Tsukamurella spp. are Neglecting Bacteria

Masoud Keikha1,2*

1Antimicrobial Resistance Research Center, Mashhad University of Medical Sciences, Mashhad, Iran
2Department of Microbiology and Virology, School of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran

*Corresponding Author: Masoud Keikha, Isfahan Medical School, Hezarjarib St. Isfahan University of Medical Sciences, Isfahan, Iran.

Received: May 17, 2018; Published: February 23, 2019

Tsukamurella that have mycolic acid (chemo type IV) have been classified as a major genus in aerobic actinomycetes families [1]. The genus Tsukamurella are gram-positive, aerobic, partially acid-fast, nonmotile, noon spore forming bacteria with a series of very long chains and unsaturated mycolic acid which live in environmental resources such as water, soil and dust; Therefore Tsukamurella spp. can enter the human via inhalation or cutaneous damage and cause of mycetoma, pulmonary infection (like tuberculosis), meningitis, peritonitis, keratitis, conjunctivitis, brain abscess, acute otitis media, bacteremia and catheter-related infections [2-4]. Tsukamurella infection are usually sporadic and people with immunodeficiency virus (HIV), transplant recipient and people who are consuming immunosuppressive drugs are most important hosts for this infection [4,5].

Tsukamurella was introduced by Collins and colleagues in 1988 whereas this group of bacteria were isolated prior in 1941 by Steinhaus, et al. from the mycetomes and ovaries of bed bugs (Cimex lectularius) as Corynebacterium paurometabolum; but presence of unsaturated mycolic acid 68 - 76 carbon can be used for differentiation of Tsukamurella from Corynebacterium [4]. So far, the genus Tsukamurella comprise of 17 different species that nine species of this genus have isolated from human infections including: Tsukamurella inchonensis, T. paurometabola, T. strandjordii, T. tyrosinosolvens, T. pulmonis, T. hongkongensis and Tsukamurella sinensis [4,6].

Tsukamurella spp. are usually misidentified as Non-tuberculosis Mycobacteria (NTM), Nocardia and Rhodococcus [7]; Tsukamurella species was identified by phenotypic methods (such as Gram and Kinyoun stains, colony morphology, resistance to lysozyme, pyrazinamidase activity, lack of aerial hyphae, growth in 25 - 35ºC, oxidase, catalase, nitrate reductase, lipase, hydrolysis of tween 80, tyrosine, urea, asesculin, casein, adenine, xanthine, hypoxanthine and carbohydrates utilization as carbon source), analysis of fatty acid and mycolic acid cell wall and molecular techniques including direct sequencing (16S rRNA pair primers: 27F:5’-AGAGTTTGATCMTGGCTCAG-3’ and 1525R:5’-AAGGAGGTGWTCCARCC-3’ and groEL by using the two primers: TB11:5′-ACCAACGATGGTGTGTCCAT-3′ and TB12:5′-CTTGTCGAACCGCATACCCT-3′ and PCR-RFLP using housekeeping genes [4,8,9]. Diagnosis based on the conventional tests are time-consuming, expensive and need to standardization and expertise technicians while molecular methods using housekeeping genes (16Sr RNA and hsp65) are simple, effective and can properly identified Tsukamurella spp. from other aerobic actinomycetes [10,11].

The best method for antibiotic susceptibility test of Tsukamurella spp. is micro-broth dilution method (based on the recommendation of Clinical and Laboratory Standards Institute (CLSI)). Given that limitation of information about of anti-drug susceptibility of the genus Tsukamurella, Susceptibility testing is necessary for Tsukamurella infections; according to the lack of information on the treatment of Tsukamurella infections, the combination of beta-lactam or macrolide with aminoglycoside antibiotics used of various antibiotic agents has recommended for treatment of this infections [4,12].

Conflict of Interest

Nil.

Citation: Masoud Keikha. “Tsukamurella spp. are Neglecting Bacteria”. EC Microbiology 15.3 (2019): 187-188.
Tsukamurella spp. are Neglecting Bacteria

Bibliography


Citation: Masoud Keikha. "Tsukamurella spp. are Neglecting Bacteria". *EC Microbiology* 15.3 (2019): 187-188.