Elizabethkingia miricola: Discrepancies in identification and antimicrobial susceptibilities

To the Editor,

We read with interest the article entitled "rpoB gene sequencing highlights the prevalence of an *E. miricola* cluster over other *Elizabethkingia* species among UK cystic fibrosis patients" by Kenna et al. (2018). We appreciate the work and would like to add a few comments.

Accurate identification of this species is essential for better treatment strategies. Commercially available identification systems based on biochemical reactions such as MicroScan, Vitek2, API/ID32 v3.1 and Phoenix100 ID/AST v5.51A lack database coverage for *E. miricola*, hence have failed to identify this species accurately (Green et al., 2008; Lin et al., 2017). MALDI-TOF MS, an excellent tool for microbe identification, is also not without issues regarding *Elizabethkingia* species identification. Although, *E. miricola* is included in the reference database of Bruker BioTyper (Eriksen et al., 2017; Han et al., 2017; Lau et al., 2016), both systems (Vitek MS or Bruker) have been able to clinch identification of *E. miricola* species with a good score after expansion of their databases with species-specific spectra (Cheng et al., 2018; Han et al., 2017; Lau et al., 2016). CDC's (Centre for disease control's) microbenet database, launched in 2013 in collaboration with Bruker Daltoniks, is a widely available tool and can be used with Bruker bioTyper for identification purposes (https://microbenet.cdc.gov/). However even with microbenet database, MALDI-TOF MS can discriminate the genus into *E. anophelis* and *E. meningoseptica* species and an *E. miricola* group but cannot differentiate the isolates of *E. miricola* group which include *E. miricola*, *E. bruuniana*, *E. occulta* and *E. ursingii species* (Cheng et al., 2018; Nicholson et al., 2018).

16S rRNA and whole genome sequencing remains the gold standard molecular identification techniques for genus *Elizabethkingia* including *E. miricola*. More recently, rpoB gene sequencing has emerged as an additional molecular identification tool differentiating the genus into three clusters: *E. anophelis*, *E. meningoseptica* and *E. miricola* cluster (comprising *E. miricola*, *E. bruuniana*, *E. occulta* and *E. ursingii*) (Cheng et al., 2018; Kenna et al., 2018; Nicholson et al., 2018).

Presently, no antibiotic guidelines exist for *Elizabethkingia* species. As the antimicrobial susceptibilities of this genus vary depending on the species, discrimination of species is important. *E. miricola*, like other *Elizabethkingia* species, has been resistant to beta-lactams, extended-spectrum cephalosporins, aminoglycosides and carbapenems. However, piperacillin has been observed as susceptible in a few studies (Han et al., 2017; Lau et al., 2016). Contrary to the findings of Kenna et al. (2018), piperacillin-tazobactam has been found sensitive while cotrimoxazole and ciprofloxacin has been found resistant in some studies (Cheng et al., 2018; Han et al., 2017). Newer quinolones such as levofloxacin and tetracyclines such as doxycycline and minocycline appear promising for *E. miricola* with their susceptibilities (Cheng et al., 2018; Han et al., 2017). More studies are needed for better insights into the susceptibility patterns of this organism as well as to formulate antibiotic guidelines.

Funding sources

None.

Conflicts of Interest

None.

G.R. Rahim
Neha Gupta*
Microbiology Department, Shah SatnamJi Speciality Hospitals, Sirsa, Haryana, India
*Corresponding author. Tel.: +91-9873268337.
E-mail address: nehagupta0606@gmail.com.

Available online 5 December 2018

https://doi.org/10.1016/j.diagmicrobio.2018.11.025

References

Cheng YH, Perng CL, Jian MJ, Lee SY, Sun JR, Shang HS. Multicentre study evaluating matrix-assisted laser desorption ionization–time of flight mass spectrometry for identification of clinically isolated *Elizabethkingia* species and analysis of antimicrobial susceptibility. Clin Microbiol Infect 2018:2–7. https://doi.org/10.1016/j.cmi.2018.04.015.

Eriksen HB, Gumpert H, Faurholt CH, Westh H. Determination of *elizabethkingia* diversity by MALDI-TOF mass spectrometry and whole-genome sequencing. Emerg Infect Dis 2017;23(2):320–3.

Green O, Murray P, Gea-Banacloche JC. Sepsis caused by *Elizabethkingia miricola* successfully treated with tigecycline and levofloxacin. Diagn Microbiol Infect Dis 2008;62(4):430–2.

Han MS, Kim H, Lee Y, Kim M, Ku NS, Choi JY, et al. Relative prevalence and antimicrobial susceptibility of clinical isolates of *Elizabethkingia* species based on 16S rRNA gene sequencing. J Clin Microbiol 2017;55(1):274–80.

Kenna DTD, Fuller A, Martin K, Perry C, Pike R, Burns PJ, et al. rpoB gene sequencing highlights the prevalence of an *E. miricola* cluster over other *Elizabethkingia* species among UK cystic fibrosis patients. Diagn Microbiol Infect Dis 2018;90(2):109–14. https://doi.org/10.1016/j.diagmicrobio.2017.10.014.

Lau SKP, Chow WN, Foo CH, Curreem SOT, Lo GCS, Teng JLL, et al. Elizabethkingia anophelis bacteremia is associated with clinically significant infections and high mortality. Sci Rep 2016;6(May):8–17. https://doi.org/10.1038/srep26045.

Lin JN, Lai CH, Yang CH, Huang YH, Lin HF, Lin HH. Comparison of four automated microbiology systems with 16S rRNA gene sequencing for identification of *Chryseobacterium* and *Elizabethkingia* species. Sci Rep 2017;7(1):7–11. https://doi.org/10.1038/s41598-017-14244-9.

Nicholson AC, Gulvik CA, Whitney AM, Humrighouse BW, Graziano J, Emery B, et al. Revisiting the taxonomy of the genus *Elizabethkingia* using whole-genome sequencing, optical mapping, and MALDI-TOF, along with proposal of three novel *Elizabethkingia* species: *Elizabethkingia bruuniana* sp. nov., *Elizabethkingia ursingii* sp. nov., and *Elizabethkingia occulta* sp. nov. Antonie Van Leeuwenhoek 2018;111(1):55–72.