used in a preliminary analysis to explore potential factors associated with leptospirosis occurrence. Results: Between 1955 and 2022, China reported 25,236,601 leptospirosis cases, with 91% occurring from July to October. The annual incidence rate peaked at 38.28/100,000 during outbreaks in the 1960s–1980s but stabilized at a low level (0.07/100,000) between 2005 and 2022, with over 99% of cases in southern China. Clustering increased over time, being greatest during the period 2015–2022 (Moran's I = 0.41, P < 0.01). Space-time cluster analysis indicated that the most likely clusters were in northern provincial-level administrative divisions (PLADs) from 1955 to 1984, in southern PLADs from 1985 to 2022. The main identified risk factors of leptospirosis occurrence were annual average precipitation (3.68, 95% CI: 2.50 to 5.12), GDP per capita (-3.70, 95% CI: − 5.97 to − 1.41), and the total power of agricultural machinery (− 2.51, 95% CI: − 3.85 to − 1.17). Conclusions: Over past 70 years, leptospirosis in China has occurred as significant outbreaks but has ultimately declined to stable, low levels of occurrence. However, a clear north–south disparity persists, with tropical and subtropical regions in southern China remaining high-risk areas. The nearly 70-year dataset underscores the complex interplay of climate and socioeconomic factors influencing the disease's occurrence. Targeted prevention and control measures are critical to prevent outbreaks, especially in regions prone to extreme climatic events like heavy rainfall and floods, which may signal the resurgence of leptospirosis.

LANGUAGE OF ORIGINAL DOCUMENT: English

Stone N.E., Picardeau M.

International Committee on Systematics of Prokaryotes Subcommittee on the taxonomy of Leptospiraceae: minutes of the closed meeting, 3 September 2024, Brussels, Belgium

(2025) International journal of systematic and evolutionary microbiology, 75 (2)

DOI: 10.1099/ijsem.0.006691

LANGUAGE OF ORIGINAL DOCUMENT: English

Kadir M.A.A., Manaf R.A., Mokhtar S.A., Ismail L.I.

Identifying leptospirosis hotspots in Selangor: uncovering climatic connections using remote sensing and developing a predictive model

(2025) PeerJ, 13 (3), art. no. e18851

DOI: 10.7717/peerj.18851

ABSTRACT: Background. Leptospirosis is an endemic disease in countries with tropical climates such as South America, Southern Asia, and Southeast Asia. There has been an increase in leptospirosis incidence in Malaysia from 1.45 to 25.94 cases per 100,000 population between 2005 and 2014. With increasing incidence in Selangor, Malaysia, and frequent climate change dynamics, a study on the disease hotspot areas and their association with the hydroclimatic factors could enhance disease surveillance and public health interventions. Methods. This ecological cross-sectional study utilised a geographic information system (GIS) and remote sensing techniques to analyse the spatiotemporal distribution of leptospirosis in Selangor from 2011 to 2019. Laboratory-confirmed leptospirosis cases (n = 1,045) were obtained from the Selangor State Health Department. Using ArcGIS Pro, spatial autocorrelation analysis (Moran’s I) and Getis-Ord Gi* (hotspot analysis) was conducted to identify hotspots based on the monthly aggregated cases for each subdistrict. Satellite-derived rainfall and land surface temperature (LST) data were acquired from NASA’s Giovanni EarthData website and processed into monthly averages. These data were integrated into ArcGIS Pro as thematic layers. Machine learning algorithms, including support vector machine (SVM), Random Forest (RF), and light gradient boosting machine (LGBM) were employed to develop predictive models for leptospirosis hotspot areas. Model performance was then evaluated using cross-validation and metrics such as accuracy, precision, sensitivity, and F1-score. Results. Moran’s I analysis revealed a primarily random distribution of cases across Selangor, with only 20 out of 103 observed having a clustered distribution. Meanwhile, hotspot areas were mainly scattered in subdistricts throughout Selangor with clustering in the central region. Machine learning analysis revealed that the LGBM algorithm had the best performance scores compared to having a cross-validation score of 0.61, a precision score of 0.16, and an F1-score of 0.23. The feature importance score indicated river water level and rainfall contributes most to the model. Conclusions. This GIS-based study identified a primarily sporadic occurrence of leptospirosis in Selangor with minimal spatial clustering. The LGBM algorithm effectively predicted leptospirosis hotspots based on the analysed hydroclimatic factors. The integration of GIS and machine learning offers a promising framework for disease surveillance, facilitating targeted public health interventions in areas at high risk for leptospirosis.

LANGUAGE OF ORIGINAL DOCUMENT: English

Paixão G., Botelho-Fontela S., Gandra F., Reis J.

Acute Leptospirosis Outbreak in Cattle: A Case Report

(2025) Veterinary Medicine and Science, 11 (2), art. no. e70206

DOI: 10.1002/vms3.70206

ABSTRACT: Leptospirosis is a globally distributed re-emerging zoonotic disease caused by Leptospira species. In cattle, the clinical course varies from a subclinical-chronic infection, commonly found in adult animals, to a severe acute syndrome mostly found in calves. The present study reports an outbreak of acute leptospirosis, following favourable climacteric conditions. Seven affected farms were monitored. Clinical observations from infected animals (n = 30) revealed two distinct patterns: lactating calves experienced hyperacute courses, often culminating in death, and older animals, mainly steers, displayed signs of apathy, anorexia, icterus and haemoglobinuria. Necropsies confirmed jaundice and haemoglobinuria, aligning with a presumptive diagnosis of leptospirosis. Haematology and serology results further supported this diagnosis. Pomona and Mozdok serovars were the most prevalent (62.5%) and had the highest mean agglutination titres, 1:1160 and 1:700, respectively. Antimicrobial treatment of sick animals consisted of oxytetracycline. Chemical metaphylaxis and prophylactic measures were established to control the outbreak in cohabiting animals.

Environmental factors like climate change are expected to contribute to more frequent leptospirosis outbreaks. Comprehensive serological surveys are recommended to develop region-specific control measures, emphasising the importance of vaccination as a practical and effective prophylactic measure.
LANGUAGE OF ORIGINAL DOCUMENT: English

Shatar L., Mustafa F.H., Suhailin F.H.

Surface Enhanced Raman Scattering (SERS) spectroscopy for Leptospira DNA detection

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DOI: 10.1109/ICP60542.2024.10877097

ABSTRACT: Surface enhanced Raman Scattering (SERS) spectroscopy is a promising biomolecule detection technique. In this work, we analyzed the vibrational modes from leptospira deoxyribonucleic acid (DNA). The metallic nanoparticles (NPs) were chemically functionalized to enable probe DNA (pDNA) immobilization. Successful hybridization between pDNA to the complementary DNA (cDNA) sequence was verified by high Raman characteristics of phosphate backbone ($PO2^{-}$) and adenine-thymine (A-T) bases pair. The finding shows the potential used of SERS spectroscopy as alternative diagnostic method for leptospirosis disease.
LANGUAGE OF ORIGINAL DOCUMENT: English

Dewi I.P., Bagaskara A.T., Anggitama A.M., Damayanti K.R.S., Mukti I.

Total atrioventricular block as a cardiac manifestation in Weil’s disease: a case report

(2025) Journal of Medical Case Reports , 19 (1), art. no. 91

DOI: 10.1186/s13256-024-04970-w

ABSTRACT: Background: Weil’s disease is an infection caused by Leptospira bacteria. Leptospirosis may cause arrhythmias, such as atrial fibrillation and ST-T segment changes. We report a rare case of total atrioventricular block induced by leptospirosis. Early diagnosis and prompt management present particular challenges. Case report: A 43-year-old Asian woman was referred from internal medicine to cardiology owing to an electrocardiogram abnormality. She complained of worsening chest discomfort 3 days earlier, accompanied by fever, nausea, and intermittent headaches. The patient appeared lethargic and jaundiced; blood pressure was 81/43 mmHg, heart rate was 41 bpm, respiratory rate was 20 times/minute, and temperature was 38.2 °C. The electrocardiogram showed a total atrioventricular block with a junctional escape rhythm of 45 bpm. Laboratory tests revealed increased renal and liver function, thrombocytopenia (98,000/µL), and positive immunoglobulin G and M anti-Leptospira. The patient was diagnosed with Weil’s disease (Faine’s score 32) and total atrioventricular block. The initial management involved fitting the patient with a transcutaneous pacemaker and giving dopamine 5 mcg/kgBW/minute, titrated to a target systolic blood pressure of > 90 mmHg. The patient was also scheduled to undergo temporary transvenous pacing. However, the patient died of suspected cardiogenic shock due to a deterioration in clinical condition. Conclusion: Leptospirosis can cause rare but fatal arrhythmias, as seen in this case of fulminant leptospirosis with total atrioventricular block. Clinicians should be vigilant and consider this potential complication in similar cases.
LANGUAGE OF ORIGINAL DOCUMENT: English

Weng Y.-T., Huang C.-K., Cheng A., Ruan S.-Y., Wang J.-T.

Next-generation sequencing for rapid etiologic diagnosis of acute respiratory distress syndrome: a case of life-threatening leptospirosis

(2025) Journal of Infection and Public Health, 18 (6), art. no. 102727

DOI: 10.1016/j.jiph.2025.102727

ABSTRACT: Leptospirosis is a zoonotic infection with public health implications and diverse clinical presentations, ranging from mild symptoms to severe, life-threatening disease. In critical cases, it can cause multiorgan failure and death. Diagnosis is typically based on clinical suspicion and confirmed by laboratory testing. However, in acute, life-threatening cases, obtaining a history of exposure and recognizing early symptoms may be challenging. Traditional diagnostic methods for identifying causative pathogens are time-consuming and limited. Next-generation sequencing (NGS) has emerged as a novel diagnostic tool that identifies pathogens using DNA or RNA from bodily fluids, offering more timely, unbiased results, especially for fastidious or non-culturable organisms.

LANGUAGE OF ORIGINAL DOCUMENT: English

de França D.A., Langoni H.

Prevalent zoonoses in Sao Paulo State, Brazil: the role of bats and molecular diagnosis

(2025) Revista do Instituto de Medicina Tropical de Sao Paulo, 67, art. no. e17

DOI: 10.1590/S1678-9946202567017

ABSTRACT: This review explores the landscape of prevalent zoonotic diseases in Sao Paulo State, Brazil, focusing on the role of bats as reservoirs and the application of molecular biology in the diagnosis. The zoonoses covered include visceral and cutaneous leishmaniasis, Chagas disease, toxoplasmosis, bartonellosis, Q fever, Brazilian spotted fever, and leptospirosis. Molecular techniques can improve public health responses by accurately identifying pathogens and tracking their transmission dynamics in populations, thus enhancing early detection, characterization of strains, and monitoring of disease outbreaks. By elucidating the epidemiology and molecular aspects of zoonoses associated with bats in Sao Paulo State, we highlight the importance of integrated surveillance systems and multidisciplinary approaches to effectively manage and prevent these diseases.

LANGUAGE OF ORIGINAL DOCUMENT: English

Khanal R., Pathak C.R.

Screening of antibodies against Leptospira Hardjo among bovine species of Nawalpur, Tanahun and Gorkha

DOI: 10.34172/ijmpes.4180

ABSTRACT: Introduction: Leptospirosis, a bacterial zoonosis, can affect livestock species with considerable losses especially cattle and buffalo. Leptospira interrogans serovar hardjo is known to be associated with reproductive disorders in bovines. Information on the seroprevalence of antibodies against this serogroup in this territory is important in managing risks and instituting control measures for the area, such as Nepal since these diseases could be overlooked due to the absence of some surveillance practices. The aim of the study was to investigate the seroprevalence of Leptospira interrogans serovar hardjo antibodies among cattle and buffalo from Nawalpur, Tanahun and Gorkha districts of Nepal in order to evaluate the extent of the disease and its effect on cattle. Methods: A total of blood samples were collected aseptically using purposive sampling from cattle and buffalo in the study area 174. These samples were analyzed serologically using PrioCHECK®L.hardjo Ab ELISA kit for antibodies to Leptospira interrogans serovar hardjo. Results: The serological analysis indicated that the seroprevalence was 1.149% which points out the existence of a natural

infection in cattle and buffalo reared without any immunization against leptospirosis. Geographical factors, especially region, combined with other factors like low immunogenicity of their vaccines offered to the animals, might explain the low level seroprevalence of the disease. Conclusion: This current study has highlighted the natural occurrence of the leptospires in the hardjo serovar in cattle and buffalo within the study region. The above studies bring out the necessity for active programs for control and preventative measures to restraints leptospirosis disease among the cattle as the disease prevalence designates low seroprevalence rate.
LANGUAGE OF ORIGINAL DOCUMENT: English

Donado-Botero R., Montoya-Jaramillo M.E., Arango C.A., Zakzuk-Martinez E.

Malaria and leptospirosis co-infection: overlapping tropical diseases in an endemic area. Case report [Coinfección de malaria y leptospirosis: superposición de enfermedades tropicales en área endémica. Reporte de caso]

(2025) Infectio, 29 (1), pp. 45 - 50
DOI: 10.22354/24223794.1215

ABSTRACT: In Colombia, undifferentiated tropical febrile illnesses are common and a matter of great concern, with Malaria and Leptospirosis being considered of national public health importance. We report a clinical case of co-infection with malaria-leptospirosis in a 21- year-old female who initially presented with acute febrile syndrome and nonspecific general symptoms, along with hemorrhagic manifestations, and had recently traveled to an endemic area. The initial diagnosis was Malaria caused by P. Vivax, but there was no expected improvement despite starting antimalarial treatment. The condition progressed to respiratory distress, persistent anemia, and severe thrombocytopenia, with high suspicion of alveolar hemorrhage. Treatment was initiated in the context of Weil's disease, and serological tests using ELISA and MAT showed positive IgM for Leptospira. The patient showed a favorable clinical evolution with antibiotic treatment. Although extremely rare, simultaneous infections are possible, and their shared clinical characteristics make them a diagnostic challenge in our region, particularly in clinically compromised patients.
LANGUAGE OF ORIGINAL DOCUMENT: Spanish