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LETTER TO EDITOR

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Diagnostic pitfalls in identification of *Elizabethkingia meningoseptica*

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To the Editor of JCCM,

Regarding the article "Emerging Infection with *Elizabethkingia meningoseptica* in Neonate. A Case Report" by Arbune *et al*. (2018) [1], there are specific facts which need clarification regarding the reporting of this organism.

First of all, Arbune reported the isolation of the organism from the cerebrospinal fluid (CSF) and blood culture of one case, and that no source of infection was identified. *Elizabethkingia meningoseptica*, although linked to meningitis and nosocomial infections, can be an environmental contaminant as well. Repeat cultures of the samples are mandatory for the confirmation of such unusual pathogens.

Secondly, at present, no antibiotic sensitivity guidelines exist for this organism. Hence, the reporting of antibiotic susceptibilities must be done along with minimum inhibitory concentration (MIC) values of the tested antimicrobials rather than merely stating they are "sensitive" or "resistant". MIC values of the tested antibiotics may help the clinicians in deciding the drug dosage. Additionally, they may contribute to the formulation of susceptibility guidelines in the future.

Thirdly, and most importantly, accurate identification is the key issue for such rare isolates. Arbune used the Vitek 2 automated system to identify *Elizabethkingia meningoseptica*. However, discrepancies in identification by the Vitek2 system have been reported in the published literature. In a study by Carvalho et al. (2017) [2], an isolate of *Chryseobacterium indologenes* was misidentified as *Elizabethkingia meningoseptica* by a Vitek 2 system with 99 % certainty of identification.

Lau *et al*. (2016) [3] reported seventeen isolates of *Elizabethkingia anopheles* and one isolate of *E. miricola* confirmed by 16S rRNA sequencing, all having been misidentified by Vitek 2 as *E. meningoseptica*. These included CSF isolates from three cases of neonatal meningitis. In a study by Lau *et al*. (2015) [4], three isolates including two CSF samples from neonatal meningitis cases that were later confirmed as *E. anophelis* by whole genome sequencing were initially misidentified as *E. meningoseptica* by the Vitek 2 system. Lo and Chang (2014) [5] also reported a 16S rRNA confirmed *Chryseobacterium gleum* isolate having been misidentified as *E. meningoseptica* by the Vitek 2 system.

The above data indicate that the Vitek 2 automated system has a high positive predictive value but also a variable number of false positives concerning the identification of *Elizabethkingia meningoseptica*. It can be concluded that the Vitek 2 system alone is not sufficient for confirmatory identification of this organism and more advanced techniques such as MALDI-TOF MS with its expanded database, as well as molecular techniques such as 16S rRNA gene sequencing and whole genome sequencing (WGS), should be considered for accurate identification.

Further comparative studies of these molecular and microbiological techniques, with updated databases to prevent pseudo-identifications leading to false reporting of outbreaks and cases of this unusual pathogen, should be undertaken.

Conflicts of interest

None declared

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