

Bacteriome analysis in ocular MALT lymphoma by 16S rRNA gene sequencing: A case report

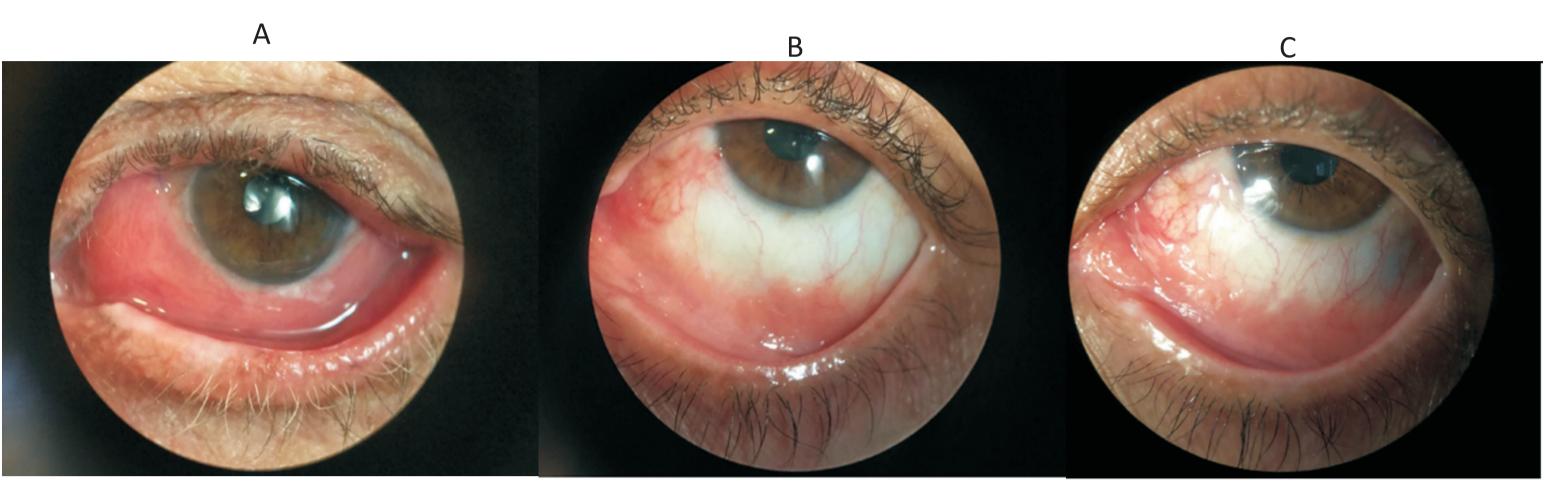
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ABSTRACT

METHODS

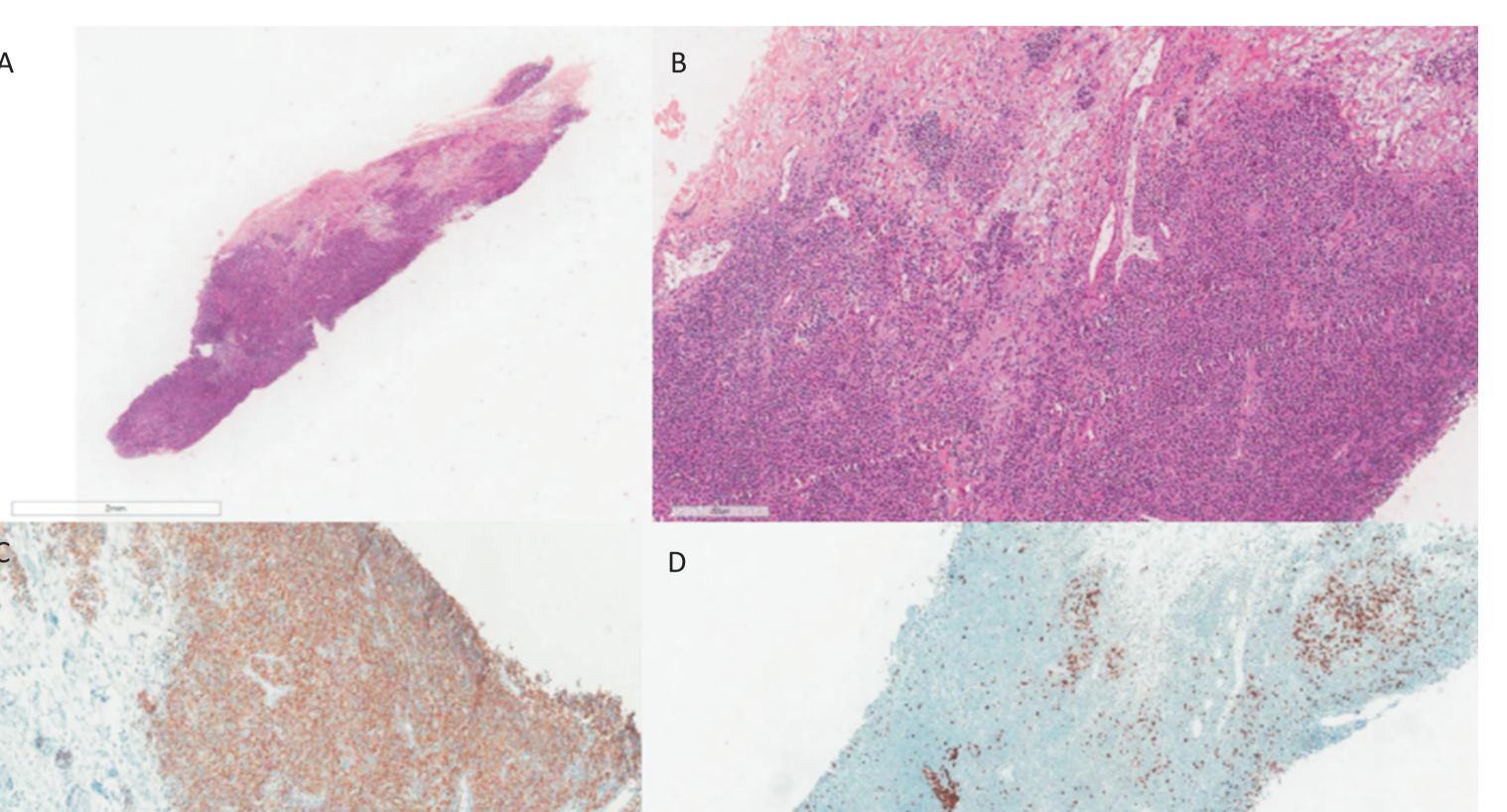
RESULTS

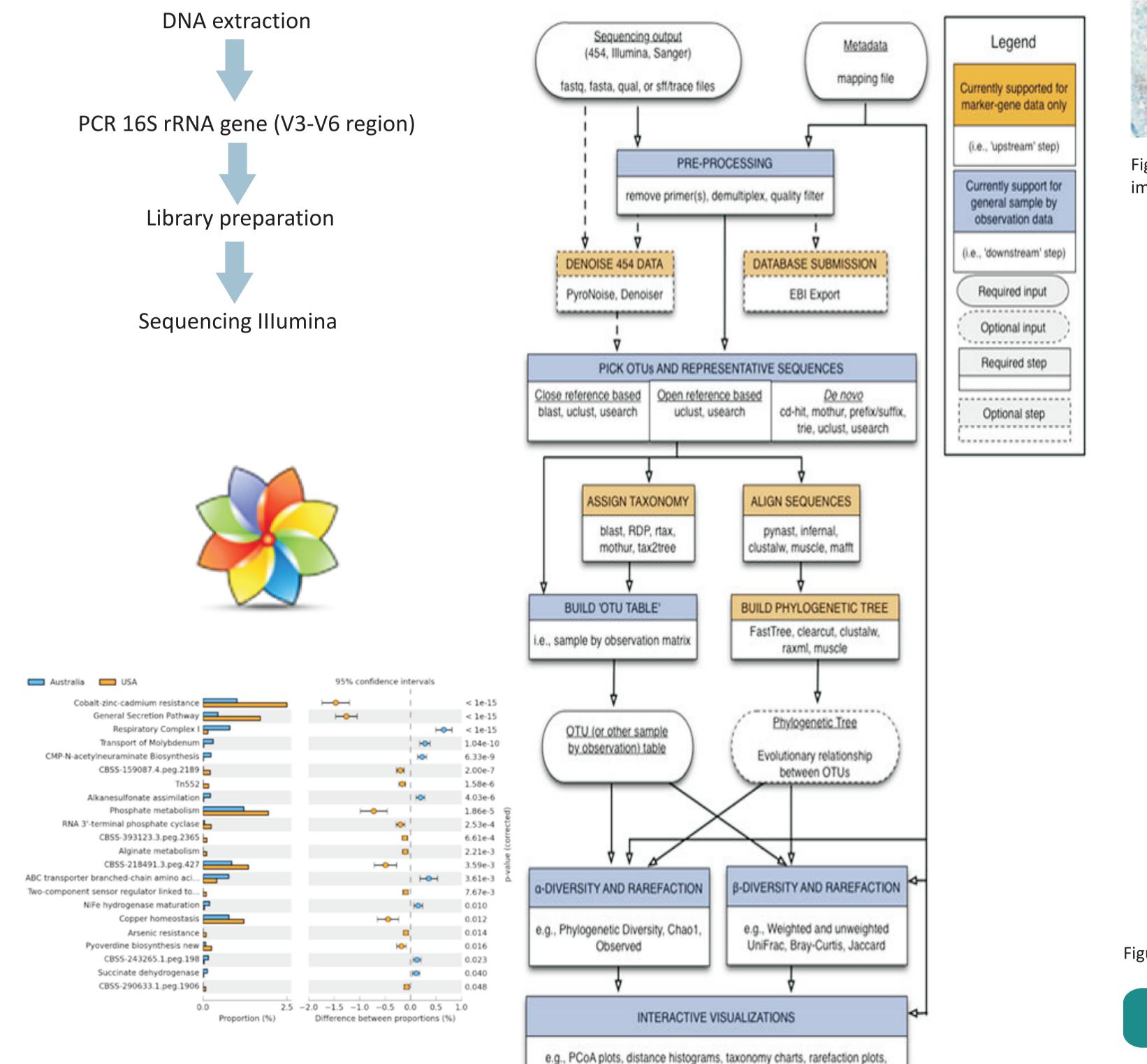
Primary ophthalmic lymphoma represents 5-15% of all extranodal and 1-2% of all non-Hodgkin's lymphomas (NHL). Mucosa-assoated lymphoid tissue (MALT) is a common histologic type of primary ophthalmic non-Hodgkin's lymphomas,



accounting for 38-100% of ocular adnexal NHL. MALT lymphoma arises in lymphoid tissue at extranodal sites (outside of lymph nodes, spleen, thymus and Waldeyer`s ring) as a result of chronic inflammation or autoimmune disorders. Helicobacter pylori-associated gastric MALT lymphoma is the classical example of chronic antigenic stimulation as the driving mechanism in the development of MALT lymphoma. However, etiologic agents in ocular MALT are undefined. Presence of Chlamydia psittaci in ocular MALT lymphoma has been reported with variable prevalence in different populations, generating conflicting assumptions about *C. psittaci* as a causative agent of ocular MALT lymphoma. Tumor regression after doxycycline therapy supports the hypothesis of bacterial infection contributing to the development of ocular MALT. Additionally, regression of lymphoma lesions after doxycycline therapy in *C. psittaci* DNAnegative patients suggests other doxycycline-sensitive bacteria may play a role in the pathogenesis of ocular MALT. In this study, we performed bacteriome analysis in ocular MALT lymphoma using high-throughput bacterial 16S rRNA gene sequencing for analysis of conjunctiva swabs before and after doxycycline treatment of a patient diagnosed with ocular MALT lymphoma.

Figura 1- (a) Left eye with subconjunctival mass. (b) Clinical remission at 8 and (c) 18-month follow-up visit





network visualization, jackknifed hierarchical clustering. Sitepainter, animations

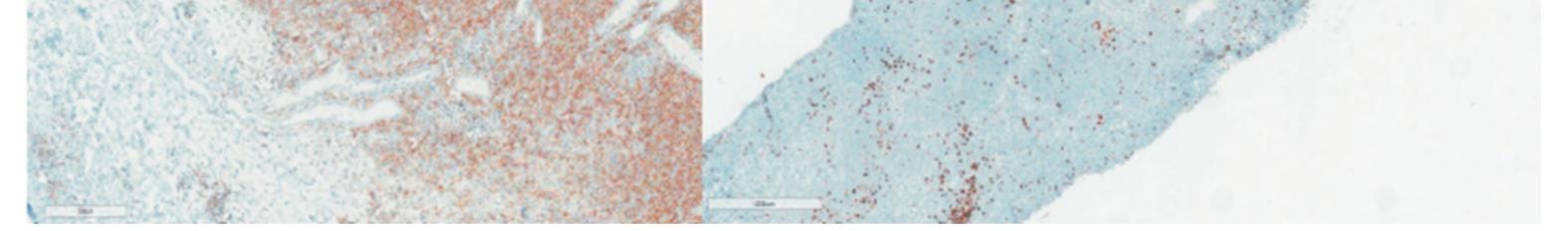


Figura 2- Histopathology analysis. Hematoxylin and eosin stain with increase of (a) 1.5 x and (b) 100 x. (c) CD20 (100 x) and (d) KI67 (100 x) immunohistochemical staining

Relative abundance 0.2 0.1 Healthy eye Healthy eye Affected eye Affected eye Value (before treatment) (before treatment) (after treatment) (after treatment) o Solibacterales g_Corynebacterium g__Flavobacterium Cloacibacterium g o_Bacillales f Bacillaceae g_Cohnella g__Sporosarcina Enterococcus a g Streptococcus Aurantimonadaceae g_Bradyrhizobium f Phyllobacteriaceae Rhizobiaceae f Sphingomonadaceae g__Novosphingobium g__Sphingomonas

fComamonadaceae		
f_Oxalobacteraceae		
fNeisseriaceae		
g_Zoogloea		

Figura 3-Heatmap generated by unsupervised hierarchical clustering analysis of ocular microbiome before and after the antibiotic treatment.

CONCLUSION

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We describe, for the first time, the predominance of Neisseriaceae bacteria in ocular MALT lymphoma, clinical evolution and microbiological assessment overtime.

Projeto Gráfico: Setor de Edição e Informação Técnico-Científica / INCA

