Metagenome techniques to reduce diagnostic delay in Acanthamoeba keratitis

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Accepted: July 6th, 2021

To the Editor,

We read with interest the article by Shah YS et al. "Delayed diagnoses of Acanthamoeba keratitis at a tertiary care medical center" [1].

The article well describes difficulties to diagnose microbial keratitis. As reported in Table 1, Acanthamoeba keratitis (AK) is usually misdiagnosed with herpetic keratitis [1]. We have had same and similar issues [2,3].

Timely diagnosis is the key for an effective treatment. However, the current conventional diagnostic methods (CDM) of stain and culture are time consuming and often with no clinically useful results [4].

Consequently, efforts need to be done to develop highly sensitive and accurate molecular diagnostic tools with the aim to provide rapid diagnosis and reduce the threat of antimicrobial resistance.

In recent years, we have started to evaluate the analysis of the metagenome [5,6].

Metagenomics analysis with next-generation sequencers is becoming more common. The first difficulties to such a new approach improved during time [7]. Nowadays, with some sets, it is possible to have results in 24-36 hours [6] with reduced costs than in the past [8].

Additionally, as recently reported by Yu-Jen et al., bacterial 16S ribosomal RNA sequencing

techniques have the potential to profile the microbiome in contact lens associated with AK to characterize the association between Acanthamoeba and the intracellular microbiome [9]. This way, metagenomics analysis will move the investigator from a hypothesis guided approach of CDM to a hypothesis-free approach, with a more comprehensive evaluation of samples [6,10].

Therefore, we hope that a widespread use of metagenomics analysis could improve the diagnosis of AK and reduce delays.

Conflict of Interest statement

Authors state no conflict of interest.

Acknowledgements

None.

Sources of Funding

None.

Disclosures

None.

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