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CORRESPONDENCE

Elizabethkingia meningoseptica diagnostic hitch

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To the editor,

With reference to the case report titled "First case of *E. meningoseptica* in Italy in a patient with necrotic hemorrhagic pancreatitis" by Montrucchio et al [1], *Elizabethkingia meningoseptica* isolate was isolated in bronchial aspirate sample. However, there are certain fallacies we would like to highlight in this context.

First and foremost, identification method for *E. meningoseptica* was not mentioned by Montrucchio et al. [1]. How *E. meningoseptica* was identified? Whether identified by Vitek2 automated system or by MALDI-TOF MS (matrix-assisted laser desorption and ionization-time of flight mass spectrometry) system? If MALDI-TOF MS was used, whether it was Vitek MS (Biomerieux) or Bruker BioTyper (Bruker Daltonics, Germany)? What was the version of MALDI-TOF MS database used? Was the isolate identification confirmed by repeat culture? If at all it was *E. meningoseptica* even after repeat culture, was the identification confirmed by 16S rRNA gene sequencing or whole genome sequencing? Answers to these queries need to be mentioned when reporting cases of such unusual pathogens as accurate identification is essential for better understanding of such isolates, their pathophysiology, clinical course and their management strategies.

Discrepancies in identification of *Elizabethkingia* species by Vitek2 or even MALDI-TOF MS have been demonstrated in some recent studies [2–5]. Most *E. meningoseptica* isolates though have been correctly identified by Vitek2 system; however, a few isolates have been misidentified as *Chryseobacterium indologenes* and *Acinetobacter baumannii* [2, 3]. MALDI-TOF MS (whether Vitek MS or Bruker Biotyper) has also shown misidentifications of few *E. meningoseptica* isolates as *Pseudoxanthomonas* species, *E. miricola, C. indologenes, Stenotrophomonas maltophilia* [2, 3].

Not only *E. meningoseptica* isolates have been misidentified, isolates of other *Elizabethkingia* species such as *E. anophelis* and *E. miricola* have been falsely identified as *E. meningoseptica* by Vitek2 and MALDI-TOF MS systems due to lack of database coverage for *Elizabethkingia* species other than *E. meningoseptica* [3–5]. Only a few studies have been done for accurate identification of these species by expanding the database of MALDI-TOF MS with species-specific spectra [3, 4].

To conclude, isolated *Elizabethkingia meningoseptica* may be a true isolate or an isolate of *Elizabethkingia species* falsely identified as *E. meningoseptica* by the automated system. Hence, *E. meningoseptica* isolate by these systems must be confirmed by 16S rRNA gene sequencing to prevent pseudo-reporting of such cases. Also, we recommend database updation of these systems for reliable identification of *Elizabethkingia species* in clinical laboratories routinely.

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Compliance with ethical standards

Conflict of interest The authors declare that they have no competing interest.

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