Methods

Case description.

Results

A 61-year-old male patient arrived at the Emergency Department due to disorientation and behavioural alteration since the previous day. His condition deteriorated rapidly, with a decreased level of consciousness. The manifestations observed indicated possible neurological pathologies, so a cranial CAT scan, laboratory tests and a lumbar puncture were requested. The cranial CAT scan was normal. Laboratory tests revealed peripheral blood neutrophilia (11.27x10ˆ3/μL). Acute phase reactants and other biochemical parameters were within normal limits. Urine drug screening showed no presence of toxic substances. Cerebrospinal fluid (CSF) analysis indicated normal, colourless appearance, glucose 98 mg/dL (40.0-70.0 mg/dL), protein 0.63 g/L (0.15-0.45 mg/dL), LDH < 25 U/L, red blood cells 5/μL, leukocytes 5/μL. Microbiological cultures, Gram, and FilmArray Meningitis/Encephalitis (ME) panel were negative. After 48 hours, a new CSF analysis showed the following results: glucose 104 mg/dL, protein 0.48 g/L, LDH <25 U/L, red blood cells 55/μL, leukocytes 10/μL. Faced with this result of leukocytes and considering the patient's symptoms, the laboratory decided to perform the ME panel, revealing a positive result for HSV-1, prompting the initiation of acyclovir treatment.

Conclusions

In a comprehensive review of the literature, we confirmed that in a patient presenting neurological symptoms with normal CSF findings and normal neuroimaging, HSV cannot be excluded. During the first two days, this patient, despite present neurological symptoms, has not a noticeable pleocytosis. However, tested positive on the second day in the ME panel. In cases of suspected HSV infection, treatment with acyclovir and repeat ME panel should be instituted. Delaying acyclovir treatment can lead to an increased risk of patient sequelae and mortality. The laboratory has a very important role in the diagnosis and follow-up of the pathology of many diseases such as this case presented, advising the addition of specific tests to ensure correct differential diagnosis.

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P1222

Ocular microbiome changes in dry eye disease

H. Kamdougha [b], B. Taminiau [a], S. Ben Amor [c], G. Daube [a], B. Menif [b]

[a] *Laboratory of Microbiology, Department of Food Sciences, Fundamental and Applied Research for Animal & Health (FARAH), Faculty of Veterinary Medicine, University of Liège, 4000 Liège, Belgium*
[b] *Laboratory of Microbiology, Habib Bourguiba University Hospital, Sfax University, Sfax, Tunisia*
[c] *Ophthalmology ward, Habib Bourguiba University Hospital, Sfax University, Sfax, Tunisia*

Background-Aim

The ocular surface microbiota brings together both commensal and pathogenic microorganisms that cohabit the eye. This microbiota significantly contributes to the eye homeostasis and its alteration may contribute to the development of various ophthalmic diseases. The aim of this study was to investigate potential association between the ocular surface microbiota and dry eye disease.

Methods

Swab samples were collected from the conjunctiva of both eyes in a cohort comprising 32 healthy volunteers (HV, n = 64) and 28 individuals diagnosed with dry eye disease (DE, n = 56) in Tunisia. 16S ribosomal RNA gene amplicon sequencing was performed targeting of the V1-V3 region. Bioinformatics and biostatistic analysis were conducted using respectively Mothur tools and R language to elucidate the taxonomic composition of the microbiota and assess community structures, correlations and differences between groups.

Results

Our data revealed a very diverse bacterial community with 28 phyla and 740 genera. The most abundant phyla were Actinobacteria (69.32 %), Firmicutes (17.2 %), and Proteobacteria (11.61 %). Corynebacterium (57.05 %), Staphylococcus (10.85 %), Cutibacterium (8.19 %), and Streptococcus (2.16 %) were the most abundant genera.

Samples from DE group exhibited significantly greater alpha-diversity compared to control samples ($P < 0.05$). Permutational multivariate analysis of beta-diversity variance also revealed a statistically significant difference in ocular surface microbiota between the two groups ($P < 0.05$). Approximately 42 bacterial genera, most of them Gram-negative bacteria (54.7 %), were significantly higher in the dry eye syndrome group, as identified by Deseq2. The Proteobacteria (18.03 % in DE vs. 5.20 % in HV, $P < 0.001$) namely Acinetobacter, Pseudomonas, Escherichia, and Bradyrhizobium; and the Firmicutes (22.19 % in DE vs. 12.22 % in HV; $P < 0.001$), namely Staphylococcus, Streptococcus, and Exiguobacterium and were significantly enriched in the DE group.

Conclusions

Our findings expand previous studies which proved the domination of ocular surface microbiota by Gram positive bacteria and supports other research that displayed the association between ocular surface microbiota alteration and dry eye diseases.

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P1223

Prevalence of rifampicin-resistant tuberculosis in ndola, zambia. A retrospective study 2020-2022

C. Mulenga [c], D. Chisompola [a], N. Mukuma [c], K. Tembo [b], E. Chinyante [c]

[a] *Pathology Laboratory Dept, Arthur Davison Children's Hospital, Ndola, Zambia*
[b] *Pathology Laboratory Dept, Healit Research International and Trace Research and Innovation, Zambia*
[c] *Pathology Laboratroy Dept, Ndola Teaching Hospital, Ndola, Zambia*

Background-Aim

Tuberculosis (TB) is a major public health problem in Zambia, with an estimated incidence of 319 per 100,000 population in 2019. Rifampicin-resistant TB, defined as tuberculosis caused by strains of Mycobacterium tuberculosis resistant to at least rifampicin, is a serious threat to TB control and poses a challenge for diagnosis and treatment. Rifampicin-resistant TB is often associated with multidrug-resistant TB (MDR-TB), which is resistant to at least rifampicin and isoniazid, the two most potent first-line anti-TB drugs. The study aims to determine the preva-