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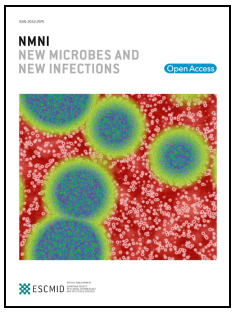


*Alloprevotella rava* isolated from a mixed infection of an elderly patient with chronic mandibular osteomyelitis mimicking oral squamous cell carcinoma

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**First clinical case report**

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

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Runnimg title: ***Alloprevotella rava*** **in chronic mandibular osteomyelitis**

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


## Abstract

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


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

## Introduction

Chronic mandibular osteomyelitis (CMO) is a serious condition requiring early and accurate diagnosis, antibiotics, and surgical management. The cases are usually mixed anaerobic infections, reinforcing the concept that osteomyelitis of the jaws are mainly related to microorganisms from the oral environment [1]. *Alloprevotella rava* is an obligatory anaerobic Gram-negative bacilli isolated from the human oral cavity, associated with oral dysbiotic infections such as dental caries and periodontitis [2,3,4]. We presented the first case of *A. rava* infection in a patient with polymicrobial CMO initially thought to be oral squamous cell carcinoma (SCC) upon the presence of 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 teeth extraction in the same region. According to her medical history, the patient's cervical lymph node was removed and received radiotherapy with a diagnosis of lymphoma, 5 years ago. The patient 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 MALDI-TOF MS (VITEK MS; bioMérieux) as *Veilonella parvula*, *Prevotella nigrescens, Klebsiella oxytoca* and *Corynebacterium durum.* The fifth bacterium, for which MALDI-TOF MS was insufficient for identification, was identified by 16S rRNA gene sequencing as *Alloprevotella rava* with 99% nucleotide identity to the strain isolated from the human oral cavity (GenBank accession no. JQ039190) [2]. The *actinomyces* strain was not isolated despite of the 14-day incubation period for anaerobic culture [5]. All isolated organisms were susceptible to amoxicillin-clavulanic acid (AMC). The patient was given empirical AMC, she was discharged on the fifth day of hospitalization with oral AMC therapy (2X1g daily) for two months. The clinical condition improved considerably, mandibular discharge and swelling disappeared.

## Discussion

In our case, three different anaerobic bacteria were isolated, consistent with the mixed anaerobic etiology of CMO. Several fastidious strictly anaerobic bacteria commonly present in the dental biofilm suggests 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 firstly isolated from dental plaque [2]. In our case *A. rava* was isolated from a pateint with CMO with a history of tooth extraction on the same area. This is the first case of CMO, which consisted of *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 from 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* was 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 genera *Alloprevotella* increment in 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 salivary microbial community was significantly decreased in Behçet's disease compared to healthy controls. Recent research, focused on the role of bacteria in oral carcinogenesis, indicated that genus *Alloprevotella* was among the bacteria that showed significantly higher abundances [[8], [9]]. However, its features related to pathogenesis have not been clarified yet.

## Conclusion

Signs and symptoms of oral SCC, which has a poor overall 5-year survival rate, and CMO can often be similar. The diagnosis of CMO is particularly important as appropriate treatment, culture-guided antibiotic therapy for the infection and surgical

management, provides successful cure. Defining of bacterial community composition associated with CMO can help understanding the mechanisms of disease and impact of the bacteria.

No conflict of interest was declared by the authors.

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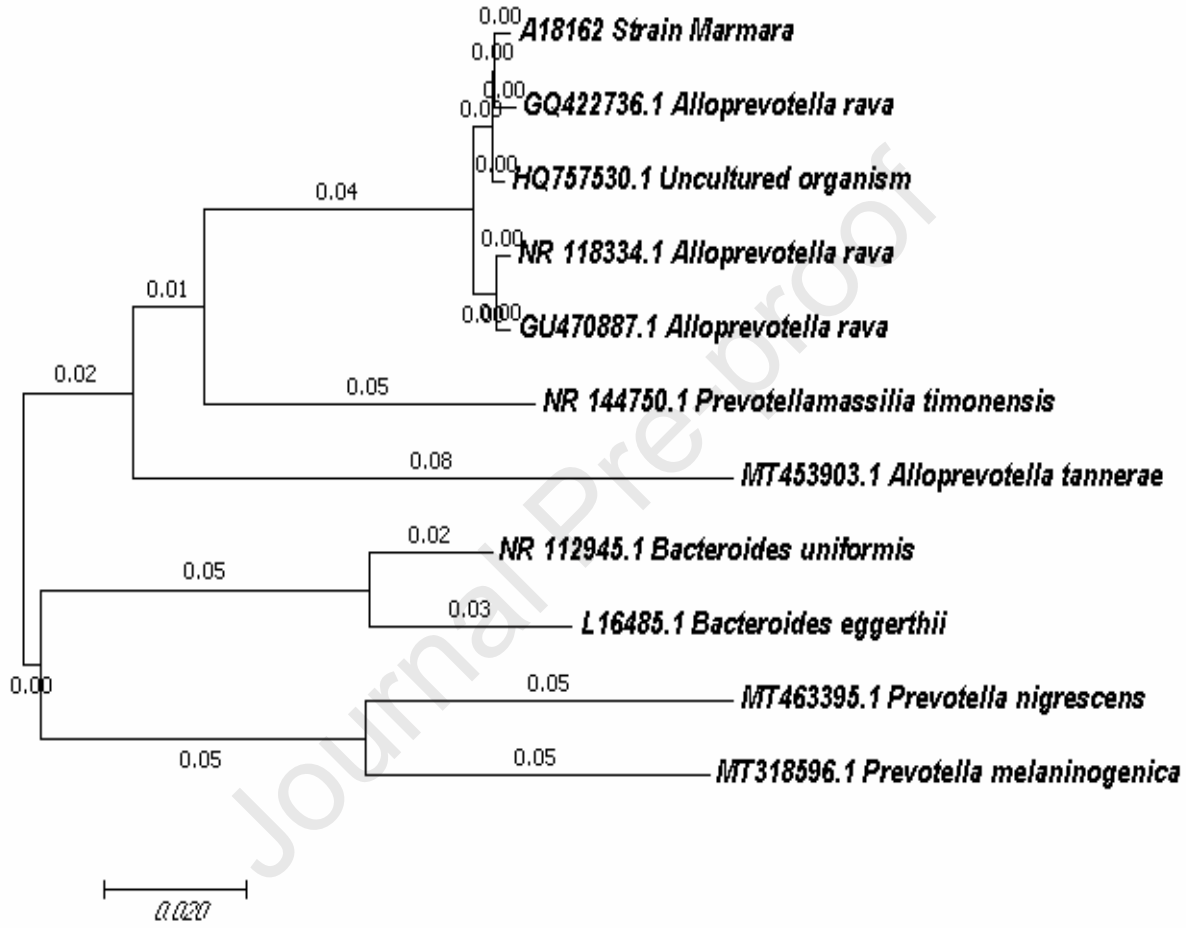


Figure 1.

Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences, showing the relationships between STRAIN MARMARA and some related taxa. GenBank accession numbers are shown in parentheses. Numbers at nodes indicate bootstrap percentages (based on 1000 replicates). Bar represents 0.02 substitutions per nucleotide position.