Alloprevotella rava isolated from a mixed infection of an elderly patient with chronic mandibular osteomyelitis mimicking oral squamous cell carcinoma

N. Ulger Toprak1, N. Duman1, B. Sacak2, M. C. Ozkan2, E. Sayın1, L. Mulazimoglu3 and G. Soyletir1

1) Department of Microbiology, 2) Department of Plastic Reconstructive and Aesthetic Surgery and 3) Department of Infectious Diseases, Marmara University School of Medicine, Istanbul, Turkey

Abstract

The anaerobic, Gram-negative bacillus Alloprevotella rava has recently been described in the human oral cavity. To our knowledge, this species has not been isolated from chronic osteomyelitis samples. We present the first case of A. rava infection in a 92-year-old woman with polymicrobial chronic mandibular osteomyelitis, mimicking oral squamous cell carcinoma.

© 2021 The Author(s). Published by Elsevier Ltd.

Keywords: Actinomycosis, Alloprevotella rava, anaerobic bacillus, chronic mandibular osteomyelitis, oral squamous cell carcinoma

Original Submission: 8 February 2021; Revised Submission: 3 April 2021; Accepted: 7 April 2021
Available online 14 April 2021

Introduction

Chronic mandibular osteomyelitis (CMO) is a serious condition requiring early and accurate diagnosis, antibiotics, and surgical management. Cases are usually mixed anaerobic infections, reinforcing the concept that osteomyelitis of the jaws is mainly related to microorganisms from the oral environment [1]. Alloprevotella rava is an obligatory anaerobic Gram-negative bacillus isolated from the human oral cavity, associated with oral dysbiotic infections such as dental caries and periodontitis [2–4]. We present the first case of A. rava infection in a patient with polymicrobial CMO initially thought to be oral squamous cell carcinoma from clinical and computed tomography findings.

Case report

A 92-year-old woman presented to our hospital with chronic, bloody discharge in the left mandibular body for 18 months, since the extraction of teeth in the same region. According to her medical history, the woman’s cervical lymph node had been removed and she had received radiotherapy with a diagnosis of lymphoma, 5 years ago. She also received medication for osteoporosis. Tissue specimens, obtained from defective bone and surrounding soft tissue, were examined histopathologically and microbiologically. Histopathology made a diagnosis of actinomycosis without any malignancy. However, microbiological examination revealed polymicrobial infection involving five bacteria. Four organisms were identified by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS; VITEK MS; bioMérieux, Marcy l’Étoile, France) as Veillonella parvula, Prevotella nigrescens, Klebsiella oxytoca and Corynebacterium durum. The fifth bacterium, mentioned as strain Marmara, for which MALDI-TOF MS was insufficient for identification, was identified by 16S rRNA gene sequencing as A. rava with 99% nucleotide identity to the strain isolated from the human oral cavity (GenBank Accession no. JQ039190) [2] (see Fig. 1). The actinomycosis strain was not isolated despite the 14-day incubation period for anaerobic culture [5]. All isolated organisms were susceptible to amoxicillin-clavulanic acid. The patient was given empirical amoxicillin-clavulanic acid, and she was discharged on the fifth day of hospitalization with oral amoxicillin-clavulanic acid therapy (2 × 1 g daily) for 2 months. Her clinical condition...
improved considerably, and mandibular discharge and swelling disappeared.

Discussion

Three different anaerobic bacteria were isolated from the samples, consistent with the mixed anaerobic aetiology of CMO. Several fastidious strictly anaerobic bacteria are commonly present in the dental biofilm, which suggests that the source of infecting pathogens in osteomyelitis of the jaws is likely to be gingivitis, chronic periodontitis, previous dental extractions or endodontic treatments [1]. Alloprevotella rava was first isolated from dental plaque [2]. In our case, A. rava was isolated from a woman with CMO with a history of tooth extraction in the same area. This is the first case of CMO involving A. rava in the world literature. However, it may not reflect the actual result because phenotypic identification systems have insufficient databases for this microorganism. Alloprevotella rava has been detected in the oral microbiota of certain patients with oral dysbiosis by molecular techniques since 2013, when it was defined [2–4]. An epidemiological study, conducted among Chinese preschool children, revealed that the relative proportions of A. rava were significantly higher in the halitosis group compared with the control group [6]. A prospective cohort study showed a relationship between an increase in dental caries and the level of the genus Alloprevotella in the oral microbiome among Japanese university students [3]. Another report indicated that the proportion of A. rava was significantly increased in saliva samples of periodontitis patients [4]. On the other hand, Coit et al. [7] reported that the abundance of A. rava in the microbial community of saliva was significantly decreased in Behçet’s disease compared with healthy controls. Recent research, focused on the role of bacteria in oral carcinogenesis, indicated that the genus Alloprevotella was among the bacteria that showed significantly higher abundances [8,9]. However, the features related to its pathogenesis have not been clarified.

Conclusion

Signs and symptoms of oral squamous cell carcinoma, which has a poor overall 5-year survival rate, and CMO can often be similar. The diagnosis of CMO is particularly important because appropriate treatment, culture-guided antibiotic therapy for the infection and surgical management provide successful cure. Defining the bacterial community composition associated with CMO can help in understanding the mechanisms of disease and the impact of the bacteria.

Conflicts of interest

The authors have declared that there are no conflicts of interest.

Acknowledgements

We thank Sedef Glover for editing the manuscript. This research did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.
References

[1] Gaetti-Jardim Júnior E, Fardin AC, Gaetti-Jardim EC, de Castro AL, Schweitzer CM, Avila-Campos MJ. Microbiota associated with chronic osteomyelitis of the jaws. Braz J Microbiol 2010;41:1056–64.

[2] Downes J, Dewhirst FE, Tanner ACR, Wade WG. Description of Alloprevotella rava gen. nov., sp. nov., isolated from the human oral cavity, and reclassification of Prevotella tannerae Moore et al. 1994 as Alloprevotella tannerae gen. nov., comb. nov. Int J Syst Evol Microbiol 2013;63:1214–8.

[3] Uchida-Fukuhara Y, Ekuni D, Islam MM, Kataoka K, Taniguchi-Tabata A, Fukuhara D, et al. Caries increment and salivary microbiome during university life: a prospective cohort study. Int J Environ Res Public Health 2020;17:3713.

[4] Sun X, Li M, Xia L, Fang Z, Yu S, Gao J, et al. Alteration of salivary microbiome in periodontitis with or without type-2 diabetes mellitus and metformin treatment. Sci Rep 2020;10:15363.

[5] Valour F, Sénéchal A, Dupieux C, Karsenty J, Lustig S, Breton P, et al. Actinomycosis: etiology, clinical features, diagnosis, treatment, and management. Infect Drug Resist 2014;7:183–97.

[6] Zhang Y, Zhu C, Feng X, Chen X. Microbiome variations in preschool children with halitosis. Oral Dis 2020. epub ahead of print.

[7] Coit P, Mumcu G, Ture-Ozdemir F, Uнал AU, Alpar U, Bostancı N, et al. Sequencing of 16S rRNA reveals a distinct salivary microbiome signature in Behçet’s disease. Clin Immunol 2016;169:28–35.

[8] Zhang L, Liu Y, Zheng Hj, Zhang CP. The oral microbiota may have influence on oral cancer. Front Cell Infect Microbiol 2020;9:476.

[9] Chattopadhyay I, Verma M, Panda M. Role of oral microbiome signatures in diagnosis and prognosis of oral cancer. Technol Cancer Res Treat 2019;18. 1533033819867354.