# Bulletin de veille risques biologiques
# N°129 – Novembre-décembre 2024

**Objectifs :** veilles spécifiques sur la thématique du risque biologique : biotechnologies (nouveaux procédés), équipements de protection individuelle (fièvre hémorragique, Ebola), protection respiratoire (ajustement), zoonoses (pathologies émergentes), légionellose (cas professionnels), endotoxines (effets toxiques/multi-expositions).

+ suivi d'organismes français et internationaux (sélection d'actualités classées par thème).

*La validation des informations fournies (exactitude, fiabilité, pertinence par rapport aux principes de prévention, etc.) est du ressort des auteurs des articles signalés dans la veille. Les informations ne sont pas le reflet de la position de l'INRS. Les éléments issus de cette veille sont fournis sans garantie d'exhaustivité.*

*Les liens mentionnés dans le bulletin donnent accès aux documents sous réserve d'un abonnement à la ressource.*

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## Sommaire :

- ## Protection individuelle : fièvre hémorragique, Ebola

Fazlalipour M, Jalali T, Hewson R, Pouriayevali MH, Salehi-Vaziri M.

**Crimean-Congo haemorrhagic fever among healthcare workers in Iran 2000-2023, a report of National Reference Laboratory.**

Bmc Infectious Diseases. 2024;24(1):7.

https://bmcinfectdis.biomedcentral.com/counter/pdf/10.1186/s12879-024-10199-1.pdf

*BackgroundCrimean-Congo haemorrhagic fever (CCHF) is a lethal acute viral zoonosis with a case fatality rate of 5-50%. Due to the potential of human-to human transmission of the disease, healthcare workers (HCWs) are at risk of occupational exposure to CCHF virus. Little is known about CCHF virus route of transmission and risks in Iranian HCWs. Therefore this study was designed to identify the routes of exposure to the CCHF virus among Iranian HCWs.MethodsFrom Oct 2000 to Feb 2023, 96 CCHF suspected healthcare workers referred to national reference laboratory were tested for CCHF virus infection by the use of RT-PCR and IgM Capture Enzyme-Linked Immunosorbent Assay (MAC-ELISA) and exposure history of cases were investigated to determine the CCHF virus routes of transmission in nosocomial settings.ResultsTwelve CCHF confirmed cases were identified including seven nurses and five physicians, with the median age of 32.5 years (range 23-53 years) and the median incubation period of 6.8 days (range from 1 to 22 days). None of the cases reported a history of tick bite or close contact with tissues or animal blood. The cases were from Razavi Khorasan (seven cases), Sistan and Baluchistan (two cases), Isfahan (one case), South Khorasan (one case) and Fars (one case). Percutaneous exposure (needle stick) (three cases), mucosal exposure (blood splash in to face) (three cases) and skin contact with blood (three cases) constituted the most prevalent routes of transmission. Since 2013, no CCHF cases have been identified among Iranian HCWs.ConclusionsIn healthcare settings, physicians and nurses are at risk of nosocomial CCHF virus infection. The routes of transmission mainly include direct exposures via needle-stick, mucosal or direct contact with the skin to infected blood. Continuous education and implementation of infection prevention and control measures are key factors to minimize the incidence of healthcare related CCHF.*

Graham A, Ettles S, McGrath M, Ogunremi T, Selkirk J, Bruce N.

**Is there sufficient evidence to inform personal protective equipment choices for healthcare workers caring for patients with viral hemorrhagic fevers?**

Canada communicable disease report = Releve des maladies transmissibles au Canada. 2025;51(1):7-15.

https://pmc.ncbi.nlm.nih.gov/articles/PMC11706576/pdf/CCDR-51-7.pdf

*BACKGROUND: Ugandan health authorities declared an outbreak of Ebola disease (EBOD), caused by the Sudan virus, in September 2022. A rapid review was conducted to update the Public Health Agency of Canada's guidelines for infection prevention and control measures for EBOD in healthcare settings to prepare for potential introduction of cases. OBJECTIVE: Summarize the available evidence on personal protective equipment (PPE) use by healthcare workers (HCWs) to prevent exposure to and transmission of viral hemorrhagic fevers (VHFs), including Ebola virus. METHODS: Electronic databases were searched to identify peer-reviewed evidence published from July 2014-October 2022. Peer-*

*reviewed primary studies and literature reviews, in English or French, reporting on PPE for VHFs and filoviruses in the healthcare context were eligible for inclusion. Literature review processes were conducted by two reviewers using DistillerSR® systematic review software and the Public Health Agency of Canada's Infection Prevention and Control Critical Appraisal Toolkit. An environmental scan of grey literature was also conducted to inform the rapid review. RESULTS: The database search yielded 417 citations and 29 studies were considered eligible for critical appraisal. In total, 20 studies were included in the narrative synthesis of evidence. The evidence base was limited regarding comparative effectiveness of types of PPE for preventing exposure to and transmission of VHFs to HCWs. Four studies reported on exposure to and transmission of a VHF. Sixteen studies provided data on other relevant topics, such as simulated contamination and lab-based tests of PPE integrity. CONCLUSION: There is limited evidence with which to draw conclusions on the comparative effectiveness of PPE to prevent exposure to and transmission of VHFs to HCWs. Additional research is required to determine the optimal PPE to protect HCWs from exposure to and transmission of VHFs.*

## Protection respiratoire : ajustement

Čuta M, Jurda M, Kováčová V, Jandová M, Bezděková V, Černý D, Urbanová P.

**Virtual fit and design improvements of a filtering half-mask for sub-adult wearers.**

Ergonomics. 2024;67(10):1267-83.

https://doi.org/10.1080/00140139.2023.2298984

*The recent pandemic has shown that protecting the general population from hazardous substances or pathogens can be a challenging and urgent task. The key element to adequate protection is appropriately sized, well-fitted and sufficiently distributed personal protective equipment (PPE). While these conditions are followed for adult PPE wearers, they are less considered when it comes to protecting subadults. In this study, the assessment of the fit and design improvements of a 3D-printed facial half mask for subadult wearers (4-18 years) is designed. The target population was represented by 1137 subadults, aged 4.06-18.94 years, for whom 3D face models were acquired. The half mask tested, which was originally provided in one subadult size, did not fit appropriately the target population. This finding prompted the creation of four size categories using the age-dependent distribution of the centroid size calculated from 7 facial landmarks. For each size category, a modified half-mask virtual design was created, including resizing and reshaping, and fit was evaluated visually and numerically using averaged and random 3D face representatives.Practitioner summary: The reason for this study was to describe procedures which led to design improvement of an existing half-mask and provide respiratory protection for subadults. To address this, fit was assessed using an innovative metric approach. Four sizes were then created based on centroid size, resulting in improved fit and design.*

d'Oro EC, De Maio C, Samuele G, Candiani G, Bono N, Miceli M, Pedeferri M.

**Setup of a method supporting the adoption of a regeneration strategy for FFP2 masks used by rescuers during the Covid-19 emergency.**

Eur Phys J Plus. 2024;139(11):10.

https://link.springer.com/article/10.1140/epjp/s13360-024-05756-1

*In the context of the Covid-19 pandemic, the chemical, biological, radiological, and nuclear unit of the Fire and Rescue Service command in Milan sought to prevent potential shortages of disposable FFP2 masks by developing a regeneration method. The method involved establishing a system to verify the protective properties of the masks, with the goal of enabling their reuse. The proposed method is based on a decontamination process that uses dry hot air combined with gaseous ozone, applied through a prototype industrial technology. Validation tests for this method involved subjecting disposable FFP2 masks to two primary stressors: usage (simulated using an artificial respirator) and decontamination. The impact of these stressors on the mechanical and physical properties of the masks was assessed using tests derived from or inspired by the European certification standards for disposable FFP2 masks. Successfully passing these tests indicates that the FFP2 masks are suitable for reuse. This study demonstrates that the decontamination process effectively inactivates E. coli and SARS-CoV-2 (the reference biological agents) and eliminates odors. Validation tests further show that a disposable FFP2 mask can undergo up to twenty decontamination cycles without any significant loss of its protective functions. However, when subjected to cycles of simulated use followed by decontamination-conditions that closely mimic real-world usage-the FFP2 masks exhibit noticeable physical deterioration after more than five cycles. This deterioration compromises the sealing and fit on the wearer's face, rendering the masks unsuitable for reuse beyond five cycles.*

Gakhal MK, Bakshi A, Gu M, Khambay BS.

**A study to determine the three-dimensional (3D) facial shape characteristics for a successful FFP3 mask fit.**

Scientific reports. 2024;14(1):28683.

https://pmc.ncbi.nlm.nih.gov/articles/PMC11577019/pdf/41598_2024_Article_80001.pdf

*A reported 20% of dental staff will fail their fit test for a disposable FFP3 respirator. This needs to be factored into future pandemic workforce and PPE supply planning. At present there are no scientifically or universally accepted facial shape criteria to design and produce facial masks that will fit the entire work force. This study presents differences in facial shape, volume and surface area between individuals who passed on several FFP3 masks (pass group) and participants who passed on only one FFP3 mask (fail group). Three dimensional images of 50 individuals, 25 in each group, were taken at rest and at maximum smile using a DI4D SNAP 6200 camera system. The images were processed, and four "average faces" were produced-pass group at rest, fail group at rest, pass group at maximum smile and fail group at maximum smile. Simple Euclidian linear and angular measurements, geodesic surface distances and volume and surface area enclosed within the mask were analysed. The results of the study show that individuals who are more likely to pass a mask fit test have longer faces, wider mouths, greater geodesic surface distances and a greater volume and surface area of soft tissue enclosed within the mask boundary. This would suggest that some manufactures masks may be too large, and they need to reduce the size of their masks or produce a category of sizes, accepting the fact that one size does not fit all.*

Janson DJ, Dhokia V, Banks K, Rodohan JHD, Clift BC.

**Personal protection equipment: pockets, perceptions and equity - the untold truth of PPE: a reflexive thematic analysis.**

International journal of occupational safety and ergonomics : JOSE. 2024:1-12.

https://doi.org/10.1080/10803548.2024.2404748

*Personal protective equipment (PPE) is worn in a range of industrial environments by women and men alike. However, the majority of PPE is designed around male anthropometrics and the impacts of this on women are largely undocumented. Reflexive thematic analysis was used to develop themes from in-depth interviews with 30 women working in diverse roles in industrial environments, around their experiences of wearing PPE. Four themes developed: 'There's nothing here for me'; 'Collateral damage'; 'Organisational culture and the burden of responsibility'; and 'Personally protective women'. The findings significantly expand upon previous literature concerning: the reduced range of PPE available for women when compared with men; considerable fit and comfort issues; and physical, day-to-day and health-related consequences. This work evidences the increased PPE-related burden on women, and demonstrates fundamental links between women wearing ill-fitting or inappropriate PPE and their reduced sense of belonging, confidence and morale.*

Lindsley WG, Blachere FM, Derk RC, Mnatsakanova A, Noti JD.

**Efficacy of powered air-purifying respirators (PAPRs) for source control of simulated respiratory aerosols.**

American Journal of Infection Control. 2024;52(12):1397-402.

https://doi.org/10.1016/j.ajic.2024.07.019

*Background: Loose-fitting powered air-purifying respirators (PAPRs) are a popular alternative to the use of filtering facepiece respirators for health care workers. Although PAPRs protect the wearer from aerosol particles, their ability to block infectious aerosol particles exhaled by the wearer from being released into the environment (called source control) is unclear. Methods: The source control performance of 4 PAPRs with loose-fitting facepieces were tested using a manikin that exhales aerosol particles. The PAPRs were tested by themselves and in combination with a faceworn product intended to provide source control (either a surgical mask or an N95 filtering facepiece respirator). Results: Two PAPR facepieces with filtration panels significantly reduced the release of exhaled aerosols into the environment, while 3 facepieces without such panels did not. Wearing a surgical mask or respirator under the facepiece significantly improved the source control performance. Conclusions: Most PAPR facepieces do not block aerosols exhaled by the wearer. Facepieces designed to filter exhaled particles can prevent aerosols from being released into the environment. Wearing a surgical mask or a filtering facepiece respirator under the facepiece can also provide source control, but PAPRs are not typically certified for use with masks and respirators. Published by Elsevier Inc. on behalf of Association for Professionals in Infection Control and Epidemiology, Inc.*

Oboho IK, Hanna J, Silva-Rodriguez D, Christie-Smith A, Psenicka A, Khongmongkhon A, et al.

**Management of a COVID-19 outbreak using a multidisciplinary approach and infection prevention control practices at a community living center in Veterans Administration Hospital, North Texas.**

Antimicrob Steward Healthc Epidemiol. 2025;5(1):e12.

https://pmc.ncbi.nlm.nih.gov/articles/PMC11748011/pdf/S2732494X24004911a.pdf

*BACKGROUND: The increase in severe acute respiratory coronavirus virus 2 (SARS-CoV-2) cases due to the omicron strain led to reduced acute care hospital beds at the Veterans Administration (VA) Hospital, North Texas; veterans with non-severe coronavirus disease 2019 (COVID-19) disease were managed at a community living center (CLC), a VA nursing home. The management of non-severe COVID-19 in VA nursing homes has not been extensively described. METHODS: We describe resident characteristics and outcomes, and infection control practices implemented during 2 COVID-19 outbreak periods (January 12-February 15, 2022, June 28-July 14, 2023). Serial testing of all CLC residents was conducted, and* *residents with polymerase chain reaction-confirmed SARS-CoV-2 (COVID-19) infection were included in the analysis. Resident data were ascertained from the COVID-19 facility dashboard and medical record system. RESULTS: From January 12 to February 15, 2022, and June 28-July 14, 2023, 62 adults residing at the CLC were diagnosed with COVID-19. Overall, the median age was 75 years [interquartile range, 71-80], and 57 (91.9%) were men. Residents were cohorted by COVID-19 test results. A multidisciplinary team was convened, and staff were fit tested for appropriate personal protective equipment (PPE) and received refresher training on hand hygiene, donning, and doffing of PPE. Thirty-seven (59.7%) residents were symptomatic. Overall, 55 (88.7%) residents were documented to have received the SARS-CoV-2 primary vaccination series. Most residents were managed at the CLC, while 12 (19.3%) were hospitalized in acute care. CONCLUSIONS: It is feasible to manage high-risk residents with non-severe COVID-19 disease in a CLC utilizing a multidisciplinary approach and implementing Infection Prevention and Control strategies.*

Yang WH, Myers WR, Bergman M, Fisher E, Ryan KJ, Vollmer B, et al.

**Evaluating source control efficacy against exhaled submicron particles: Total outward leakage of surgical masks and half facepiece respirators across a spectrum of particle sizes.**

Aerosol Science and Technology. 2024:12.

https://doi.org/10.1080/02786826.2024.2427282

*The size of airborne particles emitted from infected individuals is crucial in the transmission of respiratory viruses. The use of source control devices is essential for interrupting the transmission of exhaled submicron particles, particularly in healthcare settings with high infection risk. This study evaluated the efficacy of five types of source control devices, commonly used in healthcare settings, in mitigating the transmission of exhaled submicron particles (20-210 nm). Total outward leakage (TOL) of these devices was analyzed across different particle sizes, and the TOL mean diameter (TOLMD) was calculated to characterize particle size distribution. The devices tested included N95 filtering facepiece respirators (N95 FFRs), N95 FFRs with an exhalation valve (N95 FFRV), surgical masks (SMs), elastomeric half-mask respirators (EHMRs), and EHMRs with a SM covering the exhalation valve (EHMRSM). The study also examined the effects of faceseal and flowrate on TOL and particle size characteristics. Results indicated that TOL varied with particle size, increasing from 40 to 90 nm before stabilizing. Aerosols larger than 90 nm had significantly higher TOL compared to smaller aerosols. Higher flow rates increased TOL for EHMR and EHMRSM across all particle sizes. Improved faceseal on N95 FFRs and SMs significantly reduced TOL and decreased TOLMD. The study underscored that using well-fitting devices without exhalation valves is crucial for preventing the transmission of exhaled aerosols potentially carrying viruses, in particular for larger particle sizes. This is especially crucial in the absence of proper indoor ventilation and other control measures.*

## Zoonoses : pathologies émergentes

Al-Mustapha AI, Adesiyan IM, Orum TG, Ogundijo OA, Lawal AN, Nzedibe OE, et al.

**Lassa fever in Nigeria: epidemiology and risk perception.**

Scientific reports. 2024;14(1):14.

https://www.nature.com/articles/s41598-024-78726-3.pdf

*Annual outbreaks of Lassa fever have resulted in a public health threat in Nigeria and other endemic countries in Sub-Saharan Africa. While the Lassa Virus (LASV) is endemic in rodent populations, zoonotic* *spillover to humans causes annual outbreaks. This study reviewed the burden of Lassa fever (LF) in Nigeria between 2020 and 2023 and conducted a cross-sectional survey of Nigerians to evaluate their risk perceptions of LF. During the period under review, 28,780 suspected and 4,036 confirmed cases of LF were reported from 34 of the 37 states of Nigeria. These cases resulted in 762 deaths (a CFR of 18.9%). The overall case positivity rate was 14% (4,036/28,780), with more positive cases in 2020 (17.5%, n = 1,189/6,791). A total of 2,150 study participants were enrolled in the prospective cross-sectional study, with most of them (87.5%, n = 1,881/2,150) having previously heard of Lassa fever (LF). The numerical scoring system revealed that 35.43% (n = 762/1,881) of those aware of LF have poor knowledge of its preventive measures, route of transmission, and control measures. Approximately 6.84% (n = 147/2,150) of them were at a high risk of contracting LF, with 27.6% (n = 584/2,150) of study participants feeling concerned about contracting LF because of the presence of rodents in their immediate vicinity, occupational exposure to healthcare workers, and the probability of contamination of food by infected rodents without necessary food safety measures. Multivariable logistic regression analysis revealed that tertiary education was associated with an increased likelihood of better LF knowledge (OR: 17.32; 95% CI: 10.62, 28.26; p < 0.01) and a lower risk of contracting LF when compared to respondents with no formal education. In addition, study participants who reside in low-burden states have lower LF perception than those residents in high-LF-burden states (OR: 0.59; 95% CI: 0.38-0.91; p = 0.049). On the other hand, study participants with poor risk perception (knowledge) of LF had a higher likelihood (RR: 0.33; 95% CI: 0.20, 0.53; p < 0.01) of contracting LF when compared to those with good knowledge of LF. Similarly, those residents in low LF burden states were less likely (OR: 0.09; 95% CI: 0.05,0.17; p < 0.01) to contract LF when compared to those residents in high burden states. There is a need to improve LF diagnostics capacity, infection prevention and control measures, and implementation of the One Health approach to controlling LASV from animal reservoirs. In addition, public enlightenment campaigns to address fundamental knowledge gaps are crucial to mitigating the ongoing and future impact of LF in Nigeria.*

Amoah S, Unicorn NM, Kyeremateng ET, Desewu G, Obuam PK, Malm ROT, et al.

**Ticks and tick-borne pathogens in selected abattoirs and a slaughter slab in Kumasi, Ghana.**

Vet Med Sci. 2024;10(5):9.

https://doi.org/10.1002/vms3.70030

*Background: Ticks are vectors of pathogens that affect the health of animals and humans. With the constant trade of livestock across borders, there is the risk of new tick species invasion accompanied by the spread of infectious tick-borne pathogens. Aim: This study sought to determine the diversity of tick species within abattoirs and a slaughter slab as well as identify the pathogens carried by these ticks. Methods: The ticks were collected from slaughtered cattle, identified and screened for pathogens using PCR and sequencing. Results: A total of 371 ticks were collected from slaughtered cattle across the three sampling sites: Kumasi abattoir (288, 77.63%), Akwatia Line slaughter slab (52, 14.02%) and Suame abattoir (31, 8.35%). The predominant species was Amblyomma variegatum (85.44%) with Rhipicephalus sanguineus (s.l.) (0.27%) as the least occurring species. Total nucleic acid from the tick pools was screened for pathogens based on the nucleoprotein gene region in the S segment of the Crimean-Congo haemorrhagic fever virus (CCHFV) genome, the 295-bp fragment of the transposase gene of the Coxiella burnetii IS1111a element, the 560 bp segment of the ssrRNA gene of Babesia and Theileria, , the 345 bp fragment of the Ehrlichia genus 16SrRNA gene and the rOmpA gene (OmpA) of Rickettsia. . From the 52 tick pools screened, 40(76.92%) were found positive for pathogen DNA. The pathogens identified were Rickettsia africae (69.23%), Rickettsia aeschlimannii (7.69%), C. burnetii (5.77%), uncultured Ehrlichia sp. (5.77%), Candidatus Midichloria mitochondrii (3.85%) and CCHFV (3.85%). A significant association was observed among A. variegatum, , Hyalomma rufipes, , Hyalomma* *truncatum and occurring tick-borne pathogens R. africae, , R. aeschlimannii and uncultured Ehrlichia sp. (p < 0.001). Conclusion: The findings show the occurrence of zoonotic pathogens, suggesting an increased risk of infections among the abattoir workers. There is a need to adopt control measures within the abattoirs to prevent pathogen spread.*

Baer K, Arora I, Kimbro J, Haider A, Mott M, Marshall K, et al.

**Iquitos Virus in Traveler Returning to the United States from Ecuador.**

Emerging Infectious Disease journal. 2024;30(11):2447.

https://wwwnc.cdc.gov/eid/article/30/11/24-0708_article

https://pmc.ncbi.nlm.nih.gov/articles/PMC11521160/pdf/24-0708.pdf

*We describe the case of a returned traveler to the United States from Ecuador who had an acute febrile illness, initially diagnosed as Oropouche fever. This illness was later confirmed to be a rare infection with Iquitos virus, a related bunyavirus that shares 2 of 3 genome segments with Oropouche virus.*

Bandeira AC, Pereira FM, Leal A, Santos SPO, Barbosa AC, Souza MSPL, et al.

**Fatal Oropouche Virus Infections in Nonendemic Region, Brazil, 2024.**

Emerging Infectious Disease journal. 2024;30(11):2370.

https://wwwnc.cdc.gov/eid/article/30/11/24-1132_article

https://pmc.ncbi.nlm.nih.gov/articles/PMC11521185/pdf/24-1132.pdf

*We report acute Oropouche virus infections in 2 previously healthy women from a nonendemic region of Brazil outside the Amazon Basin. Infections rapidly progressed to hemorrhagic manifestations and fatal outcomes in 4–5 days. These cases highlight the critical need for enhanced surveillance to clarify epidemiology of this neglected disease.*

Barbarin A, Fisher T, Reiskind M, Williams C, Ayres B, Burkhalter K, Nicholson W.

**Heartland Virus Infection in Elderly Patient Initially Suspected of Having Ehrlichiosis, North Carolina, USA.**

Emerging Infectious Disease journal. 2024;30(12):2625.

https://wwwnc.cdc.gov/eid/article/30/12/24-0646_article

https://pmc.ncbi.nlm.nih.gov/articles/PMC11616643/pdf/24-0646.pdf

*We report a patient in North Carolina, USA, with Heartland virus infection whose diagnosis was complicated by previous Ehrlichia chaffeensis infection. We identified E. ewingii–infected and Bourbon virus–infected tick pools at the patient's residence. Healthcare providers should consider testing for tickborne viruses if ehrlichiosis is suspected.*

Barrio T, Benestad S, Douet J-Y, Huor A, Lugan S, Aron N, et al.

**Zoonotic Potential of Chronic Wasting Disease after Adaptation in Intermediate Species.**

Emerging Infectious Disease journal. 2024;30(12):2691.

https://wwwnc.cdc.gov/eid/article/30/12/24-0536_article

https://pmc.ncbi.nlm.nih.gov/articles/PMC11616668/pdf/24-0536.pdf

*Chronic wasting disease (CWD) is an emerging disease in Europe. We report an increase in interspecies transmission capacity and zoonotic potential of a moose CWD isolate from Europe after passage in an ovine prion protein–expressing host. Those results indicated some CWD prions could acquire enhanced zoonotic properties following adaptation in an intermediate species.*

Brambilla M, Bisaglia C, Filisetti A, Giovinazzo S, Lazzari A, Mancini P, et al., editors.

**Hepatitis E Virus Detection in Swine Slurries of Abruzzo: Considerations on Virus Occurrence and Workers' Exposure.**

7th Ragusa International Conference on Safety, Health and Welfare in Agriculture and Agro-Food Systems (SHWA); 2023 Sep 06-09; Ragusa, ITALY: Springer International Publishing Ag.

https://link.springer.com/chapter/10.1007/978-3-031-63504-5_45

*Pigs and wild boars are the main reservoirs of the Hepatitis E virus (HEV). In Abruzzo, the majority of pigs is reared in a few specialised structures, mainly devoted to animal reproduction and fattening. As seroprevalence studies on blood donors highlight significant exposure to the virus in Abruzzo, the One Health FOOD-WAT HEV project has focused on HEV presence in slurry samples from specialised rearing units to underpin the factors potentially influencing virus circulation in pig farms. Four sampling campaigns were conducted in 19 intensive swine farming units throughout the Abruzzo Region in July and November 2021, May and November 2022. Slurry samples were processed by concentration, nucleic acid extraction and nested RT-PCR to detect HEV presence. Frequency analysis and binary logistic regression focused on any possible connection between breeding site characteristics, geographical location of the farm, and HEV presence. HEV detection in swine slurry revealed a significant virus circulation throughout the Abruzzo territory: 18.9% of the collected samples resulted positive for HEV, almost all of which were from the sampling in May 2022. The chi(2)test revealed a significant relation between HEV detection and the housing structures with partly slatted floors, which were nearly fourfold more likely to provide HEV-positive slurry samples. Such findings underline the importance of good farming practices (i.e., adoption of biosafety procedures and rapid manure removal from the pens) as the first countermeasure to reduce workers' exposure.*

Calin R, Périllaud-Dubois C, Marot S, Kerrou K, Peytavin G, Bachir M, et al.

**Mpox Hepatic and Pulmonary Lesions in HIV/Hepatitis B Virus Co-Infected Patient, France.**

Emerging Infectious Disease journal. 2024;30(11):2445.

https://wwwnc.cdc.gov/eid/article/30/11/24-1331_article

https://pmc.ncbi.nlm.nih.gov/articles/PMC11521180/pdf/24-1331.pdf

*We report a case of persistent disseminated mpox evolving over &gt;6 months in an HIV/hepatitis B virus co-infected patient in France who had &lt;200 CD4+ cells/mm3, pulmonary and hepatic necrotic lesions, persistent viremia, and nasopharyngeal excretion. Clinical outcome was favorable after 90 days of tecovirimat treatment and administration of human vaccinia immunoglobulins.*

Castilletti C, Huits R, Mantovani RP, Accordini S, Alladio F, Gobbi F.

**Replication-Competent Oropouche Virus in Semen of Traveler Returning to Italy from Cuba, 2024.**

Emerging Infectious Disease journal. 2024;30(12):2684.

https://wwwnc.cdc.gov/eid/article/30/12/24-1470_article

https://pmc.ncbi.nlm.nih.gov/articles/PMC11616654/pdf/24-1470.pdf

*A febrile man in Italy who had traveled to Cuba in July 2024 was diagnosed with Oropouche fever. Reverse transcription PCR detected prolonged shedding of Oropouche virus RNA in whole blood, serum, urine, and semen. Sixteen days after symptom onset, replication-competent virus was detected in semen, suggesting risk for sexual transmission.*

Castonguay AC, Chowdhury S, Shanta IS, Schrijver B, Schrijver R, Wang SY, Magalhaes RJS.

**A Generalizable Prioritization Protocol for Climate-Sensitive Zoonotic Diseases.**

Tropical Medicine and Infectious Disease. 2024;9(8):16.

https://mdpi-res.com/d_attachment/tropicalmed/tropicalmed-09-00188/article_deploy/tropicalmed-09-00188.pdf?version=1724219762

*Emerging and re-emerging zoonotic diseases pose a significant threat to global health and economic security. This threat is further aggravated by amplifying drivers of change, including climate hazards and landscape alterations induced by climate change. Given the complex relationships between climate change and zoonotic disease health outcomes, a structured decision-making process is required to effectively identify pathogens of greatest concern to prioritize prevention and surveillance efforts. Here, we describe a workshop-based expert elicitation process in six steps to prioritize climate-sensitive zoonoses based on a structured approach to defining criteria for climate sensitivity. Fuzzy analytical hierarchy process methodology is used to analyze data provided by experts across human, animal, and environmental health sectors accounting for uncertainties at different stages of the prioritization process. We also present a new interactive expert elicitation interface that facilitates data collection and real-time visualization of prioritization results. The novel approach presented in this paper offers a generalized platform for prioritizing climate-sensitive zoonoses at a national or regional level. This allows for a structured decision-making support process when allocating limited financial and personnel resources to enhance preparedness and response to zoonotic diseases amplified by climate change.*

de França DA, Kmetiuk LB, Rodrigues OJD, Panazzolo GAK, Morikawa VM, Dure AID, et al.

***Coxiella burnetii* (Q fever) exposure in wildlife professionals.**

Frontiers in public health. 2024;12:7.

https://www.frontiersin.org/journals/public-health/articles/10.3389/fpubh.2024.1466981/pdf

*Introduction Although occupational exposure to Coxiella burnetii has been studied previously, the zoonotic risk in wildlife environments remains unclear and has yet to be fully established.Methods Accordingly, the present study aimed to serologically assess professionals with daily contact with free-living and captive wildlife in Paran & aacute; State, Brazil, along with the potential associated risk factors for C. burnetii exposure.Results Overall, 25 out of 309 (8.1%) wildlife professionals were seropositive, including 6/54 (11.1%) national and 7/125 (5.6%) state park employees, 6/92 (6.5%) zookeepers, and 6/38 (15.8%) animal service workers, with titers ranging from 32 to 128. No statistical association was found between seropositivity and associated risk factors, including the working location.Discussion Our results differ from those of previous studies in Brazil, which found 8/893 (0.9%) indigenous, 1/18 (5.5%) police officers, and 44/200 (22.0%) former Black slaves to be seropositive. This study is the first serological investigation of C. burnetii among park rangers, zookeepers, and animal service workers in Brazil, showing no statistically significant risk factors for seropositivity. As the seroprevalence in this study was higher than that in previous surveys of healthy (asymptomatic) human populations, C. burnetii exposure may also be an occupational risk for wildlife professionals owing to their contact with the natural environment in Brazil.*

Douglas KO, Punu G, Van Vliet N.

**Prioritization of zoonoses of wildlife origin for multisectoral one health collaboration in Guyana, 2022.**

One Health. 2024;18:8.

https://www.sciencedirect.com/science/article/pii/S2352771424000569?via%3Dihub

*Background: The human population in Guyana, located on the South American continent, is vulnerable to zoonotic diseases due to an appreciable reliance on Neotropical wildlife as a food source and for trade. An existing suboptimal health surveillance system may affect the effective monitoring of important zoonotic diseases. To effectively address this deficit, a One Health zoonotic disease prioritization workshop was conducted to identify nationally significant zoonoses. Methods: Prioritization of zoonotic diseases was conducted for the first time in Guyana & Caribbean region using literature review, prioritization criteria and a risk prioritization tool in combination with a consultative One Health workshop. This involved multisectoral experts from varied disciplines of social, human, animal, and environmental health to prioritize zoonotic diseases using a modified semi-quantitative One Health Zoonotic Disease Prioritization (OHZDP) tool. The inclusion and exclusion criteria were applied to pathogen hazards in existence among wildlife in Guyana during the hazard identification phase. Results: In total, fifty zoonoses were chosen for prioritization. Based on their weighted score, prioritized diseases were ranked in order of relative importance using a one-to-five selection scale. In Guyana, this zoonotic disease prioritization method is the first significant step toward bringing together specialists from the fields of human, animal, and environmental health. Following discussion of the OHZDP Tool output among disease experts, a final zoonotic disease list, including tuberculosis, leptospirosis, gastroenteritis, rabies, coronavirus, orthopoxvirus, viral hemorrhagic fevers, and hepatitis were identified as the top eight priority zoonoses in Guyana. Conclusions: This represents the first prioritization of nationally significant zoonotic diseases in Guyana and the English-speaking Caribbean. This One Health strategy to prioritize these eight zoonoses of wildlife origin is a step that will support future tracking and monitoring for disease prevalence among humans and wildlife and can be used as a decision-making guide for policymakers and stakeholders in Guyana.*

Gajda-Sawicka E, Kowalec M, Sienko A, Ochab A, Zuk M, Bielat U, et al.

**Assessment of occupational exposure of soldiers to Lyme disease and *Borrelia miyamotoi* disease in selected military training areas from northern Poland.**

Exp Appl Acarol. 2025;94(1):25.

https://link.springer.com/article/10.1007/s10493-024-00980-x

*Ixodes ricinus tick is a vector of bacteria of Borreliella genus and Borrelia miyamotoi. Exposure to ticks constitutes occupational risk to soldiers, but the current knowledge on this subject is still limited. Therefore, the aim of this study was to evaluate tick abundance and prevalence of infection with Borreliella spp. and/or B. miyamotoi. Ticks were collected from vegetation on Drawsko, Ustka and Orzysz military training areas. Additionally, ticks infesting soldiers were also obtained. Ticks were examined by nested PCR and sequencing of flaB gene fragment. General Linear Models of One Variable was used for analysis of mean tick abundance and Maximum Likelihood technique based on log-linear analysis of contingency tables was used for analysis of prevalence of pathogens in ticks. Molecular phylogenetic analyses were also performed. 852 I. ricinus were collected from vegetation from three military areas. The overall mean abundance of ticks was almost 4 ticks/100 m2. Season of study had a significant effect on density of total ticks, infected nymphs and females and infected nymphs, which were higher in spring-early summer. Total prevalence of pathogens was 25.7% in 711 questing ticks, and 16.0% in 282 I. ricinus collected from soldiers. Six species of Borreliella and Borrelia were identified with predominance of B. afzelii. It should be assumed that there is a risk for soldiers of acquiring infection after tick bite. The awareness of presence of pathogens in ticks should be raised in military.*

Grubaugh N, Torres-Hernández D, Murillo-Ortiz M, Dávalos D, Lopez P, Hurtado I, et al.

**Dengue Outbreak Caused by Multiple Virus Serotypes and Lineages, Colombia, 2023–2024.**

Emerging Infectious Disease journal. 2024;30(11):2391.

https://wwwnc.cdc.gov/eid/article/30/11/24-1031_article

https://pmc.ncbi.nlm.nih.gov/articles/PMC11521178/pdf/24-1031.pdf

*Dengue cases rose to record levels during 2023–2024. We investigated dengue in Valle del Cauca, Colombia, to determine if specific virus serotypes or lineages caused its large outbreak. We detected all 4 serotypes and multiple lineages, suggesting that factors such as climatic conditions were likely responsible for increased dengue in Colombia.*

Guagliardo SA, Connelly CR, Lyons S, Martin S, Sutter R, Hughes H, et al.

**Reemergence of Oropouche Virus in the Americas and Risk for Spread in the United States and Its Territories, 2024.**

Emerging Infectious Disease journal. 2024;30(11):2241.

https://wwwnc.cdc.gov/eid/article/30/11/24-1220_article

https://pmc.ncbi.nlm.nih.gov/articles/PMC11521165/pdf/24-1220.pdf

*Oropouche virus has recently caused outbreaks in South America and the Caribbean, expanding into areas to which the virus was previously not endemic. This geographic range expansion, in conjunction with the identification of vertical transmission and reports of deaths, has raised concerns about the broader threat this virus represents to the Americas. We review information on Oropouche virus, factors influencing its spread, transmission risk in the United States, and current status of public health response tools. On the basis of available data, the risk for sustained local transmission in the continental United States is considered low because of differences in vector ecology and in human–vector interactions when compared with Oropouche virus–endemic areas. However, more information is needed about the drivers for the current outbreak to clarify the risk for further expansion of this virus. Timely detection and control of this emerging pathogen should be prioritized to mitigate disease burden and stop its spread.*

Hoa HTT, Dung NT, Hung LM, Hong NTT, Quy VT, Thao NT, et al.

**Emerging Monkeypox Virus Sublineage C.1 Causing Community Transmission, Vietnam, 2023.**

Emerging Infectious Disease journal. 2024;30(11):2385.

https://wwwnc.cdc.gov/eid/article/30/11/24-0729_article

https://pmc.ncbi.nlm.nih.gov/articles/PMC11521191/pdf/24-0729.pdf

*We studied a community cluster of 25 mpox cases in Vietnam caused by emerging monkeypox virus sublineage C.1 and imported into Vietnam through 2 independent events; 1 major cluster carried a novel APOBEC3-like mutation. Three patients died; all had advanced HIV co-infection. Viral evolution and its potential consequences should be closely monitored.*

Jirawattanadon P, Bunyaratavej S, Leeyaphan C, Chongtrakool P, Sitthinamsuwan P, Panjapakkul W, et al.

**Clinical Manifestations, Antifungal Drug Susceptibility, and Treatment Outcomes for Emerging Zoonotic Cutaneous Sporotrichosis, Thailand.**

Emerging Infectious Disease journal. 2024;30(12):2583.

https://wwwnc.cdc.gov/eid/article/30/12/24-0467_article

https://pmc.ncbi.nlm.nih.gov/articles/PMC11616660/pdf/24-0467.pdf

*We analyzed clinical manifestations, antifungal susceptibility, and treatment outcomes of cutaneous sporotrichosis in Thailand during 2018–2022. The study included 49 patients whose mean age was 58.7 (SD 16.9) years; 65.3% were female and 34.7% male. A history of cat exposure was reported in 32 (65.3%) patients who had a significantly higher prevalence of upper extremity lesions than did those without cat contact (90.6% vs. 41.7%; adjusted odds ratio 18.9 [95% CI 3.2–92.9]). Among patients &gt;60 years of age, lesions were more likely to be nonpustular than for patients &lt;60 years of age (82.1% vs. 52.4%; p = 0.033). All 9 isolates tested for antifungal drug susceptibility exhibited an itraconazole MIC of &lt;1 µg/mL. Oral itraconazole monotherapy was effective; the median time-to-cure was 180 days (interquartile range 141–240 days). Physicians should heighten their awareness of potential sporotrichosis causes, particularly when a history of animal contact exists.*

Kälber KA, Enk A, Michel J, Schrick L, Winkler JK.

**Orf-Virus-Infektion bei einer 53-jährigen Frau.**

Dermatologie. 2025;76(1):34-6.

https://pmc.ncbi.nlm.nih.gov/articles/PMC11711704/pdf/105_2024_Article_5412.pdf

*The orf virus is one of the parapoxviruses. It occurs worldwide and its natural reservoir are sheep and goats. Infections in humans can occur through direct or indirect contact with affected animals. The infectious ulcerations usually heal spontaneously after a few weeks in immunocompetent patients. An infection must be reported to the responsible professional association if the exposure occurs in the occupational environment, for example in farmers.*

Kharwadkar S, Weinstein P, Stanhope J.

**Drivers of human *Leptospira* infection in the Pacific Islands: A systematic review.**

Epidemiology & Infection. 2024;152:19.

https://www.cambridge.org/core/services/aop-cambridge-core/content/view/B5D2A4B3FFE91138EB08C70C6B34D02D/S0950268824001250a.pdf/div-class-title-drivers-of-human-span-class-italic-leptospira-span-infection-in-the-pacific-islands-a-systematic-review-div.pdf

*Leptospirosis is a bacterial zoonosis that poses an increasing global public health risk. Pacific Island communities are highly vulnerable to leptospirosis outbreaks, yet the local drivers of infection remain poorly understood. We conducted a systematic review to identify the drivers of human Leptospira infection in the Pacific Islands. There were 42 included studies from which findings were synthesized descriptively. In tropical Pacific Islands, infections were a product of sociodemographic factors such as male gender/sex, age 20 to 60 years, Indigenous ethnicity, and poverty; lifestyle factors such as swimming, gardening, and open skin wounds; and environmental factors, including seasonality, heavy rainfall, and exposure to rodents, cattle, and pigs. Possible mitigation strategies in these islands include strengthening disease reporting standards at a regional level; improving water security, rodent control, and piggery management at a community level; and information campaigns to target individual-level drivers of infection. By contrast, in New Zealand, exposures were predominantly occupational, with infections occurring in meat and farm workers. Accordingly, interventions could include adjustments to occupational practices and promoting the uptake of animal vaccinations. Given the complexity of disease transmission and future challenges posed by climate change, further action is required for leptospirosis control in the Pacific Islands.*

La THA, McMillan IA, Dahal P, Burger AH, Belcaid M, Phelps DM, et al.

**Tracking sero-molecular trends of swine brucellosis in Hawai'i and the central Pacific.**

Frontiers in public health. 2024;12:11.

https://www.frontiersin.org/journals/public-health/articles/10.3389/fpubh.2024.1440933/pdf

*Introduction: Brucellosis is a zoonotic disease of mammals caused by bacterial species of the Brucella genus. The reservoir for disease is typically mammals, with species of Brucella found infecting amphibians, bats, and marine mammals. Brucella spp. can pass directly to humans through contact* *with infected animals or their products. Brucella spp. can cause chronic debilitating infections in mammals, including humans, and is associated with spontaneous abortions in infected animals, causing reduced fecundity. In Hawai'i, terrestrial species that could harbor Brucella spp. include swine, cattle, horses, and axis deer among others. The numerous feral swine in Hawai'i are known to carry Brucella suis, with evidence supporting infections in cattle. Brucella suis also poses infection risk to humans, dogs, and potentially horses across the state. Methods: In this study, 3,274 feral swine serum samples collected from 5 of the 8 main islands over a 15-year span were analyzed for exposure to B. suis. Of the 558 watersheds in the state, 77 were sampled as part of this effort. Spatial analysis was used to identify watersheds of concern. MLVA and whole genome SNP analysis was used for molecular epidemiological analysis. Results: Statewide seropositivity rates were triple that of feral swine found in the conterminous United States. Smoothed positivity rates were highest on Maui, followed by O'ahu, and the island of Hawai'i. Island-by-island analysis found high brucellosis positivity levels associated with specific watersheds and agricultural areas. Local spatial autocorrelation identified hot spots on O'ahu and Hawai'i. MLVA analysis of available B. suis from Hawai'i found molecular epidemiological connections with B. suis found in French Polynesia and the mainland US while differing from those in Tonga, Western Polynesia. Strains from Hawai'i are phylogenetically closest to strains from the United States. MLVA and SNP analysis found B. suis strains from Hawai'i fell into the genetic group that contains biovar 1 B. suis. Discussion: This work identified islands and watersheds of high brucellosis seropositivity in feral swine of Hawai'i, highlighting the magnitude of the zoonotic risk. Introduction of strains in recent history is unlikely due to modern animal trade and disease control practices. Genomic analysis of strains in Hawai'i and the Pacific area can provide hidden historical and local clues to brucellosis epidemiology in the state.*

Loevinsohn G, Paulino CT, Spring J, Hughes H, Restrepo AC, Mayfield H, et al.

**Chikungunya Outbreak Risks after the 2014 Outbreak, Dominican Republic.**

Emerging Infectious Disease journal. 2024;30(12):2679.

https://wwwnc.cdc.gov/eid/article/30/12/24-0824_article

https://pmc.ncbi.nlm.nih.gov/articles/PMC11616656/pdf/24-0824.pdf

*The 2014 chikungunya outbreak in the Dominican Republic resulted in intense local transmission, with high postoutbreak seroprevalence. The resulting population immunity will likely minimize risk for another large outbreak through 2035, but changes in population behavior or environmental conditions or emergence of different virus strains could lead to increased transmission.*

Méndez M, Colanzi R, Suárez J, Penagos H, Hernandez C, Garcia-Redondo R, et al.

**Lobomycosis in Amazon Region, Bolivia, 2022.**

Emerging Infectious Disease journal. 2024;30(12):2660.

https://wwwnc.cdc.gov/eid/article/30/12/24-1089_article

https://pmc.ncbi.nlm.nih.gov/articles/PMC11616652/pdf/24-1089.pdf

*We report a patient with lobomycosis caused by Paracoccidioides loboi fungi in the Andes-Amazon region of Bolivia. We examined clinical, epidemiologic, and phylogenetic data and describe potential* *transmission/environmental aspects of infection. Continued surveillance and identification of lobomycosis cases in South America are crucial to prevent the spread of this disease.*

Onafruo D, Dreyfus A, Erume J, Kankya C, Jubara A, Kokas I, et al.

***Leptospira* seroprevalence and associated risk factors among slaughterhouse workers in Western Bahr El Ghazal State, South Sudan.**

PLoS neglected tropical diseases. 2024;18(12):13.

https://journals.plos.org/plosntds/article/file?id=10.1371/journal.pntd.0012700&type=printable

*Background Leptospirosis is a neglected re-emerging and occupational zoonotic disease worldwide. In Africa, contact with livestock is postulated as a potential source of environmental contamination and a source of human Leptospira exposure, though pathways remain unknown. Recently, we confirmed Leptospira exposure and shedding among slaughtered cattle in Western Bahr El Ghazal. In the current study, we sought to determine corresponding occupational leptospiral seropositivity, associated risk factors and the prevalence of febrile illness among slaughterhouse workers.Methods Between 27th February and 30th March 2023, we collected blood and interviewed 250 consenting slaughterhouse workers of the same facilities from which the cattle samples were collected. The workers were screened for leptospiral antibodies using the Microscopic agglutination test (MAT), based on a panel of 12 including those previously reported in livestock in South Sudan and the East African Region.Results Of the 250 participants, 16 were seropositive 16/250, (6.4%, 95% CI = 3.2-10.2). Two seropositive individuals 0.8% (2/250) had MAT titers >= 800, indicative of probable recent leptospiral infection. Moreover, 42.4% (106/250) of the respondents reported experiencing fever in the past one month and 36.0% (90/250) sought medical attention. Among those seeking medical care for febrile illnesses, diagnostic tests revealed 9.2% (23/250) with malaria, 7.6% (19/250) with typhoid, 16.8% (42/250) with both malaria and typhoid coinfections, 1.6% (4/250) with brucellosis, and no cases of leptospirosis had been considered. Most seropositive individuals reacted to serovar L. borgpetersenii Tarassovi 2.4% (6/250) and L. interrogans sv Australis 2.4% (6/250). The factors associated with seropositivity included flaying, with persons who flay animals having 14.9 times, (95% CI, 2.5-88.9) greater odds of being seropositive than persons who do not flay animals (P = 0.003), people who wore an apron/overall were 10.6 times (95% CI, 1.6-67.6) more likely to be seropositive than people who did not wear an apron/overall (P = 0.012). An increase in the number of carcasses handled per day by one increases the odds of exposure by 2.7 times (95% CI, 1.6-4.5), (P = 0.001).Conclusion Finding seropositive workers in cattle slaughter facilities in Western Bahr El Ghazal, South Sudan, and similar serogroups as previously found in the cattle slaughtered at these facilities implies activities like animal slaughter that bring humans into close contact with animals could be one pathway for human Leptospira exposure in South Sudan. This could also highlight leptospirosis as a potential public health threat to those in frequent contact with cattle, including farmers, those in animal transportation, and veterinarians. The role of leptospirosis in cases of undifferentiated fever in South Sudan may also be worth investigating, especially in cases where occupational exposure is suspected. Further research including animals, the general public, farmers, and hospitalized patients is proposed to fully understand the burden of human leptospirosis. Including the serovar and serogroup Tarassovi and Australis in future vaccine development and serodiagnostic panels for South Sudan is highly recommended.*

Piche-Ovares M, García MP, Moreira-Soto A, Figueroa-Romero MD, Merino-Sarmiento NS, Marcelo-Ñique AI, et al.

**Rio Mamore Hantavirus Endemicity, Peruvian Amazon, 2020.**

Emerging Infectious Disease journal. 2024;30(12):2532.

https://wwwnc.cdc.gov/eid/article/30/12/24-0249_article

https://pmc.ncbi.nlm.nih.gov/articles/PMC11616641/pdf/24-0249.pdf

*To explore hantavirus infection patterns in Latin America, we conducted molecular and serologic hantavirus investigations among 3,400 febrile patients from Peru during 2020&ndash;2021. Reverse transcription PCR indicated that a patient from Loreto, in the Peruvian Amazon, was positive for Rio Mamore hantavirus (serum, 3.8 &times; 103 copies/mL). High genomic sequence identity of 87.0%&ndash;94.8% and phylogenetic common ancestry with a rodent-associated Rio Mamore hantavirus from Loreto in 1996 indicated endemicity. In 832 samples from Loreto, hantavirus incidence based on IgM ELISA of pooled Sin Nombre (SNV) and Andes virus (ANDV) nucleoproteins and immunofluorescence assay&ndash;based end-point titration using SNV/ANDV/Hantaan/Puumala/Saarema/Dobrava/Seoul hantaviruses was 0.5%. Across 3 ecologically distinct departments in Peru, SNV/ANDV IgG ELISA/IFA&ndash;based reactivity was 1.7%, suggesting circulation of antigenically distinct New World hantaviruses. Testing for arboviruses, nonendemic pathogens, and antigen-free ELISA corroborated nonspecific reactivity in 2 IgG and several IgM ELISA&ndash;positive serum samples. Hantavirus diagnostics and surveillance should be strengthened in Peru and across Latin America.*

Segaloff H, Wu K, Williams S, Shaw S, Miko S, Parnell L, et al.

**Human and Canine Blastomycosis Cases Associated with Riverside Neighborhood, Wisconsin, USA, December 2021–March 2022.**

Emerging Infectious Disease journal. 2024;30(12):2633.

https://wwwnc.cdc.gov/eid/article/30/12/24-0390_article

https://pmc.ncbi.nlm.nih.gov/articles/PMC11616636/pdf/24-0390.pdf

*We investigated a blastomycosis cluster among humans and canines in a neighborhood in Wisconsin, United States. We conducted interviews and collected serum specimens for Blastomyces antibody testing by enzyme immunoassay. Although no definitive exposure was identified, evidence supports potential exposures from the riverbank, riverside trails or yards, or construction dust.*

Usuga J, Limonta D, Perez-Restrepo L, Ciuoderis K, Moreno I, Arevalo A, et al.

**Co-Circulation of 2 Oropouche Virus Lineages, Amazon Basin, Colombia, 2024.**

Emerging Infectious Disease journal. 2024;30(11):2375.

https://wwwnc.cdc.gov/eid/article/30/11/24-0405_article

https://pmc.ncbi.nlm.nih.gov/articles/PMC11521167/pdf/24-0405.pdf

*In early 2024, explosive outbreaks of Oropouche virus (OROV) linked to a novel lineage were documented in the Amazon Region of Brazil. We report the introduction of this lineage into Colombia and its co-circulation with another OROV lineage. Continued surveillance is needed to prevent further spread of OROV in the Americas.*

Wainaina M, Wasonga J, Cook EAJ.

**Epidemiology of human and animal leptospirosis in Kenya: A systematic review and meta-analysis of disease occurrence, serogroup diversity and risk factors.**

PLoS neglected tropical diseases. 2024;18(9):20.

https://journals.plos.org/plosntds/article/file?id=10.1371/journal.pntd.0012527&type=printable

*Background Leptospirosis is a priority zoonotic disease in Kenya, but an in-depth review of its presence in humans, animals and the environment is lacking. Therefore, we conducted this systematic review and meta-analysis to understand the epidemiological situation to date.Methodology We searched for literature in African journals online, AGRIS, Embase, the Leptospira WOAH reference laboratory library, ProMED-mail, PubMed, Scopus, Web of Science, and the institutional repositories of 33 academic institutions and included 66 publications on leptospirosis in Kenya which spanned from 1951 to 2022. The review was registered on the International Platform of Registered Systematic Review and Meta-analysis Protocols (INPLASY).Findings Most investigations were done in rural and urban areas in western, southern, central, and coastal areas in Kenya and the largely pastoral eastern and northern areas were under-represented. A wide host range of domestic animals and wildlife was revealed, and occupational exposure was an important risk factor for humans. The microscopic agglutination test (MAT) was the most frequent test, particularly common in studies conducted during the 1980s and 1990s. However, varying MAT panels and cut-off titres were observed. The overall seroprevalence in cattle was 28.2% (95% confidence intervals [CI]: 12.0-53.0; heterogeneity: I2 = 96.7%, tau 2 = 1.4), and 11.0% in goats (95% CI: 5.4-21.2; heterogeneity: I2 = 78.8%, tau 2 = 0.4). Molecular tests were seldom used to determine species and illustrate strain diversity. There was a lack of awareness of leptospirosis among farmers and health practitioners.Conclusion The widespread presence of leptospires and inadequate diagnostic capacity demonstrate that leptospirosis is a common but underreported disease in Kenya. Raising awareness and boosting the country's diagnostic capacity is crucial to timely detection and disease control. Leptospirosis is a prevalent but understudied zoonotic disease in Kenya. A comprehensive review of the presence of the disease in various hosts is therefore needed to catalogue the research efforts and inspire future scientific inquiry on this neglected tropical disease. We therefore undertook this comprehensive review of published literature in leading databases and institutional repositories of relevant Kenyan higher institutions of learning. Literature spanning more than 70 years was identified and study areas showed a regional bias towards central, western, southern and coastal regions. The arid and semi-arid areas in the northern and eastern regions with large animal and wildlife populations that could facilitate leptospiral transmission were under-represented, and the inclusion of these pastoral regions could give a better picture of the country's leptospirosis risk profile. Summary estimates in cattle and goats revealed considerable pooled seroprevalence of leptospirosis and the need for control in animal hosts. A low awareness among farmers, and animal and public health practitioners was found, demonstrating the need for education initiatives that can facilitate at-risk populations such as farmers. Additionally, the country lacks the capacity for MAT testing, and recent efforts to culture for leptospires are non-existent. Understanding the circulating serovars and strain diversity is crucial to the effective control of leptospirosis. Investments in diagnostics for peripheral and central laboratories are vital for public health response.*

Waranius B, Tillman C, Van Houten C, Harrist A, Digianantonio R, Hasel H, et al.

**Human Case of Leptospirosis During a Canine Disease Outbreak - Wyoming, 2023.**

Mmwr-Morbidity and Mortality Weekly Report. 2024;73(27):602-6.

https://pmc.ncbi.nlm.nih.gov/articles/PMC11254349/pdf/mm7327a1.pdf

*Leptospirosis is a zoonotic bacterial disease spread through the urine of infected animals; the typical incubation period is 5-14 days. In approximately 90% of human cases, illness is asymptomatic or mild, characterized by fever, chills, myalgia, nausea, vomiting, diarrhea, headache, calf pain, and conjunctival suffusion, but severe illness can progress to multiorgan dysfunction and death. Although Wyoming is considered a low-risk area for leptospirosis because of its cold and semiarid climate, the Wyoming Department of Health was notified of a probable human case in August 2023, the first reported in the state since 1983. The patient had occupational exposure to dogs but did not report other risk factors. The same week that the human patient's illness began, public health authorities received notification of an increase in canine leptospirosis cases. Public health authorities investigated to determine potential sources of infection, identify additional cases, and recommend control measures. After public health outreach activities were implemented, canine vaccination practices changed substan-tially in the affected city: a survey conducted after the outbreak revealed that all responding veterinary clinics in the affected city were recommending the vaccine more frequently to dog owners and reporting higher levels of owner compliance with vaccination recommendations. Increased vaccination coverage offers protection from leptospirosis for both dogs and persons exposed to them. Leptospirosis should be considered in the differential diagnosis of persons with occupational exposure to animals and clinically compatible signs and symptoms, including fever, chills, myalgia, nausea, vomiting, diarrhea, headache, calf pain, and conjunctival suffusion, irrespective of geographic location.*

Xu Q, Nabeshima T, Hamada K, Sugimoto T, Tun MMN, Morita K, et al.

**Transmission of Severe Fever with Thrombocytopenia Syndrome Virus to Human from Nonindigenous Tick Host, Japan.**

Emerging Infectious Disease journal. 2024;30(11):2419.

https://wwwnc.cdc.gov/eid/article/30/11/24-0912_article

https://pmc.ncbi.nlm.nih.gov/articles/PMC11521155/pdf/24-0912.pdf

*We report a human case of severe fever with thrombocytopenia syndrome virus infection transmitted by a tick, confirmed by viral identification. Haemaphysalis aborensis, a tick species not native to Japan that has been observed to transmit the virus to humans, is now recognized as a potential vector of this virus in Japan.*

Zychowski D, Bamunuarachchi G, Commins S, Boyce R, Boon ACM.

**Evidence of Human Bourbon Virus Infections, North Carolina, USA.**

Emerging Infectious Disease journal. 2024;30(11):2396.

https://wwwnc.cdc.gov/eid/article/30/11/24-0499_article

https://pmc.ncbi.nlm.nih.gov/articles/PMC11521162/pdf/24-0499.pdf

*Bourbon virus is a tickborne virus that can cause human disease. Cases have been reported in Kansas, Oklahoma, and Missouri, USA. We identified Bourbon virus–specific neutralizing antibodies in patients from North Carolina. Bourbon virus infections are likely more common than previously thought, highlighting the need for improved diagnostics and surveillance.*

## Légionellose

Mohamed HM, Zielinski L, Diedhiou A, Clemmons N, Smith JC, Rinsky JL, et al.

**Cluster of Legionellosis Cases Associated with Manufacturing Process, South Carolina, USA, 2022.**

Emerging infectious diseases. 2025;31(1):41-9.

https://pmc.ncbi.nlm.nih.gov/articles/PMC11682818/pdf/24-0916.pdf

*Evolving technology and the development of new devices that can aerosolize water present a risk for new sources of Legionella bacteria growth and spread within industrial settings. We investigated a cluster of legionellosis among employees of a manufacturing facility in South Carolina, USA, and found 2 unique equipment sources of Legionella bacteria. The cluster of cases took place during August-November 2022; a total of 34 cases of legionellosis, including 15 hospitalizations and 2 deaths, were reported. Legionella pneumophila was isolated*

## Endotoxines

Madsen AM, Rasmussen PU, Delsuz MS, Frederiksen MW.

**A cross-sectional study on occupational hygiene in biowaste plants.**

Annals of work exposures and health. 2024:15.

https://academic.oup.com/annweh/article-abstract/68/9/967/7766093

*Recycling demands are increasing and new biowaste plants are established. The aim of this study is to obtain knowledge about occupational hygiene in biowaste pretreatment plants. At 6 plants, bioaerosol exposure, hand hygiene, and bioaerosol concentrations in work areas were investigated repeatedly. The total inflammatory potential (TIP) of exposures was measured using the human HL-60 cell line. Exposure to airborne bacteria, bacteria able to grow anaerobic, fungi(37 degrees C), endotoxin, and TIP differed between plants and was lowest in a plant transporting waste in closed pipes compared to plants where waste was delivered on the receiving hall floor. Conversely, high exposures were measured in a plant that also processes compost. All microbial components had an impact on TIP of workers' exposure with main effects of fungi and endotoxin. Seasonality was found for several exposures and TIP, and they were lowest in the winter. Concentrations of bacteria and fungi on workers' hands at the end of the workday were 15 times higher for production than for nonproduction workers. In work areas, the concentrations of airborne fungi were highest in the waste-receiving area. Bacteria (3.2 mu m) and anaerobic bacteria (4.0 mu m) were present as larger airborne particles than fungi (2.8 mu m), and bacteria were largest in the waste-receiving area. The microbial community compositions of exposures and work areas differed between plants and work areas. In conclusion, measures to reduce exposure should focus on the waste-receiving area and on the production workers. Differences in exposures and community compositions were found between seasons, work areas, work groups, and plants.*

# Biotechnologies

## Nouveaux procédés

Ali A, Shahbaz M, Ölmez F, Fatima N, Umar UUD, Ali MA, et al.

**RNA interference: a promising biotechnological approach to combat plant pathogens, mechanism and future prospects.**

World Journal of Microbiology & Biotechnology. 2024;40(11):23.

https://link.springer.com/article/10.1007/s11274-024-04143-3

*Plant pathogens and other biological pests represent significant obstacles to crop Protection worldwide. Even though there are many effective conventional methods for controlling plant diseases, new methods that are also effective, environmentally safe, and cost-effective are required. While plant breeding has traditionally been used to manipulate the plant genome to develop resistant cultivars for controlling plant diseases, the emergence of genetic engineering has introduced a completely new approach to render plants resistant to bacteria, nematodes, fungi, and viruses. The RNA interference (RNAi) approach has recently emerged as a potentially useful tool for mitigating the inherent risks associated with the development of conventional transgenics. These risks include the use of specific transgenes, gene control sequences, or marker genes. Utilizing RNAi to silence certain genes is a promising solution to this dilemma as disease-resistant transgenic plants can be generated within a legislative structure. Recent investigations have shown that using target double stranded RNAs via an effective vector system can produce significant silencing effects. Both dsRNA-containing crop sprays and transgenic plants carrying RNAi vectors have proven effective in controlling plant diseases that threaten commercially significant crop species. This article discusses the methods and applications of the most recent RNAi technology for reducing plant diseases to ensure sustainable agricultural yields.*

Ambily B, Mol VPL, Sini H, Nevin KG.

**CRISPR-based microalgal genome editing and the potential for sustainable aquaculture: a comprehensive review.**

J Appl Phycol. 2024:21.

https://link.springer.com/article/10.1007/s10811-024-03376-x

*Microalgae are a diverse collection of unicellular photosynthetic organisms that grow in a wide range of environments, from hot springs to snow and ice. They have great potential for renewable energy generation as well as being potential sources of a wide range of metabolites including lipids, proteins, pigments, and bioactive compounds. Microalgae have received a lot of interest in recent years as a resource for sustainable aquaculture and as a potential solution to the environmental and dietary challenges created by traditional aquaculture practices. Recent biotechnology advancements have enabled scientists to modify the genetic composition of microalgae through CRISPR technology, specifically focusing on genes or metabolic pathways that provide unprecedented accuracy and efficiency for the production of bioactive substances and biorefineries. CRISPR-based microalgal genetic engineering could eventually help to ease pressure on wild fish populations, preserve natural aquatic ecosystems, and improve the nutritional value of farmed fish for human consumption. This review also highlights the challenges and limitations of applying CRISPR technology in microalgae, including the* *risk of off-target effects that can alter unintended genomic regions, leading to unpredictable outcomes. Likewise, the efficient delivery of CRISPR components into microalgal cells remains a critical challenge, necessitating the development of species-specific delivery methods to enhance the precision and efficacy of CRISPR-based modifications. Overall, this review shows the potential of microalgae in sustainable aquaculture, and provides an assessment of current developments and successes in CRISPR-based genome editing in microalgae as well as the potential future uses of its metabolic engineering and gene editing strategies.*

Bhowmick K, Roy D, Rana D, Ghosh A, Sadhukhan S, Chakraborty M, et al.

**Potential microbes in bioremediation: A review.**

Mater Today Sustain. 2024;28:17.

https://www.sciencedirect.com/science/article/abs/pii/S2589234724003683?via%3Dihub

*Over the past few decades, the soaring environmental pollution due to hastened industrialization and pernicious agricultural processes has become a substantial obstacle. The existence of detrimental contaminants like nuclear wastes, heavy metals, pesticides, hydrocarbons, oils, and dyes has been withering the environment and human health. In this context, microbial bioremediation has established itself as the most comprehensive biotechnological process for environmental restoration. The application of microbial communities in bioremediation is gaining momentum as an astounding, environmentally sound, and economically efficient means to mitigate the harmful effects of toxic pollutants. Microorganisms serve as invaluable resources for environmental restoration and remediation of polluted soil, showcasing their presence across a wide range of environmental conditions. Precisely microorganisms are distributed all over the biosphere due to their diverse metabolic activity and can easily grow in a wide range of environmental conditions which in an environment often create a variety of enzymes that can eliminate hazardous contaminants by using them as a substrate for growth. To enhance the metabolic potential of microbes, currently, different methods and strategies like biostimulation, bioaugmentation, bioventing, etc. are applied. The present review focuses on microbial diversity in bioremediation, different techniques applied, and the bioremediation of different environmental pollutants. It additionally attempted to highlight the monitoring of the bioremediation processes and their sustainability.*

Boyadzhieva I, Berberov K, Atanasova N, Krumov N, Kabaivanova L.

**Extracellular Haloalkalophilic Pectinase Produced by *Virgibacillus salarius* Strain 434-A Useful Tool for Biotechnological Applications.**

Appl Sci-Basel. 2024;14(20):15.

https://mdpi-res.com/d_attachment/applsci/applsci-14-09295/article_deploy/applsci-14-09295.pdf?version=1728722488

*Featured Application Microbial enzyme production falls into the so-called white biotechnology field, a part of modern biotechnology. Different applications of microbial enzymes have significant importance in regard to sustainable production, replacing hazardous chemicals. The newly isolated and purified haloalkalophilic pectinase enzyme revealed unique characteristics, making it suitable for application in the pretreatment of wastewaters from the textile, fabric, and paper industries, containing pectinecious wastes, in this way hindering environmental pollution. Its potential uses in the food-processing industry include improving the quality of fruit juices and wine in a cost-effective and sustainable manner.Abstract The interest in microbial pectinases is increasing due to their use in the* *biotechnological and food industries in response to global demand. In this study, among the 22 halophilic bacterial strains screened, 20 showed pectinase activity. The highest activity was measured for Virgibacillus salarius strain 434. As pectinase production meets many parameter optimization constraints, optimal production conditions for maximizing the yield of the pectinase synthesized using the investigated strain were followed. Enzyme purification was accomplished at up to 11.5-fold via ultrafiltration and gel filtration chromatography, until the enzyme's specific activity had increased 10-fold (104.3 U/mg). The enzyme's molecular weight was determined to be 68 kDa. Km and Vmax values of 0.38 mg/mL and 120 U/mg, respectively, were determined. The purified pectinase from Virgibacillus salarius strain 434 showed good thermal stability. A half-life of 20 min at 70 degrees C and high catalytic activity under haloalkaline conditions (pH 9 and 70 g L-1 NaCl) were observed. Its storage stability at -20 degrees C exceeded 2 months. This demonstrates its potential for application in industries where these extremes are present, as the harsh conditions in industrial processes require novel pectinases with unique properties instead of the use of hazardous chemicals.*

Bulkowska K, Zielinska M.

**Recovery of Biogas and Other Valuable Bioproducts from Livestock Blood Waste: A Review.**

Energies. 2024;17(23):25.

https://mdpi-res.com/d_attachment/energies/energies-17-05873/article_deploy/energies-17-05873.pdf?version=1732288355

*The anaerobic digestion (AD) of livestock blood represents a sustainable solution for the management of waste generated by the meat processing industry while simultaneously generating renewable energy. The improper treatment of livestock blood, which is rich in organic matter and nutrients, can result in environmental risks such as water pollution, soil degradation, and greenhouse gas emissions. This review examines a range of AD strategies, with a particular focus on technological advances in reactor design, pretreatment, and co-digestion, with the aim of optimizing process efficiency. While the high protein content of blood has the potential to enhance biogas production, challenges such as ammonia inhibition and process instability must be addressed. Innovations such as bio-carriers, thermal pretreatment, and co-digestion with carbon-rich substrates have demonstrated efficacy in addressing these challenges, resulting in stable operation and enhanced methane yields. The advancement of AD technologies is intended to mitigate the environmental impact of livestock blood waste and facilitate the development of a circular bioeconomy. Furthermore, the possibility of utilizing slaughterhouse blood for the recovery of valuable products, including proteins, heme iron, and bioactive peptides, was evaluated with a view to their potential applications in the pharmaceutical and food industries. Furthermore, the potential of utilizing protein-rich blood as a substrate for mixed culture fermentation in volatile fatty acid (VFA) biorefineries was explored, illustrating its viability in biotechnological applications.*

Cao HX, Michels D, Vu GTH, Gailing O.

**Applications of CRISPR Technologies in Forestry and Molecular Wood Biotechnology.**

Int J Mol Sci. 2024;25(21):25.

https://mdpi-res.com/d_attachment/ijms/ijms-25-11792/article_deploy/ijms-25-11792.pdf?version=1730537316

*Forests worldwide are under increasing pressure from climate change and emerging diseases, threatening their vital ecological and economic roles. Traditional breeding approaches, while valuable, are inherently slow and limited by the long generation times and existing genetic variation of trees.*

*CRISPR technologies offer a transformative solution, enabling precise and efficient genome editing to accelerate the development of climate-resilient and productive forests. This review provides a comprehensive overview of CRISPR applications in forestry, exploring its potential for enhancing disease resistance, improving abiotic stress tolerance, modifying wood properties, and accelerating growth. We discuss the mechanisms and applications of various CRISPR systems, including base editing, prime editing, and multiplexing strategies. Additionally, we highlight recent advances in overcoming key challenges such as reagent delivery and plant regeneration, which are crucial for successful implementation of CRISPR in trees. We also delve into the potential and ethical considerations of using CRISPR gene drive for population-level genetic alterations, as well as the importance of genetic containment strategies for mitigating risks. This review emphasizes the need for continued research, technological advancements, extensive long-term field trials, public engagement, and responsible innovation to fully harness the power of CRISPR for shaping a sustainable future for forests.*

Harris CG, Semprini L, Rochefort WE, Fogg KC.

**Statistical optimization of cell-hydrogel interactions for green microbiology - a tutorial review.**

RSC Sustain. 2024;2(12):3750-68.

https://pubs.rsc.org/en/content/articlepdf/2024/su/d4su00400k

*In this tutorial mini-review, we explore the application of Design of Experiments (DOE) as a powerful statistical tool in biotechnology. Specifically, we review the optimization of hydrogel materials for diverse microbial applications related to green microbiology, the use of microbes to promote sustainability. Hydrogels, three-dimensional polymers networks with high water retention capabilities, are pivotal in the immobilization of microorganisms and provide a customizable environment essential for directing microbial fate. We focus on the application of DOE to precisely tailor hydrogel compositions for a range of fungi and bacteria either used for the sustainable production of chemical compounds, or the elimination of hazardous substances. We examine a variety of DOE design strategies such as central composite designs, Box-Behnken designs, and optimal designs, and discuss their strategic implementation across diverse hydrogel formulations. Our analysis explores the integral role of DOE in refining hydrogels derived from a spectrum of polymers, including natural and synthetic polymers. We illustrate how DOE facilitates nuanced control over hydrogel properties that cannot be achieved using a standard one factor at a time approach. Furthermore, this review reveals a conserved finding across different materials and applications: there are significant interactions between hydrogel parameters and cell behavior. This highlights the intricacies of cell-hydrogel interactions and the impact on hydrogel material properties and cellular functions. Lastly, this review not only highlights DOE's efficacy in streamlining the optimization of cell-hydrogel processes but also positions it as a critical tool in advancing our understanding of cell-hydrogel dynamics, potentially leading to innovative advancements in biotechnological applications and bioengineering solutions.*

Huang H, Lu JJ, Jin LL, Ren HQ.

**The Future of Environmental Engineering Technology: A Disruptive Innovation Perspective.**

Engineering. 2024;41:153-60.

https://www.sciencedirect.com/science/article/pii/S2095809924003783?via%3Dihub

*Scientific and technological revolutions and industrial transformations have accelerated the rate of innovation in environmental engineering technologies. However, few researchers have evaluated the current status and future trends of technologies. This paper summarizes the current research status in eight major subfields of environmental engineering-water treatment, air pollution control, soil/solid* *waste management, environmental biotechnology, environmental engineering equipment, emerging contaminants, synergistic reduction of pollution and carbon emissions, and environmental risk and intelligent management-based on bibliometric analysis and future trends in greenization, low carbonization, and intelligentization. Disruptive technologies are further identified based on discontinuous transformation, and ten such technologies are proposed, covering general and specific fields, technical links, and value sources. Additionally, the background and key innovations in disruptive technologies are elucidated in detail. This study not only provides a scientific basis for strategic decision-making, planning, and implementation in the environmental engineering field but also offers methodological guidance for the research and determination of breakthrough technologies in other areas. (c) 2024 THE AUTHORS. Published by Elsevier LTD on behalf of Chinese Academy of Engineering and Higher Education Press Limited Company. This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/4.0/).*

Kamboj A, Sadh PK, Chawla P, Saharan BS, Seth CS, Sridhar K, et al.

**Sustainable management of rice by-products: Environmental challenges, industrial applications, and circular bio-economy innovations.**

Biocatal Agric Biotechnol. 2024;62:27.

https://www.sciencedirect.com/science/article/abs/pii/S1878818124004146?via%3Dihub

*The agricultural sector plays an essential role in both human and economic growth, offering sustenance, employment, income, raw materials, technological progress, and sustainability. The growing awareness of the necessity to enhance agricultural production is gaining attention, primarily driven by the imperative to adequately nourish the continuously expanding global population. Diverse agricultural practices are causing harmful environmental consequences, posing a significant risk to ecological stability through issues such as soil degradation, water pollution, habitat loss, and biodiversity decline. Timely and effective agricultural waste management has become essential for preventing adverse environmental and health impacts. Biomass from rice crop harvesting and processing has been found in abundance around the world. Because of the abundance of this biomass in nature, researchers are harnessing it for various objectives, including global energy requirements, while supporting environmental sustainability. Due to this rationale, within the frameworks of emerging sustainable and circular models, the prioritization of agricultural waste valorization has gained prominence as a pivotal strategy aimed at advancing sustainable management and circular economy. This review mainly emphasizes on the rice bio-waste, its environmental and health-related issues, policies to control stubble burning, reduce pollution in the air, and sustainable management of the biowaste into wealth using different approaches worldwide. We also investigated the potential contribution of rice-by-products wastes to bioenergy production (bioethanol, biogas, and biofuel), enzymes, nanoparticles, construction materials, animal husbandry, bioplastics, and other value-added products. We recommend that proper management of rice by-products may produce innovative bio-ingredients and biodegradable materials, and enhance green growth and a circular bioeconomy.*

*Kasapgil E, Garay-Sarmiento M, Rodriguez-Emmenegger C.*

***Advanced Antibacterial Strategies for Combatting Biomaterial-Associated Infections: A Comprehensive Review.***

*Wiley Interdiscip Rev-Nanomed Nanobiotechnol. 2024;16(6):27.*

*https://doi.org/10.1002/wnan.2018*

*Biomaterial-associated infections (BAIs) pose significant challenges in modern medical technologies, being a major postoperative complication and leading cause of implant failure. These infections significantly risk patient health, resulting in prolonged hospitalization, increased morbidity and mortality rates, and elevated treatment expenses. This comprehensive review examines the mechanisms driving bacterial adhesion and biofilm formation on biomaterial surfaces, offering an in-depth analysis of current antimicrobial strategies for preventing BAIs. We explore antimicrobial-eluting biomaterials, contact-killing surfaces, and antifouling coatings, emphasizing the application of antifouling polymer brushes on medical devices. Recent advancements in multifunctional antimicrobial biomaterials, which integrate multiple mechanisms for superior protection against BAIs, are also discussed. By evaluating the advantages and limitations of these strategies, this review aims to guide the design and development of highly efficient and biocompatible antimicrobial biomaterials. We highlight potential design routes that facilitate the transition from laboratory research to clinical applications. Additionally, we provide insights into the potential of synthetic biology as a novel approach to combat antimicrobial resistance. This review aspires to inspire future research and innovation, ultimately improving patient outcomes and advancing medical device technology.*

*Katalevskiy AD, Smirnov KV, Smirnova NN.*

***MEMBRANES IN BIOTECHNOLOGY: CURRENT STATE AND PROSPECTS.***

*Izv Vyss Uchebnykh Zaved Khim Khimichesk Tekhnol. 2025;68(1):6-22.*

*https://ctj-isuct.ru/article/download/5737/3591*

*Membranes have always been an important part of a diverse range of biotechnological processes. Nowadays, reverse osmosis, ultrafiltration, microfiltration, gas separation, chromatography, pervaporation, electrodialysis and other membrane-based processes are integral part of biotechnological production, enabling the resolution of various technological challenges. First membrane systems, used in biotechnology was taken from other fields. However, over the past 45 years, new materials and components have been developed for specific biotechnological applications. Membranes are highly suitable for use with biomolecules: relatively low temperature and pressure, no need for phase transitions or addition of chemical compounds. As a result, the risks of degradation, denaturation or inactivation of biotechnological products are reduced to a minimum. Currently, membrane-based technologies offer the best solutions for processes such as sterilizing filtration, clarification, cell culture cultivation, virus removal, and protein concentration and purification. Processes involving membrane bioreactors and membrane chromatography are becoming more and more common. In the review, the current state of development in membrane technology is presented, as well as the description of materials used for membranes and the characteristics of the membrane systems used in commercial production. Appliance for membrane separation processes can be quite expensive, but it is more energy-efficient than traditional separation methods. Due to their design, membrane systems are typically compact and have a modular structure, which allows to use of the same equipment to solve various tasks. It is discussed that future developments in membrane technology will be able to meet the increasing demands for higher productivity, lower production costs, and accelerate the development of the biotechnology.*

Luo X, Pang ZR, Li JH, Anh M, Kim BS, Gao G.

**Bioengineered human arterial equivalent and its applications from vascular graft to in vitro disease modeling.**

iScience. 2024;27(11):34.

https://doi.org/10.1016/j.isci.2024.111215

*Arterial disorders such as atherosclerosis, thrombosis, and aneurysm pose significant health risks, necessitating advanced interventions. Despite progress in artificial blood vessels and animal models aimed at understanding pathogenesis and developing therapies, limitations in graft functionality and species discrepancies restrict their clinical and research utility. Addressing these issues, bioengineered arterial equivalents (AEs) with enhanced vascular functions have been developed, incorporating innovative technologies that improve clinical outcomes and enhance disease progression modeling. This review offers a comprehensive overview of recent advancements in bioengineered AEs, systematically summarizing the bioengineered technologies used to construct these AEs, and discussing their implications for clinical application and pathogenesis understanding. Highlighting current breakthroughs and future perspectives, this review aims to inform and inspire ongoing research in the field, potentially transforming vascular medicine and offering new avenues for preclinical and clinical advances.*

Manikandan A, Muthusamy S, Wang ES, Ivarson E, Manickam S, Sivakami R, et al.

**Breeding and biotechnology approaches to enhance the nutritional quality of rapeseed byproducts for sustainable alternative protein sources- a critical review.**

Front Plant Sci. 2024;15:26.

https://www.frontiersin.org/journals/plant-science/articles/10.3389/fpls.2024.1468675/pdf

*Global protein consumption is increasing exponentially, which requires efficient identification of potential, healthy, and simple protein sources to fulfil the demands. The existing sources of animal proteins are high in fat and low in fiber composition, which might cause serious health risks when consumed regularly. Moreover, protein production from animal sources can negatively affect the environment, as it often requires more energy and natural resources and contributes to greenhouse gas emissions. Thus, finding alternative plant-based protein sources becomes indispensable. Rapeseed is an important oilseed crop and the world's third leading oil source. Rapeseed byproducts, such as seed cakes or meals, are considered the best alternative protein source after soybean owing to their promising protein profile (30%-60% crude protein) to supplement dietary requirements. After oil extraction, these rapeseed byproducts can be utilized as food for human consumption and animal feed. However, anti-nutritional factors (ANFs) like glucosinolates, phytic acid, tannins, and sinapines make them unsuitable for direct consumption. Techniques like microbial fermentation, advanced breeding, and genome editing can improve protein quality, reduce ANFs in rapeseed byproducts, and facilitate their usage in the food and feed industry. This review summarizes these approaches and offers the best bio-nutrition breakthroughs to develop nutrient-rich rapeseed byproducts as plant-based protein sources.*

Maria TC, Maldaner Pereira PA, Pepe ESG, Lemos EGM.

**Biochemical study and digestion profile of olive oil by LipBK: Revealing the potential applications of a new acid/broad thermal range true lipase.**

Int J Biol Macromol. 2025;297:139892.

https://www.sciencedirect.com/science/article/abs/pii/S0141813025004416?via%3Dihub

*This study characterized a novel bacterial lipase with high biotechnological potential, focusing on industrial and environmental applications. Bacterial isolates were screened using olive oil as a substrate, and the strain with the highest hydrolytic halo was identified as Burkholderia sp. via 16S rRNA analysis. The secreted lipase was purified and exhibited high hydrolytic activity, specifically targeting long-chain fatty acids. Gas chromatography analyses confirmed its ability to hydrolyze fatty acids present in olive oil, while kinetic parameters and substrate preferences were assessed using synthetic substrates. Optimal activity was observed at pH 4.5 and temperatures between 40 and 60 °C. The enzyme demonstrated remarkable thermal stability, retaining over 78 % residual activity after 24 h at 30, 40, 60, and even 70 °C. It also displayed broad pH stability, with increased relative activity at pH 6.5 over time. LipBK showed resilience in the presence of metallic ions, salts, EDTA, and non-ionic detergents, with enhanced activity in the presence of additives like KCl, $CaCl_2$, and Triton X-100. These properties highlight its robustness and suitability for applications in acidic and thermally variable environments, such as biodiesel production, waste treatment, and sustainable industrial processes, contributing to global sustainability goals.*

Mu YF, Ma LW, Yao J, Luo D, Ding XG.

**Bioengineered Extracellular Vesicle Hydrogel Modulating Inflammatory Microenvironment for Wound Management.**

Int J Mol Sci. 2024;25(23):13.

https://mdpi-res.com/d_attachment/ijms/ijms-25-13093/article_deploy/ijms-25-13093.pdf?version=1733407274

*Chronic wounds, frequently arising from conditions like diabetes, trauma, or chronic inflammation, represent a significant medical challenge due to persistent inflammation, heightened infection risk, and limited treatment solutions. This study presents a novel bioengineered approach to promote tissue repair and improve the healing environment. We developed a bioactive hydrogel patch, encapsulated zeolitic imidazolate framework-8 (ZIF-8) into extracellular vesicles (EVs) derived from anti-inflammatory M2 macrophages, and synthesized ZIF@EV, then embedded it in the sodium alginate matrix. This hydrogel structure enables the controlled release of therapeutic agents directly into the wound site, where it stimulates endothelial cell proliferation and promotes new blood vessel formation. These processes are key components of effective tissue regeneration. Crucially, the EV-infused patch influences the immune response by polarizing macrophages towards an M2 phenotype, shifting the wound environment from inflammation toward regenerative healing. When applied in a murine model of chronic wounds, the EV hydrogel patch demonstrated notable improvements in healing speed, quality, and tissue integration compared to traditional approaches such as growth factor therapies and foam dressings. These promising findings suggest that this bioactive hydrogel patch could serve as a versatile, practical solution for chronic wound management, providing an adaptable platform that addresses both the biological and logistical needs of wound care in clinical settings.*

Onn SM, Koh GJ, Yap WH, Teoh ML, Low CF, Goh BH.

**Recent advances in genetic engineering of microalgae: bioengineering strategies, regulatory challenges and future perspectives.**

J Appl Phycol. 2024:18.

https://link.springer.com/article/10.1007/s10811-024-03367-y

*Microalgae are being studied for nutraceuticals, medicines, and other industrial applications due to their metabolic capabilities in generating a wide range of bioproducts. However, inadequate yield and productivity are recurring issues for the commercial use of microalgae and their bioproducts. Despite promising global market, the industrial biotechnology sector has been slow in adapting to genetically modified (GM) microalgae due to various regulatory and scalability challenges. In this review, genetic modification tools like CRISPR, ZFN, TALEN, RNAi, synthetic biology, metabolic engineering techniques and high throughput screening platforms in different microalgal strains are discussed. Recent progress in microalgal genetic engineering and strain improvement in industrial applications such as biomass production, biomolecules production and process improvement are also highlighted. Lastly, the regulatory issues and biosafety issues in the use of genetically engineered microalgae in industrial and commercial applications, as well as the risk assessments such as hazard and exposure assessments are described.*

Pathakakula S, Lakshmanan N, Thiruvenkatasamy S, Subramaniam G, Narayanan MB, Kalichamy C.

**Mutation Breeding on Medicinal *Solanum* Species: Advances, Applicability and Challenges.**

Plant Breed. 2024:13.

https://doi.org/10.1111/pbr.13253

*Medicinal Solanum species, belonging to the Solanaceae family, are extensively utilized in traditional medicine because of their therapeutic properties, including anti-inflammatory, antioxidant and anticancer activities. Enhancing these species through the integration of conventional breeding techniques with modern biotechnological tools presents promising strategies for developing improved varieties with higher yields, better quality and reduced thorniness. Induced mutagenesis has emerged as a highly effective approach for improving specific traits in these cultivars while preserving their well-adapted genetic backgrounds. This review explores various mutagenesis methods, including physical, chemical and insertional methods, highlighting their efficacy in the enhancement of medicinal Solanum species. It also addresses the challenges and potential risks associated with mutation breeding. Recent advancements in sequencing technologies, such as MutMap, MutChromeSeq and whole-genome sequencing-based mapping, offer unprecedented opportunities for accurately detecting large-scale mutagenesis-induced variations in other solanaceous crops, including tomato, brinjal and chilli. The combination of well-characterized mutant resources with innovative mapping techniques holds significant potential for rapidly improving the quality and yield of medicinal Solanum species. Overall, this comprehensive analysis provides valuable insights for researchers and practitioners involved in the cultivation and enhancement of medicinal Solanum species through mutation breeding techniques.*

Phogat S, Lankireddy SV, Lekkala S, Anche VC, Sripathi VR, Patil GB, et al.

**Progress in genetic engineering and genome editing of peanuts: revealing the future of crop improvement.**

Physiol Mol Biol Plants. 2024;30(11):1759-75.

https://link.springer.com/article/10.1007/s12298-024-01534-6

*Peanut (Arachis hypogaea L.), also known as groundnut, is cultivated globally and is a widely consumed oilseed crop. Its nutritional composition and abundance in lipids, proteins, vitamins, and essential mineral elements position it as a nutritious food in various forms across the globe, ranging from nuts and confections to peanut butter. Cultivating peanuts provides significant challenges due to abiotic and biotic stress factors and health concerns linked to their consumption, including aflatoxins and allergens. These factors pose risks not only to human health but also to the long-term sustainability of peanut* *production. Conventional methods, such as traditional and mutation breeding, are time-consuming and do not provide desired genetic variations for peanut improvement. Fortunately, recent advancements in next-generation sequencing and genome editing technologies, coupled with the availability of the complete genome sequence of peanuts, offer promising opportunities to discover novel traits and enhance peanut productivity through innovative biotechnological approaches. In addition, these advancements create opportunities for developing peanut varieties with improved traits, such as increased resistance to pests and diseases, enhanced nutritional content, reduced levels of toxins, anti-nutritional factors and allergens, and increased overall productivity. To achieve these goals, it is crucial to focus on optimizing peanut transformation techniques, genome editing methodologies, stress tolerance mechanisms, functional validation of key genes, and exploring potential applications for peanut improvement. This review aims to illuminate the progress in peanut genetic engineering and genome editing. By closely examining these advancements, we can better understand the developments achieved in these areas.*

Ravikumar M, Velmurugan K, John AJ, Selvarajan E.

**Microalgae to remove pharmaceutical and personal care products (PPCPs) from wastewater.**

Biocatal Agric Biotechnol. 2024;62:14.

https://www.sciencedirect.com/science/article/abs/pii/S1878818124003992?via%3Dihub

*Substances used for medicinal, cosmetic, hygiene, and health care objectives are included in the category of pharmaceuticals and personal care products (PPCPs). They are a major source of public concern because of their ubiquitous manufacturing, usage, and careless disposal of expired products into the environment. Many PPCPs, including antibiotics, analgesics, endocrine disruptors, and microbial/disinfecting agents, are commonly detected in freshwater systems, groundwater, and wastewater treatment effluents in amounts ranging from nanograms per liter to milligrams per milliliter. Additionally, these compounds frequently show persistence and accumulate in biological tissue, eventually finding their way into crops, vegetables, and drinking water supplies. Because many PPCPs are known to have the ability to upset ecosystems and/or provide health hazards, they are categorized as "emerging contaminants." The research on the occurrence, fate, and possible health and environmental hazards related to PPCPs in both aquatic and terrestrial habitats is thoroughly reviewed in this work. It also covers reported cases of danger or health concerns in humans, although a full assessment may not be possible given the limitations of the data at hand. This review aims to provide a comprehensive and well-focused overview of the current understanding of bioremediation strategies for the removal of pharmaceuticals and personal care products (PPCPs), with an emphasis on the application of macroalgae, microalgae, and aquatic macrophytes. It examines the physicochemical properties of PPCPs and their potential risks to environmental and human health. Additionally, the review explores the potential and challenges associated with the broader application of biotechnologies employing algae and aquatic macrophytes. This includes research efforts to correlate the operational parameters of these biotechnologies with the primary mechanisms responsible for PPCP removal. In conclusion, algae and macrophytes present promising, eco-friendly solutions for wastewater treatment, significantly contributing to the mitigation of PPCP contamination.*

Roca A, Monge-Olivares L, Matilla MA.

**Antibiotic-producing plant-associated bacteria, anti-virulence therapy and microbiome engineering: Integrated approaches in sustainable agriculture.**

Microbial biotechnology. 2024;17(10):9.

https://doi.org/10.1111/1751-7915.70025

*Plant health is crucial for maintaining the well-being of humans, animals and the environment. Plant pathogens pose significant challenges to agricultural production, global food security and ecosystem biodiversity. This problem is exacerbated by the impact of climate change, which is expected to alter the emergence and evolution of plant pathogens and their interaction with their plant hosts. Traditional approaches to managing phytopathogens involved the use of chemical pesticides, but alternative strategies are needed to address their ongoing decline in performance as well as their negative impact on the environment and public health. Here, we highlight the advancement and effectiveness of biocontrol strategies based on the use of antimicrobial-producing plant-associated bacteria, anti-virulence therapy (e.g. quorum quenching) and microbiome engineering as sustainable biotechnological approaches to promote plant health and foster sustainable agriculture. Notably, Enterobacterales are emerging as important biocontrol agents and as a source of new antimicrobials for potential agricultural use. We analysed here the genomes of over 250 plant-associated enterobacteria to examine their potential to synthesize secondary metabolites. Exploration of the plant microbiome is of major interest in the search for eco-friendly alternatives for reducing the use of chemical pesticides. Antimicrobial-producing plant-associated bacteria, anti-virulence therapy and microbiome engineering as sustainable biotechnological approaches to promote plant health and foster sustainable agriculture.*

Sanchez-Hernandez JC, Megharaj M.

**Insect farming: A bioeconomy-based opportunity to revalorize plastic wastes.**

Environ Sci Ecotechnol. 2025;23:100521.

https://www.sciencedirect.com/science/article/pii/S2666498424001352?via%3Dihub

*Managing plastic waste is one of the greatest challenges humanity faces in the coming years. Current strategies-landfilling, incineration, and recycling-remain insufficient or pose significant environmental concerns, failing to address the growing volume of plastic residues discharged into the environment. Recently, increasing attention has focused on the potential of certain insect larvae species to chew, consume, and partially biodegrade synthetic polymers such as polystyrene and polyethylene, offering novel biotechnological opportunities for plastic waste management. However, insect-assisted plastic depolymerization is incomplete, leaving significant amounts of microplastics in the frass (or manure), limiting its use as a soil amendment. In this perspective, we propose a novel two-step bioconversion system to overcome these limitations, using insects to sustainably manage plastic waste while revalorizing its by-products (frass). The first step involves pyrolyzing microplastic-containing frass from mealworms (Tenebrio molitor larvae) fed on plastic-rich diets to produce biochar with enhanced adsorptive properties. The second stage integrates this biochar into the entomocomposting of organic residues, such as food waste, using black soldier fly (Hermetia illucens) larvae to produce nutrient-rich substrates enriched with carbon and nitrogen. This integrated system offers a potential framework for large-scale industrial applications, contributing to the bioeconomy by addressing both plastic waste and organic residue management. We critically examine the advantages and limitations of the proposed system based on current literature on biochar technology and entomocomposting. Key challenges and research opportunities are identified, particularly concerning the physiological and toxicological processes involved, to guide future efforts aimed at ensuring the scalability and sustainability of this innovative approach.*

Shi K, Xu JM, Cui HL, Cheng HY, Liang B, Wang AJ.

**Microbiome regulation for sustainable wastewater treatment.**

Biotechnology advances. 2024;77:19.

https://www.sciencedirect.com/science/article/abs/pii/S0734975024001526?via%3Dihub

*Sustainable wastewater treatment is essential for attaining clean water and sanitation, aligning with UN Sustainable Development Goals. Wastewater treatment plants (WWTPs) have utilized environmental microbiomes in biological treatment processes in this effort for over a century. However, the inherent complexity and redundancy of microbial communities, and emerging chemical and biological contaminants, challenge the biotechnology applications. Over the past decades, understanding and utilization of microbial energy metabolism and interaction relationships have revolutionized the biological system. In this review, we discuss how microbiome regulation strategies are being used to generate actionable performance for low-carbon pollutant removal and resource recovery in WWTPs. The engineering application cases also highlight the real feasibility and promising prospects of the microbiome regulation approaches. In conclusion, we recommend identifying environmental risks associated with chemical and biological contaminants transformation as a prerequisite. We propose the integration of gene editing and enzyme design to precisely regulate microbiomes for the synergistic control of both chemical and biological risks. Additionally, the development of integrated technologies and engineering equipment is crucial in addressing the ongoing water crisis. This review advocates for the innovation of conventional wastewater treatment biotechnology to ensure sustainable wastewater treatment.*

Sukma ACT, Budiyono B, Al-Baarri AN.

**Recent Advances in Bioethanol Production from Rice Straw: Strategies, New Concepts, and Challenges.**

Int J Environ Res. 2025;19(1):36.

https://link.springer.com/article/10.1007/s41742-024-00681-8

*Second-generation bioethanol has garnered considerable interest among researchers due to its utilization of lignocellulosic biomass, such as rice straw, which is both cost-effective and readily available. Nonetheless, the economic viability of large-scale production of second-generation bioethanol remains a significant challenge. There is an urgent need for cost efficiency across three critical stages: pretreatment, hydrolysis, and fermentation. This paper reviews recent advancements in bioethanol production from rice straw and proposes a novel approach to enhance economic feasibility. The inherent recalcitrance of rice straw necessitates the implementation of an appropriate pretreatment method, as this step is crucial for the success of the hydrolysis process. While chemical pretreatment is frequently employed, it often results in increased waste generation and maintenance costs, thereby elevating the overall production expenses. Optimizing reactor configurations for enzyme production, hydrolysis, and fermentation can lead to substantial reductions in production costs. Although enzymatic hydrolysis utilizing commercial enzymes is the predominant method, on-site enzyme production has demonstrated significant cost advantages. Consolidated bioprocessing (CBP) integrates enzyme production, hydrolysis, and fermentation within a single reactor using a single strain or microbial consortium. However, the productivity of bioethanol production from rice straw via CBP is currently low. The proposed novel CBP aims to address the limitations of the original CBP by integrating pretreatment, enzyme production, hydrolysis, and fermentation in a single reactor with a microbial consortium. This innovative approach is expected to minimize contamination risks and reduce equipment installation costs, thereby improving cost-effectiveness. Nevertheless, the implementation of the novel CBP presents challenges, including the establishment of a stable and efficient microbial consortium and the determination of optimal process parameters. Addressing these challenges is essential for the successful application of the novel CBP at an industrial scale.*

Tanwar SN, Parauha YR, There Y, Swart HC, Dhoble SJ.

**Plant-Based Biosynthesis of Metal and Metal Oxide Nanoparticles: An Update on Antimicrobial and Anticancer Activity.**

ChemBioEng Rev. 2024;11(6):80.

https://doi.org/10.1002/cben.202400012

*Nanotechnology has changed and developed all the sectors and working fields. Nanoparticles are one of the important evolutionary materials that have application in almost all the working areas such as catalysis, bioengineering, photoelectricity, antibacterial, anticancer, and medical imaging due to their unique physical and chemical properties. Traditionally used chemical and physical method of synthesis of nanoparticles have several disadvantages like using different chemicals, high cost, and most importantly they are hazardous to the environment. Counter to these disadvantages, a more eco-friendly, easy, and cost-effective green synthesis method is widely employed nowadays. Various parts of a plant are used as a fuel for reducing the metal ion salt. Plant extracts act as reducing, stabilizing, and capping agents. Besides these advantages, photosynthesized nanoparticles are nontoxic, more stable, and more uniform in size than their counterparts prepared by the traditional method. In this present review, the synthesis of various plant extract-mediated metal and metal oxide nanoparticles is discussed along with their different applications. This review provides a comprehensive overview of key findings in green synthesis of metal and metal oxide nanoparticles and attempts to determine their possible synthesis mechanism. This article also focuses on factors affecting their synthesis, characterization, potential applications, and prospects. When it comes to finding novel ways to battle newly developing pathogenic strains and illnesses, nanoparticles are the first line of defense. Plant-based nanoparticles are showing more significance over chemically or physically synthesized nanoparticles. Several plant species and their constituent parts have found several applications in medicine. They are more biocompatible and show less toxicity.*

Ugya AY, Sheng YY, Chen H, Wang Q.

**Microalgal bioengineering: A futuristic tool for carbon capture.**

Results Eng. 2024;24:12.

https://www.sciencedirect.com/science/article/pii/S2590123024012453?via%3Dihub

*Microalgae is a sustainable tool for carbon capture and bioprospecting due to its unique characteristics, but its scale-up application has been hindered by different challenges. This study alluded to the potential for overcoming existing barriers and easing the application of microalgae-based solutions in carbon capture technologies. The mechanisms by which different bioengineering techniques enhance the photosynthetic efficiency, carbon fixation pathways, and stress tolerance in microalgae, leading to carbon capture, were also explored. These bioengineering techniques were deciphered towards scale-up cultivation of microalgal resources and application in carbon capture. The success of scale-up applications was linked to the implementation of metabolic and genetic engineering strategies. These strategies tend to enhance the economic and environmental feasibility of microalgae-based carbon capture technologies. The engineering of microalgae stress responsive mechanisms was shown to improve biomass productivity and resilience of microalgae. The pathway towards the eradication of issues related to the technical feasibility of microalgae scale-up application in carbon capture was identified. The study buttressed the role of policy and regulatory frameworks in enhancing the feasibility of microalgae usage as a tool in scale-up carbon capture. But to ascertain a scale-up application of microalgae-based technology for carbon capture, research direction should focus on the use of bioengineering techniques to ease the integration of microalgae systems into industrial processes.*

# *Organismes français et internationaux - Actualités*

Suivi d'organismes français et internationaux. Sélection d'actualités classées par thème.

Pour information – interruption des mises à jour des publications des CDC (US) :

AP, Trump administration freezes many health agency reports and online posts, 22/01/2025.

## Biotechnologies

Institut Pasteur,

L'immunité humorale de la peau, façonnée par le microbiote, et son potentiel pour le développement d'approches vaccinales novatrices, 16/12/2024.

Une nouvelle méthode pour produire des thérapies à base d'ADN, 04/11/2024.

## Coqueluche

Institut Pasteur, La vaccination rend-elle moins virulente la bactérie causant la coqueluche ?, 17/12/2024.

## Entérobactéries

INPSQ, Mesures de prévention et de contrôle des entérobactéries productrices de carbapénémases : Gestion des environnements aqueux des milieux de soins, 15/01/2025.

## Fièvre paratyphoïde B

Institut Pasteur, Fièvre paratyphoïde B : retracer l'histoire de la maladie pour mieux la surveiller, 19/12/2024.

## Gestion de crise sanitaire

Institut Pasteur, Leçons de la crise Covid : agir tôt, identifier vite et surveiller l'impact pour mieux protéger, 09/12/2024.

## Grippe aviaire

CDC (US),

First H5 Bird Flu Death Reported in United States, 06/01/2025.

CDC confirms H5N1 Bird Flu Infection in a Child in California, 22/11/2024.

## Infections à pneumocoques

HAS, Pneumocoques : élargir la vaccination à tous les adultes de 65 ans et plus, 28/01/2025.

## Infections respiratoires aigües

HCSP, Stock stratégique de l'État d'antiviraux contre la grippe, 21/12/2024.

Santé Publique France,

Infections respiratoires aiguës (grippe, bronchiolite, COVID-19). Bulletin, 22 janvier 2025.

Face à la circulation active des virus de la grippe, la campagne de vaccination contre la grippe est prolongée jusqu'au 28 février 2025, 22/01/2025.

## Légionellose

HSE (UK),

Company failed to manage legionella risk as prisoner dies, 03/12/2024.

Residents put at risk of deadly disease as company fined £900k, 22/10/2024.

## Maladies vectorielles et zoonoses

ANSES,

Influenza D : une transmission possible des bovins aux porcs, 03/12/2024.

Virus influenza de la grippe du porc : éviter la transmission entre animaux et humains, 21/11/2024.

HAS, Vaccination contre la dengue : la HAS publie ses recommandations, 17/12/2024.

HCSP, Mesures de prévention pour les voyageurs vis-à-vis de la maladie à virus Oropouche, 10/12/2024.

INSPQ, Fièvre oropouche, dernière mise à jour le 27/01/2025.

OMS,

L'OMS préqualifie un test de diagnostic pour une administration plus sûre des traitements contre le paludisme à P. vivax, 08/01/2025.

Des efforts accrus doivent être déployés à l'échelle mondiale pour endiguer la menace croissante que représente le paludisme, 11/12/2024.

Lignes directrices de l'OMS sur le paludisme, 30/11/2024.

## Mayotte – surveillance sanitaire suite cyclone Chido

Santé Publique France,

Mayotte : comment s'adapte la surveillance sanitaire après le passage du cyclone Chido ?, 03/01/2025.

Chido à Mayotte. Bulletin du 23 janvier 2025, 24/01/2025.

- ## Mélioïdose

ANSES, Mélioïdose : une maladie tropicale ignorée, 17/01/2025.

- ## Mpox

OMS,

Deuxième réunion du Comité d'urgence du Règlement sanitaire international (2005) concernant la recrudescence de la mpox (variole simienne) en 2024, 28/11/2024.

Rassemblements dans le contexte de l'épidémie de mpox (variole simienne) de 2024: recommandations de santé publique, 22/11/2024.

L'OMS ajoute le vaccin LC16m8 contre la mpox au protocole d'autorisation d'utilisation d'urgence, 19/11/2024.

Des doses de vaccin ont été allouées aux neuf pays africains les plus durement touchés par la recrudescence de la mpox (variole simienne), 06/11/2024.

CDC (US),

California confirms first clade I mpox case, 16/11/2024.

Santé Publique France,

Cas de Mpox en France. 1er janvier - 8 janvier 2025, 08/01/2025.

Face au premier cas de Mpox de clade I b identifié en France, les autorités sanitaires rappellent l'importance de la vaccination pour les publics cibles, 07/01/2025.

- ## Protection respiratoire

IRSST, La santé est dans l'air : maîtrisez votre APR, 15/01/2025.

- ## Rougeole

OMS, Les cas de rougeole sont en hausse dans le monde entier, avec 10,3 millions de personnes infectées en 2023, 14/11/2024.

CDC (US), Measles cases surge worldwide, infecting 10.3 million people in 2023, 14/11/2024.

- ## Tuberculose

Kansas Department of Health and Environment (US), Kansas City Area TB Outbreak, 01/2025.

OMS, L'OMS annonce la première préqualification d'un test de diagnostic de la tuberculose, 05/12/2024.

- **VIH**

HAS, Virus de l’immunodéficience humaine (VIH) : de nouvelles recommandations pour la prise en charge thérapeutique, curative et préventive des personnes vivant avec le VIH et des personnes exposées au VIH, 20/11/2024.

INSERM, VIH : une bataille qui ne faiblit pas, 18/12/2024.