

sis of VL in Sudan. A total of 198 VL suspects were tested by microscopy of lymph node aspirates (the reference test), direct agglutination test-DAT (in house production) and rK28 antigen-based rapid diagnostic test (OnSite Leishmania rK39-Plus, CTK Biotech, USA). LAMP was performed on peripheral blood (whole blood and buffy coat) previously processed by: i) a direct boil and spin method, and ii) the QIAamp DNA Mini Kit (QIAGEN). Ninety seven of the VL suspects were confirmed as cases by microscopy of lymph node aspirates. The sensitivity and specificity for each of the tests were: rK28 RDT 98.81% and 100%; DAT 88.10% and 78.22%; LAMP-boil and spin 97.65% and 99.01%; LAMP-QIAGEN 100% and 99.01%.

Conclusions/Significance: The excellent performance of LAMP using peripheral blood indicates that it can be included in the algorithm for diagnosis of VL, avoiding the need for invasive lymph node aspiration. The simplicity of the test makes it a promising candidate for confirmatory diagnosis in settings that are lower than the reference laboratory.

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Prediction and validation of the structural features of Ov58GPCR, an immunogenic antigen of *Onchocerca volvulus*: implications in onchocerciasis control efforts



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Onchocerciasis is a severely debilitating yet neglected tropical disease (NTD) that creates social stigma, generates and perpetuates poverty, and leads ultimately to irreversible unilateral or bilateral blindness if untreated. Consequently, the disease is a major impediment to socioeconomic development. Many control programs have been launched for the disease with moderate successes achieved. This mitigated hit is partially due to the lingering need for reliable, non-invasive and easily-applicable tools for mapping endemic regions and post-elimination surveillance. In this work, bioinformatics analyses combined with immunological assays were applied in a bid to develop potential tools for diagnosis and assessing the success of drug treatment programs. Comparisons of more than two groups in case of paired data were made using repeated measures ANOVA on ranks. The diagnostic performance of the total IgG was assessed for each study peptide using receiver operating curve (ROC) analyses. We report that (i) the *O. volvulus* antigen, Ov58GPCR is a G-protein coupled receptor (GPCR) conserved in related nematodes, (ii) synthetic peptides predicted to be in the extracellular domain (ECD) of Ov58GPCR are indeed immunogenic epitopes in patients, (iii) synthetic peptide cocktails discriminate between untreated patients, treated patients and healthy African controls, (iv) polyclonal antibodies against one of the peptides or against the bacterially-expressed ECD reacted specifically with the native antigen in *O. volvulus* total and surface extracts, (v) Ov58GPCR is transcribed in both the larvae and adult parasite stages, (vi) IgG and IgE responses to recombinant the ECD decline with Ivermectin treatment compliance. All these findings suggest that the extracellular domain and synthetic peptides of Ov58GPCR and the specific immune response it generated could be harnessed for use in the context of diagnosis and surveillance for the disease.

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Under your skin: An Atypical Mycobacterium Infection



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Introduction: A 47 year old male from Dubai with a PMH of ESRD on dialysis presented to the Emergency Department with left eye blindness and diffuse, tender subcutaneous nodules one month after being appropriately treated for a dialysis-line associated blood stream infection.

Methods: Upon gathering further history, he worked as an administrator at a Seaport in Dubai. He had no recent travel history. He was in a monogamous relationship with his wife of 20 years. He did not use IV drugs. Initial concern was for recurrence of his dialysis line-associated blood stream infection with subsequent endocarditis. Blood cultures were drawn, broad spectrum antibiotics were started, and a trans-esophageal echocardiogram were obtained in addition to basic blood work. His CBC showed no signs of infection with a normal white blood cell count. Trans-esophageal echocardiogram showed no evidence of thrombus, and blood cultures remained negative. HIV, hepatitis B and C, and tuberculosis testing were all negative as well. Leukemia and lymphoma phenotyping showed no evidence of a hematologic malignancy. A skin biopsy was ultimately done, revealing an infection with mycobacterium abscessus.

Conclusions: Mycobacterium abscessus is a rare, rapidly growing mycobacterial infection. It most commonly causes pulmonary infections, but can also manifest as a skin infection, particularly in disseminated disease. It typically is found in immunocompromised individuals. Our patient was started on broad coverage with amikacin, cefoxitin, and clarithromycin. Over the next several weeks, he had gradual improvement in the skin disease. Further workup showed a lymphopenia with a CD4 count of 198. No clear cause has yet been identified for his lymphopenia, but further investigations are still ongoing.

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Serious infections by the intracellular bacterial pathogens *Legionella*, *Listeria*, and *Salmonella* in patients receiving anti-TNF therapy



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Anti-TNF agents are widely used in inflammatory diseases and have been associated with serious intracellular infections. This study is aimed at characterising the clinical presentation, analysing the treatment options, and assessing the different outcomes of infections by the intracellular bacteria *Legionella*, *Listeria*, and *Salmonella* in patients treated with anti-TNFs.

PubMed was used to search for peer-reviewed papers of relevance. This study found 70 papers which fulfilled the criteria, in which 31 cases of serious infection by *Legionella*, 57 cases of serious infection by *Listeria*, and 16 cases of serious infection by *Salmonella* were described.

The overwhelming majority of the patients taking anti-TNFs with serious infection were also receiving concomitant immunosuppressive drugs, especially steroids. The typical patient is a male in his 50s, suffering from RA, and taking Infliximab. All of the patients infected with *Legionella* had pneumonia and were treated with either a quinolone, or a macrolide, or a combination involving at least one of them. The majority of patients infected with *Listeria* had bacteremia and/ or meningitis and/ or CNS involvement; they were mainly treated with ampicillin +/-

gentamicin or amoxicillin +/- gentamicin. The majority of patients infected with Salmonella had bacteremia, being septic arthritis also very common; most were treated with fluoroquinolones. Altogether, 17 patients died, and others developed complications.

This study further revealed that a critical step towards successfully treating these patients is to achieve an accurate diagnosis quickly; instituting effective empirical antibiotic therapy is also paramount.

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Molecular Detection and Antibiotics Resistance Pattern of Extended-Spectrum Beta-Lactamase Producing *Escherichia coli* in a Tertiary Hospital in Enugu, Nigeria

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Background and Purpose: We looked for the extended-spectrum beta-lactamase producing *Escherichia coli* from clinical specimens in a tertiary hospital in Enugu, Nigeria. This is to enhance antibiotic stewardship in clinical practice.

Methodology: The study protocol was approved by Health Research and Ethics committee of the University of Nigeria Teaching Hospital (UNTH), Enugu. All hospitalized patients in UNTH from whose specimens *Escherichia coli* was isolated during the period of the study. These samples were cultured in 5% sheep Blood agar and MacConkey and incubated at 35–37°C for 24 hours. *Escherichia coli* was identified with standard biochemical tests and confirmed using API 20E. The antibiotic susceptibility testing was done by disc diffusion method and interpreted according to the Clinical and Laboratory Standard Institute guideline. ESBL production was confirmed using Chromogenic agar. The ESBL bla genes were detected with polymerase chain reaction. Data analysis was with appropriate descriptive and inferential statistics.

Results and Discussions: Out of the 200 isolates, 70 (35.00%) were confirmed positive for ESBL production. Forty-two (60.00%) of the isolates were from female patients while 28 (40.00%) were from male patients. Sixty-eight (97.14%) of the isolates were susceptible to imipenem while all of the isolates were resistant to ampicillin, chloramphenicol and tetracycline. The ESBL genes detected were blaCTX-M (n = 26; 37.14%), blaTEM (n = 7; 10.00%), blaSHV (n = 2; 2.86%), blaCTX-M/TEM (n = 7; 10.0%), blaCTX-M/SHV (n = 14; 20.0%) and blaCTX-M/TEM/SHV (n = 10; 14.29%). The most associated risk factors to infections caused by ESBL producing *Escherichia coli* was previous antibiotics use for the past 3 months followed by admission in the intensive care unit, recent surgery and urinary catheterization.

Conclusions: ESBLs was detected in 4 of every 10 *Escherichia coli* with the predominant gene detected being CTX-M. This knowledge will enable appropriate measures towards improvement of patient health care, antibiotic stewardship, and infection control in the hospital.

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Biometric Fingerprint Identification for Health Workers: A bacteriological Analysis of Sensor Devices

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Biometric fingerprint identification is expanding both primary care and secondary care facilities. The procedures of fingerprint capturing and reading require physical contact between skin and surface of the hardware devices. The aim of the study was to assess, if there was any bacterial contamination of the fingerprint sensors of biometric devices installed in our hospital.

Materials and Methods: Samples for microbiological examination were taken in sterile cotton swabs from all the biometric fingerprint devices.

Results: A total of 73 biometric devices were studied for bacterial contamination. Of the samples taken, 4 out of 73 (5.48%) yielded growth of Methicillin- Sensitive *Staphylococcus aureus*, 1 out of 73 (1.37%) yielded growth of *Proteus Mirabilis*.

Conclusion: the possibility of transmission of infection via biometric devices, even though minimal does exist and appropriate measures may be taken for prevention.

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The impact of water treatment, water reuse and the potential exposure to the risk of antibiotic resistome: the Transmission Antibiotic Resistance from the Environment to Humans

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Sewage treatment plants (WWTPs) and their water reuse are hot spots of antibiotics resistance (AR). The presence in antibiotic-resistant bacteria (ARB) could be the result of overuse and misuse of antibiotics in humans, animal feeding and agriculture, biocides and the incomplete removal of antimicrobials from WWTPs. WWTPs areas ripe for bacteria to shuffle and share their resistance genes. These hot spots of potential resistance transmission included a modern WWTPs and their water reuse in agriculture and food production, If these bacteria happen to come into contact with other microbes that carry resistance genes, those genes can pop over in one step. that such gene-transfer events are generally rare, but they are more likely to occur in these hot spots if the water reuse are hot spots of resistance gene transfer, We speculated that bacteria present in WWTP-where human regularly receive antibiotics- would see even more pressure to share resistance genes. We should concern about such bacteria getting into the food system. This explains why AR is so persistent in the environment. The nonexistence of a important overlap of ARB and antibiotic resistome between the human microbiome and potential environmental sources should not be interpreted as an indication of risk absence. The times of yore decade has eye witnessed a disintegrate of study regarding AR in the environment, mainly in areas under human activities, which they are now recognized. However, a key issue refers to the risk of transmission of resistance to humans, for which a quantitative model is urgently needed. t conclusion is that the risks of spread of AR from the environment to humans must be managed under the precautionary principle, because it may be too late to act if we wait until we have concrete risk values.

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