

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

Gislaine Curty¹, Evandro Lucena², Luciana Barreto³, Luciana W. Pinto⁴, Gilberto Z. Figueiredo⁵, Marcelo A. Soares¹, Fábio E. Leal^{1*}.
¹Programa de Oncovirologia, ²Pesquisa Clínica, ³Hematologia, ⁴Divisão de Patologia, Instituto Nacional de Câncer, Rio de Janeiro, Brazil; ⁵Oftalmologia, Fundação Hilton Rocha, Belo Horizonte, Brazil.

ABSTRACT

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

RESULTS

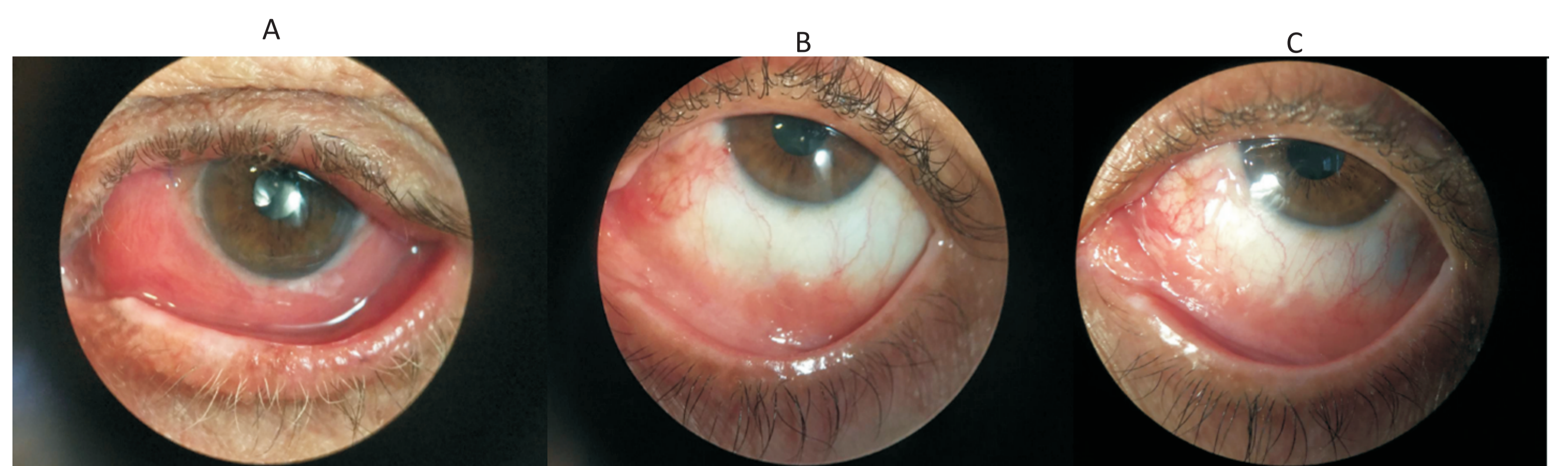


Figura 1- (a) Left eye with subconjunctival mass. (b) Clinical remission at 8 and (c) 18-month follow-up visit

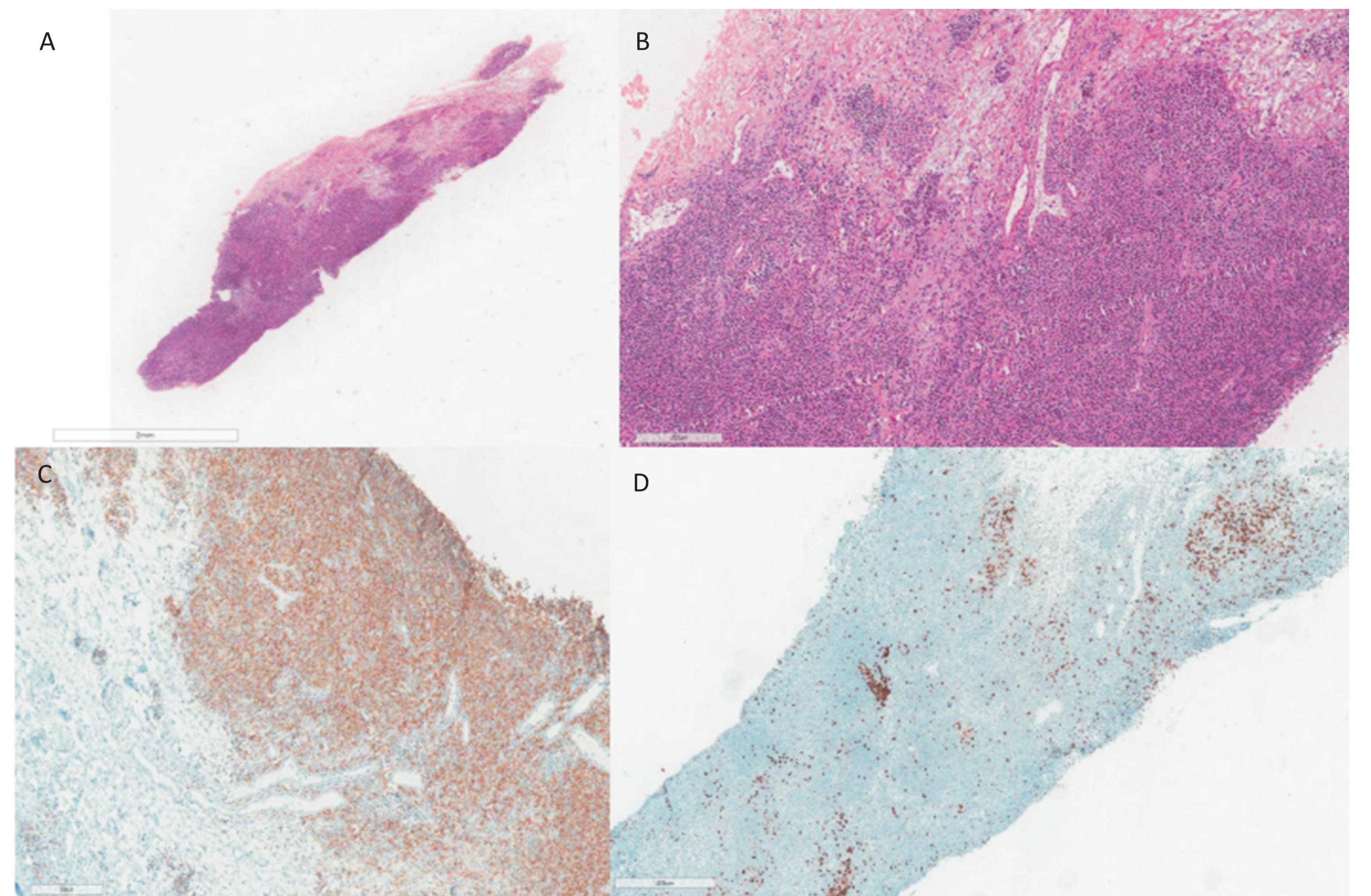


Figura 2- Histopathology analysis. Hematoxylin and eosin stain with increase of (a) 1.5 x and (b) 100 x. (c) CD20 (100 x) and (d) KI67 (100x) immunohistochemical staining

METHODS

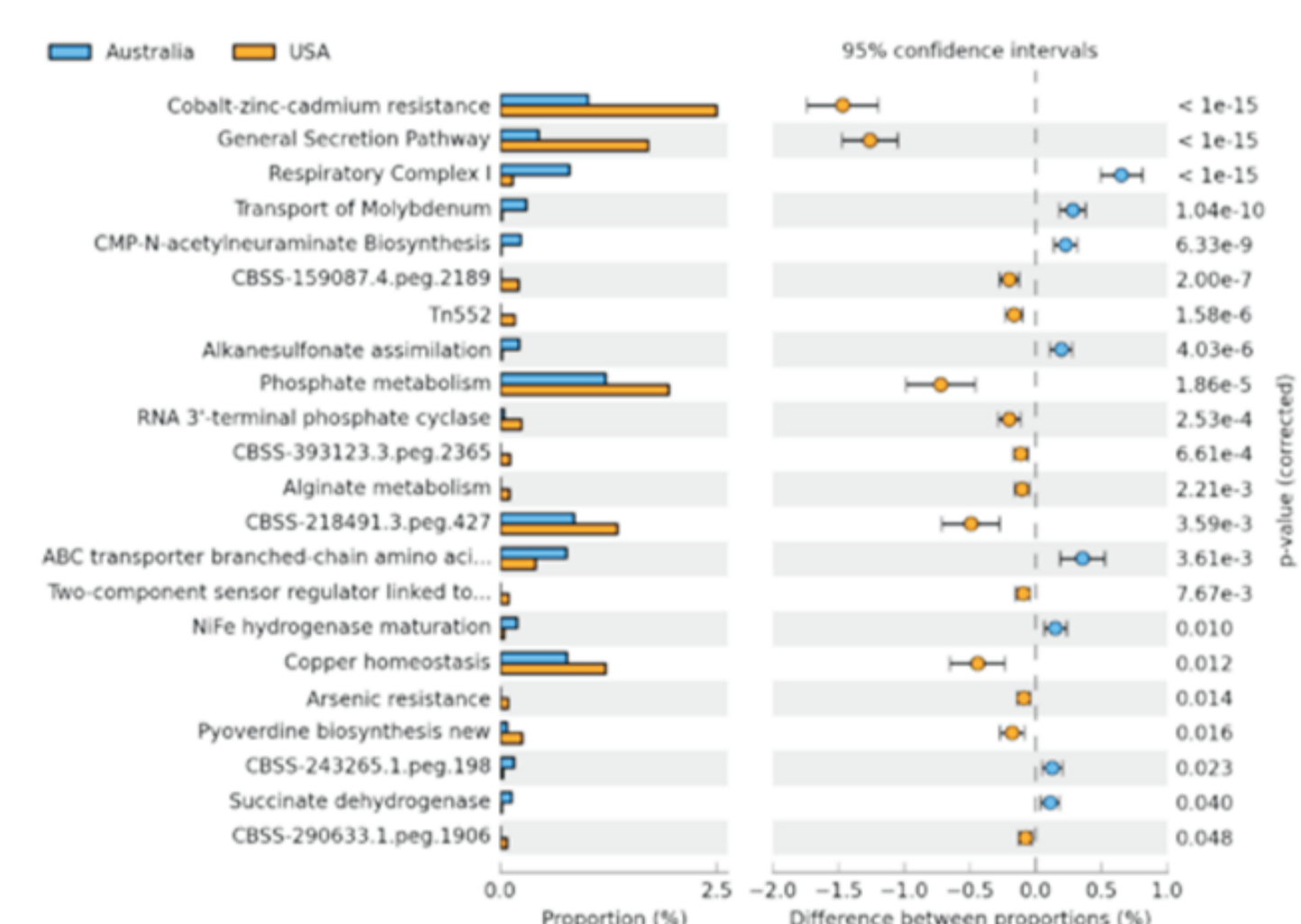
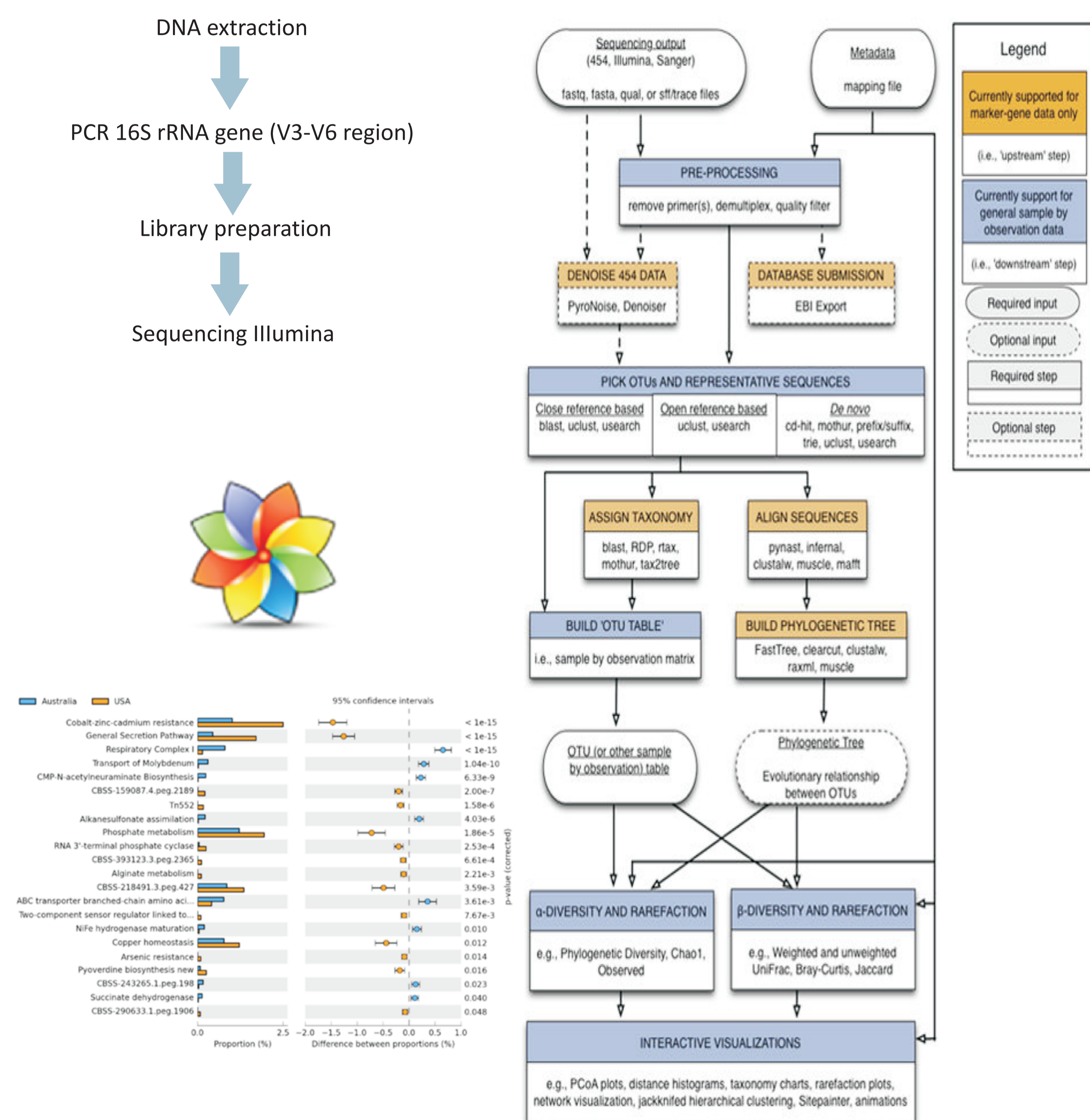


Figura 3- Heatmap generated by unsupervised hierarchical clustering analysis of ocular microbiome before and after the antibiotic treatment.

CONCLUSION

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