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**Search details**

Blind cultures positive for actinomyces meyeri.

**Resources searched**

NHS Evidence; TRIP Database; Cochrane Library; CINAHL; EMBASE; MEDLINE; Google Scholar

*Database search terms*: actinomyces adj2 meyeri*; “actinomyces meyeri”*; ACTINOMYCES; ACTINOMYCOSIS; meyeri*; actino*; positive adj2 culture*; blind*; blind* adj2 culture*; positive; culture*; *ACTINOMYCOSIS/di [Diagnosis]; *ACTINOMYCOSIS/mi [Microbiology]; *ACTINOMYCOSIS/pa [Pathology]; ACTINOMYCOSIS/ip [ip=Isolation & Purification]; ACTINOMYCIES/cy.ip.pa [cy=Cytology, ip=Isolation & Purification, pa=Pathology] df/fs.; mi/fs.; pa/fs; ip.fs.

*Google search string*: ((actinomyces OR actinomycosis) meyeri) ~blind ~culture ~positive

**Summary**

There is not much research into actinomyces meyeri and what there is only rarely covers pathological or microbiological examination not cover and blind positive cultures not at all.

**Guidelines**

None found.

**Evidence-based reviews**

None found.
1. Comparison of SmartGene IDNS Software vs. GeneBank for interpretation of partial 16S rRNA gene sequences for bacterial pathogen identification in a clinical laboratory

Author(s): Lloyd T., Church D.

Citation: International Journal of Antimicrobial Agents, July 2009, vol./is. 34/(S85), 0924-8579 (July 2009)

Publication Date: July 2009

Abstract: Objectives: CLS uses partial 16S rRNA gene sequencing to identify bacterial pathogens that are difficult to ID by conventional biochemical methods. Sequence data is blasted using GeneBank (National Center for Biotechnology Information; NCBI). SmartGene IDNS software was compared to GeneBank for sequence interpretation since this program contains >100,000 rRNA quality controlled pathogen gene sequences (SmartGene Inc., Raleigh, N.C.). Methods: Clinical isolate 500 bp 16 S rRNA forward/reverse sequences were randomly selected from the 2008 repository that previously were blasted using GeneBank. These sequences were re-interpreted using SmartGene. Blast results were compared to determine ID agreement at the >99% and >97% levels. Discordant sequence results were sent to SmartGene to resolve. Results: A total of fifty-one bacterial pathogens (i.e., 102 partial 16S rRNA sequences) were blasted using both methods. 35/51 (68.6%) were Gram-positive and 12/51 (23.5%) were Gram-negative pathogens. Clinical isolates sources included; 24 (47.1%) from blood, 18 (35.3%) from deep wounds, fluids and tissues, and 9 (17.6%) from lower respiratory specimens. SmartGene IDNS identified 50/51 (98%) of these isolates; 42/50 (88%) at >99%, 5/50 (10%) at >97%, and 3 (6%) at <=96% agreement. Discordant results occurred for Corynebacterium tuberculostercium. SmartGene identified 6/50 (12%) isolates to the genus [i.e., Eubacterium spp (2), Actinomyces spp. (1), Dialister spp. (1), Eggerthella spp. (1) and Lautropia spp. (1)], and 44/50 (88%) isolates to the species level. SmartGene provided an updated ID for 4 isolates including; Aggregatibacter aphrophilus, Granulicatella adiacens/Abiotrophia paradiacens, Parvimonas micra, Actinomyces meyeri/odontolyticus. SmartGene allows rapid online editing of sequence data uploaded directly from the genetic analyzer. Conclusions: SmartGene IDNS provides accurate and efficient ID of diverse pathogen groups for clinical microbiology laboratories using molecular ID methods.

Source: EMBASE

Full Text:
Available in fulltext at ULHT journal article requests. Complete the online form to obtain articles.

2. Actinomyces meyeri cutaneous actinomycosis.

Author(s): Hermida MD, Della Giovanna P, Lapadula M, Garcia S, Cabrera HN

Citation: International Journal of Dermatology, February 2009, vol./is. 48/2(154-6), 0011-9059;1365-4632 (2009 Feb)

Publication Date: February 2009

Abstract: Actinomyces meyeri cutaneous actinomycosis is a very rare disease. It often results from contiguous dissemination of an underlying focus. We report a case of pulmonary actinomycosis with secondary cutaneous involvement which led to the diagnosis. A 51-year-old man presented with an indurated, erythematous plaque on his right chest wall. He had been diagnosed with pneumoniae one month prior ago and received antibiotic treatment but symptoms persisted. Fibrobroncoscopy was normal and bronchoalveolar lavage samples were negative. The cutaneous plaque evolved with fistulization and drainage of serohematic material with white grains. Actinomyces meyeri was cultured from bacteriologic samples. Ceftriaxone and doxiciclin were administered for a total of 12 months with complete resolution of the clinical condition.

Source: MEDLINE

Full Text:
3. Actinomycosis: An overview: Medical education [Turkish] Aktinomikoza Genel Bir Bakis

Author(s): Kaya D., Demirezen S., Beksar M.S.

Citation: Turkiye Klinikleri Journal of Medical Sciences, 2009, vol./is. 29/2(510-519), 1300-0292 (2009)

Publication Date: 2009

Abstract: Actinomycosis is a chronic, suppurative, granulomatous and spreading disease which is caused by anaerobic bacteria of the family Actinomycetaceae in humans and other homoiothermic animals. Actinomyces israelii is the most common agent of actinomycosis. Other Actinomyces species responsible for actinomycosis are A. odontolyticus, A. meyeri, A. naeslundii and A. viscosus. Actinomycosis is an endogenous infection and is induced by some predisposing factors that introduce Actinomyces species, which are the normal inhabitants of the host, into the mucosa. Based on the site of involvement, the four common forms are cervicofacial, abdominal, toracic and pelvic actinomycosis. Cerebral, cutaneous or disseminated actinomycosis are extremely rare. Purulent matter, sputum, vaginal discharge, fistulae content or tissue biopsy specimens are generally used to diagnose actinomycosis. However, it is very difficult to identify Actinomyces in these samples because of other filamentous and anaerobic bacteria. Furthermore, actinomycosis is frequently undiagnosed or misdiagnosed and thus is not treated correctly due to the number of other fungal infections which may present with similar manifestations. In most cases, definitive diagnosis is made after surgical resection. Thus, it is very important to know the general features of actinomycosis forms and the diagnostic methods. In this review, the clinical features of actinomycosis forms, general features of Actinomyces species that are responsible for human actinomycosis, the diagnostic tools for actinomycosis and the treatment of actinomycosis are discussed in detail in the light of the literature. Copyright 2009 by Turkiye Klinikleri.

Source: EMBASE

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Author(s): Bauer P, Sultan S, Atienza P

Citation: Gastroenterologie Clinique et Biologique, January 2006, vol./is. 30/1(29-32), 0399-8320:0399-8320 (2006 Jan)

Publication Date: January 2006

Abstract: INTRODUCTION: Primary anal actinomycosis of cryptoglandular origin, mainly due to Actinomyces israelii, a specific and rare cause of anal suppurative disease, needs to be recognized because it can be cured using specific treatments.METHOD: Data were reviewed from 6 patients with actinomycotic anal abscesses of obvious cryptoglandular origin observed in a single proctology unit between 1983 and 2000. Therapeutic management included conventional surgical treatment of anal sepsis followed by a specific oral antibiotic therapy maintained until the surgical wound had completely healed.RESULTS: All but one of the patients were men (median age, 53 years). All abscesses, except one, were indolent. No patient presented macroscopic "sulphur granules" in the pus, but one presented "watery pus". The diagnosis was established by histological study of the surgically excised tissue or by anaerobic culture of the pus. In the one HIV-positive patient, an uncommon organism was isolated: Actinomyces meyeri. Two cases of recurrence were observed without evidence of Actinomyces infection.CONCLUSION: Actinomycosis should be suspected particularly in indolent anal suppuration. The absence of macroscopic "sulphur granules" does not mean this diagnosis...
can be ruled out. Careful histological examination of the excised tissue and appropriate anaerobic cultures of pus should be carried out to achieve complete eradication of this rare, but easily curable disease.

**Source:** MEDLINE

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5. *Actinomyces meyeri* isolation from synovial fluid of a patient with metastatic squamous cell lung carcinoma.

**Author(s):** Cetin ES, Kaya S, Demirci M, Aridogan BC

**Citation:** Saudi Medical Journal, December 2005, vol./is. 26/12(1997-9), 0379-5284;0379-5284 (2005 Dec)

**Publication Date:** December 2005

**Source:** MEDLINE

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6. Molecular evaluation of residual endodontic microorganisms after instrumentation, irrigation and medication with either calcium hydroxide or Septomixine.

**Author(s):** Tang G, Samaranayake LP, Yip HK

**Citation:** Oral Diseases, November 2004, vol./is. 10/6(389-97), 1354-523X;1354-523X (2004 Nov)

**Publication Date:** November 2004

**Abstract:** BACKGROUND AND OBJECTIVE: The correct choice of antimicrobial agents as inter-appointment medicaments is as important as the instrumentation and irrigation to remove pathogens from infected root canals. Calcium hydroxide [Ca(OH)2] and framycetin sulfate (Septomixine) are common endodontic medicaments. Therefore, we evaluated the efficacy of either calcium hydroxide or Septomixine in eliminating residual intra-canal bacteria, particularly Actinomyces spp., during inter-appointment interval in endodontic therapy using molecular methods.METHODS: A total of 31 single-rooted teeth with primary root canal infections were studied immediately after opening the canals and subsequently after instrumentation, irrigation with sterile saline and 1-week medication with either Ca(OH)2 (n = 25) or Septomixine (n = 6). Whole bacterial genomic DNA was isolated directly from samples and PCR with universal primers performed to detect total intra-canal bacteria. The variable regions of 16S rDNA of bacteria were amplified and labeled with digoxigenin for further hybridization to detect Actinomyces spp. A total of seven oligonucleotide probes specific for A. bovis, A. gerencseriae, A. israelii, A. meyeri, catalase-negative A. naeslundii (genospecies 1 and 2), catalase-positive A. naeslundii genospecies 2 and A. odontolyticus were used to detect Actinomyces spp. in 22 of 31 medicated root canals [Ca(OH)2: n = 17; Septomixine: n = 5].RESULTS: The PCR results showed that 25 of 31 examined canals were positively detected with residual microorganisms after instrumentation, irrigation with sterile saline and 1-week medication with either Ca(OH)2 (n = 20) or Septomixine (n = 5). Thus, only six canals [Ca(OH)2: n = 5, Septomixine: n = 1] were aseptic after treatment. Hybridization results showed higher detection frequency of both A. odontolyticus and A. gerencseriae after treatment. Significant correlation was found between exposed pulp before treatment and positive detection of Actinomyces spp., particularly A. odontolyticus on the second visit (P < 0.05).CONCLUSION: The conventional, 1-week medication of either Ca(OH)2 or Septomixine in endodontic therapy may not effectively inhibit residual bacterial growth in all root canals during inter-appointment intervals. Further investigations using, for instance quantitative real-time PCR analyses, are required to substantiate the present findings.

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7. Direct detection of cell surface interactive forces of sessile, fimbriated and non-fimbriated Actinomyces spp. using atomic force microscopy.

Author(s): Tang G, Yip HK, Samaranayake LP, Chan KY, Luo G, Fang HH

Citation: Archives of Oral Biology, September 2004, vol./is. 49/9(727-38), 0003-9969:0003-9969 (2004 Sep)

Publication Date: September 2004

Abstract: Actinomyces species are predominant early colonizers of the oral cavity and prime mediators of inter-bacterial adhesion and coaggregation. Previous workers have evaluated the adhesion of Actinomyces spp. by quantitative assessment of sessile, as opposed to planktonic cells attached to substrates, but did not quantify the cell surface interactive forces. Therefore we used atomic force microscopy to directly detect the interactive force between an approaching silicon tip and sessile Actinomyces spp. adhering to a substrate, at nanonewton (nN) range force levels. A total of eight strains each belonging to fimbriated and non-fimbriated Actinomyces species were employed, namely A. bovis, A. gerencseriae, A. israelii, A. meyeri, A. naeslundii genospecies 1 and 2, A. odontolyticus and A. viscosus. The sterile mica discs, used as the adhesion substrate, were immersed in mono-species bacterial suspensions for five days to obtain a thin bacterial biofilm. Interactive forces were measured using a silicon nitride cantilever attached to a Nanoscope IIIA atomic force microscope. The interactive forces between the approaching silicon nitride tip and bacterial biofilm surfaces were randomly quantified at three different locations on each cell; namely, the cell surface proper, the periphery of the cell and the substrate and, the interface between two cells. When the interactive forces at these locations of the same species were compared, significantly higher force levels at the cell-cell interface than the other two locations were noted with A. gerencseriae (P < 0.001), A. viscosus (P < 0.01) and A. israelii (P < 0.05). When the interactive forces of different Actinomyces spp. at an identical location were compared, fimbriated A. naeslundii genospecies 2 showed the greatest interactive force at the cell surface proper (~32.6 +/- 8.7 nN, P < 0.01). A. naeslundii genospecies 1, 2 and A. viscosus demonstrated greater interactive force at the cell-mica periphery than the other five species (P < 0.05); A. viscosus (~34.6 +/- 10.5 nN) displayed greater interactive force at the cell-cell interface than the others (P < 0.01), except for A. gerencseriae (P > 0.05). These data indicate that fimbriated Actinomyces spp., including A. naeslundii genospecies 1, 2 and A. viscosus exert higher cell surface interactive forces than those devoid of fimbriae and, such variable force levels may modulate their adhesion and coaggregation during biofilm formation.

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8. Direct detection of Actinomyces spp. from infected root canals in a Chinese population: a study using PCR-based, oligonucleotide-DNA hybridization technique.

Author(s): Tang G, Samaranayake LP, Yip HK, Chu FC, Tsang PC, Cheung BP

Citation: Journal of Dentistry, November 2003, vol./is. 31/8(559-68), 0300-5712;0300-5712 (2003 Nov)

Publication Date: November 2003

Abstract: OBJECTIVES: The poor sensitivity of phenotypic identification techniques has hampered the taxonomic differentiation of Actinomyces. Hence we developed a sensitive and specific, PCR-based oligonucleotide-DNA hybridization technique to detect Actinomyces spp. and, used this method to detect these organisms in samples directly obtained from infected root canals.METHODS: A total of 32 samples from 28 Chinese patients, with primary root canal infections, aseptically exposed at the first patient visit, were studied. Whole bacterial genomic DNA was isolated directly from paper point
samples. The variable regions of 16S ribosomal DNA of bacteria were amplified and labeled with digoxigenin for further hybridization and detection. A total of seven oligonucleotide probes specific for A. bovis, A. gerencseriae, A. israelii, A. meyeri, catalase-negative A. naeslundii (genospecies 1 and 2), catalase-positive A. naeslundii genospecies 2 and A. odontolyticus were used. RESULTS: 16 of the 32 teeth were infected with one or more Actinomyces species. The prevalence rates of the examined species were: A. odontolyticus 31.3%, A. meyeri 9.4%, A. naeslundii 9.4%, A. israelii 6.3% and A. gerencseriae 3.1%; no A. bovis was detected in any of the canals. Furthermore, A. odontolyticus was isolated more frequently from root canals with caries or a history of caries (Fisher's exact test: P=0.0496; Odds ratio=9.00, 95% confidence interval: 0.97-83.63), and A. naeslundii was significantly associated with traumatized teeth (Fisher's exact test: P=0.0121; Odds ratio=57.00, 95% confidence interval: 2.10-1546.90). However, no significant correlation was found between Actinomyces spp. and clinical symptoms and signs, such as pain, swelling, percussion to tenderness, sinus and periapical radiolucency. CONCLUSION: Actinomyces spp. may be important pathogens of root canal infections. A. naeslundii in particular may be related with traumatized teeth. A. odontolyticus appears to be involved in infections related to caries, exposure of dentinal tubules during cavity preparation and/or leaking restoration, but further clarification with large samples is necessary.

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9. Usefulness of the MicroSeq 500 16S ribosomal DNA-based bacterial identification system for identification of clinically significant bacterial isolates with ambiguous biochemical profiles.

Author(s): Woo PC, Ng KH, Lau SK, Yip KT, Fung AM, Leung KW, Tam DM, Que TL, Yuen KY

Citation: Journal of Clinical Microbiology, May 2003, vol./is. 41/5(1996-2001), 0095-1137:0095-1137 (2003 May)

Publication Date: May 2003

Abstract: Due to the inadequate automation in the amplification and sequencing procedures, the use of 16S rRNA gene sequence-based methods in clinical microbiology laboratories is largely limited to identification of strains that are difficult to identify by phenotypic methods. In this study, using conventional full-sequence 16S rRNA gene sequencing as the "gold standard," we evaluated the usefulness of the MicroSeq 500 16S ribosomal DNA (rDNA)-based bacterial identification system, which involves amplification and sequencing of the first 527-bp fragment of the 16S rRNA genes of bacterial strains and analysis of the sequences using the database of the system, for identification of clinically significant bacterial isolates with ambiguous biochemical profiles. Among 37 clinically significant bacterial strains that showed ambiguous biochemical profiles, representing 37 nonduplicating aerobic gram-positive and gram-negative, anaerobic, and Mycobacterium species, the MicroSeq 500 16S rDNA-based bacterial identification system was successful in identifying 30 (81.1%) of them. Five (13.5%) isolates were misidentified at the genus level (Granulicatella adiacens was misidentified as Abiotrophia defective, Helcococcus kunzii was misidentified as Clostridium hastiforme, Olsenella uli was misidentified as Atopobium rimaee, Leptotrichia buccalis was misidentified as Fusobacterium mortiferum, and Bregyella zoothelcum was misidentified as Rimerella anatipestifer), and two (5.4%) were misidentified at the species level (Actinomyces odontolyticus was misidentified as Actinomyces meyeri and Arcobacter cryaerophilus was misidentified as Arcobacter butzleri). When the same 527-bp DNA sequences of these seven isolates were compared to the known 16S rRNA gene sequences in the GenBank, five yielded the correct identity, with good discrimination between the best and second best match sequences, meaning that the reason for misidentification in these five isolates was due to a lack of the 16S rRNA gene sequences of these bacteria in the database of the MicroSeq 500 16S rDNA-based bacterial identification system. In conclusion, the MicroSeq 500 16S rDNA-based bacterial identification system is useful for identification of most clinically important bacterial strains with ambiguous biochemical profiles, but the database of the MicroSeq 500 16S rDNA-
based bacterial identification system has to be expanded in order to encompass the rarely encountered bacterial species and achieve better accuracy in bacterial identification.

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10. **Genotypic diversity of clinical Actinomyces species: phenotype, source, and disease correlation among genospecies.**

**Author(s):** Clarridge JE 3rd, Zhang Q

**Citation:** Journal of Clinical Microbiology, September 2002, vol./is. 40/9(3442-8), 0095-1137;0095-1137 (2002 Sep)

**Publication Date:** September 2002

**Abstract:** We determined the frequency distribution of Actinomyces spp. recovered in a routine clinical laboratory and investigated the clinical significance of accurate identification to the species level. We identified 92 clinical strains of Actinomyces, including 13 strains in the related Arcanobacterium-Actinobaculum taxon, by 16S rRNA gene sequence analysis and recorded their biotypes, sources, and disease associations. The clinical isolates clustered into 21 genogroups. Twelve genogroups (74 strains) correlated with a known species, and nine genogroups (17 strains) did not. The individual species had source and disease correlates. Actinomyces turicensis was the most frequently isolated species and was associated with genitourinary tract specimens, often with other organisms and rarely with inflammatory cells. Actinomyces radingae was most often associated with serious, chronic soft tissue abscesses of the breast, chest, and back. Actinomyces europaeus was associated with skin abscesses of the neck and genital areas. Actinomyces lingnae, Actinomyces gravenitzii, Actinomyces odontolyticus, and Actinomyces meyeri were isolated from respiratory specimens, while A. odontolyticus-like strains were isolated from diverse sources. Several of the species were commonly coisolated with a particular bacterium: Actinomyces israelii was the only Actinomyces spp. coisolated with Actinobacillus (Haemophilus) actinomycetemcomitans; Actinomyces meyeri was coisolated with Peptostreptococcus micros and was the only species other than A. israelii associated with sulfur granules in histological specimens. Most genogroups had consistent biotypes (as determined with the RapID ANA II system); however, strains were misidentified, and many codes were not in the database. One biotype was common to several genogroups, with all of these isolates being identified as A. meyeri. Despite the recent description of new Actinomyces spp., 19% of the isolates recovered in our routine laboratory belonged to novel genospecies. One novel group with three strains, Actinomyces houstonensis sp. nov., was phenotypically similar to A. meyeri and A. turicensis but was genotypically closest to Actinomyces neuii. A. houstonensis sp. nov. was associated with abscesses. Our data documented consistent site and disease associations for 21 genogroups of Actinomyces spp. that provide greater insights into appropriate treatments. However, we also demonstrated a complexity within the Actinomyces genus that compromises the biochemical identification of Actinomyces that can be performed in most clinical laboratories. It is our hope that this large group of well-defined strains will be used to find a simple and accurate biochemical test for differentiation of the species in routine laboratories.

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Author(s): Woo PC, Fung AM, Lau SK, Hon E, Yuen KY

Citation: Diagnostic Microbiology & Infectious Disease, June 2002, vol./is. 43/2(113-8), 0732-8893;0732-8893 (2002 Jun)

Publication Date: June 2002

Abstract: Traditional ways of identification of anaerobic Gram-positive non-sporulating bacilli by isolation of the organism and studying it phenotypically by elucidation of its morphologic and biochemical characteristics and metabolic end products are associated with a need for special equipment and expertise, and strains that are "unidentified" because of ambiguous biochemical profiles. In this study, an anaerobic Gram-positive non-sporulating bacterium was isolated from the intrauterine contraceptive device of a 36-year old woman with pyosalpinx. The Vitek system (ANI) showed that it was 99% Propionibacterium granulosum; whereas the API system (20A) showed that it was 78% Actinomyces meyeri/odontolyticus. The 16S ribosomal RNA gene of the strain was amplified and sequenced. There was 0 base difference between the isolate and A. odontolyticus (GenBank Accession no. AJ234047), indicating the isolate most closely resembled a strain of A. odontolyticus. Identification of the organism in this study was important because the duration of antibiotic therapy would be entirely different. In the present case, identification of the bacterium as A. odontolyticus inferred that the patient suffered from an intermediate form of pelvic actinomycosis. A prolonged course of antibiotics would be more desirable, as the relapse rate of actinomycosis after a short course of antibiotics is high.

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12. Microbiota of periapical lesions refractory to endodontic therapy.

Author(s): Sunde PT, Olsen I, Debelian GJ, Tronstad L

Citation: Journal of Endodontics, April 2002, vol./is. 28/4(304-10), 0099-2399;0099-2399 (2002 Apr)

Publication Date: April 2002

Abstract: The periapical microbiota of 36 teeth with refractory apical periodontitis was investigated. None of the teeth had responded to conventional endodontic or long-term (> 6 months), calcium-hydroxide treatment. Eight patients had received antibiotics systemically. After anaerobic culture, a total of 148 microbial strains were detected among 67 microbial species. One of the 36 lesions was culture-negative. Approximately half (51.0%) of the bacterial strains were anaerobic. Gram-positive species constituted 79.5% of the flora. Faculative organisms, such as Staphylococcus, Enterococcus, Enterobacter, Pseudomonas, Stenotrophomonas, Sphingomonas, Bacillus, or Candida species were recovered from 27 of the lesions (75%). Sulfur granules were found in 9 lesions (25%). In these granules Actinomyces israelii, A. viscosus, A. naeslundii, and A. meyeri were identified. Other bacterial species, both gram-positive and gram-negative, were detected in the granules as well. Two sulfur granules did not contain Actinomyces. Scanning electron microscopy demonstrated rod- and spirochete-like cells in the granules, and transmission electron microscopy revealed organisms with copious amounts of extracellular material. Outer membrane vesicles were also seen. Some of the granules were calcified. This study demonstrated a wide variety of microorganisms, particularly gram-positive ones, in the periapical lesions of teeth with refractory apical periodontitis.

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13. Diagnosis of pelvic actinomycosis by 16S ribosomal RNA gene sequencing and its clinical significance

Author(s): Woo P.C.Y., Fung A.M.Y., Lau S.K.P., Hon E., Yuen K.-Y.

Citation: Diagnostic Microbiology and Infectious Disease, 2002, vol./is. 43/2(113-118), 0732-8893 (2002)

Publication Date: 2002

Abstract: Traditional ways of identification of anaerobic Gram-positive non-sporulating bacilli by isolation of the organism and studying it phenotypically by elucidation of its morphologic and biochemical characteristics and metabolic end products are associated with a need for special equipment and expertise, and strains that are "unidentified" because of ambiguous biochemical profiles. In this study, an anaerobic Gram-positive non-sporulating bacterium was isolated from the intrauterine contraceptive device of a 36-year old woman with pyosalpinx. The Vitek system (ANI) showed that it was 99% Propionibacterium granulosum; whereas the API system (20A) showed that it was 78% Actinomyces meyeri/odontolyticus. The 16S ribosomal RNA gene of the strain was amplified and sequenced. There was 0 base difference between the isolate and A. odontolyticus (GenBank Accession no. AJ234047), indicating the isolate most closely resembled a strain of A. odontolyticus. Identification of the organism in this study was important because the duration of antibiotic therapy would be entirely different. In the present case, identification of the bacterium as A. odontolyticus inferred that the patient suffered from an intermediate form of pelvic actinomycosis. A prolonged course of antibiotics would be more desirable, as the relapse rate of actinomycosis after a short course of antibiotics is high. 2002 Elsevier Science Inc. All rights reserved.

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14. Abdominal actinomycosis: complication of endoscopic stenting in chronic pancreatitis?

Author(s): Harsch IA, Benninger J, Niedobitek G, Schindler G, Schneider HT, Hahn EG, Nusko G

Citation: Endoscopy, December 2001, vol./is. 33/12(1065-9), 0013-726X;0013-726X (2001 Dec)

Publication Date: December 2001

Abstract: Pancreatic endotherapy is frequently performed in patients with chronic pancreatitis and stenoses of the main pancreatic duct. In a patient with long-standing chronic pancreatitis and treatment with pancreatic stents, metastatic pancreatic head carcinoma was suspected because of infiltration of the neighboring organs and hepatic lesions. Ultrasound-guided aspiration of one liver lesion revealed grains typical for actinomycosis. In the light of this case, an extracted pancreatic stent was microbiologically investigated for actinomycetes in another patient who had a suspicious lesion of the pancreatic head. Microbiological examination of the extracted pancreatic stent revealed colonization by Actinomyces meyeri, Klebsiella oxytoca, and mixed cultures of anaerobic and saprophytic Gram-positive bacteria. In the following weeks, she developed a septic clinical picture with multiple abscesses of the liver. Actinomycoses meyeri, Corynebacterium species, Candida and Enterococci were cultivated in the aspirates. It seems possible, that treatment with pancreatic stents could have caused invasion of actinomycetes into the parenchyma of the pancreas, which was already harmed by the chronic inflammation, followed by the typical infiltrative growth and hematologic or biliary seeding into the liver.

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Identification of clinical isolates of actinomyces species by amplified 16S ribosomal DNA restriction analysis.

Author(s): Hall V, Talbot PR, Stubbs SL, Duerden BI

Citation: Journal of Clinical Microbiology, October 2001, vol./is. 39/10(3555-62), 0095-1137:0095-1137 (2001 Oct)

Publication Date: October 2001

Abstract: Amplified 16S ribosomal DNA (rDNA) restriction analysis (ARDRA), using enzymes HaeIII and HpaII, was applied to 176 fresh and 299 stored clinical isolates of putative Actinomyces spp. referred to the Anaerobe Reference Unit of the Public Health Laboratory Service for confirmation of identity. Results were compared with ARDRA results obtained previously for reference strains and with conventional phenotypic reactions. Identities of some strains were confirmed by analysis of partial 16S rDNA sequences. Of the 475 isolates, 331 (70%) were clearly assigned to recognized Actinomyces species, including 94 isolates assigned to six recently described species. A further 52 isolates in 12 ARDRA profiles were designated as apparently resembling recognized species, and 44 isolates, in 18 novel profiles, were confirmed as members of genera other than Actinomyces. The identities of 48 isolates in nine profiles remain uncertain, and they may represent novel species of Actinomyces. For the majority of species, phenotypic results, published reactions for the species, and ARDRA profiles concurred. However, of 113 stored isolates originally identified as A. meyeri or resembling A. meyeri by phenotypic tests, only 21 were confirmed as A. meyeri by ARDRA; 63 were reassigned as A. turicensis, 7 as other recognized species, and 22 as unidentified actinomycetes. Analyses of incidence and clinical associations of Actinomyces spp. add to the currently sparse knowledge of some recently described species.

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