Journal diphtheria pdf 2020

Articles and comments you currently do not have access to this article. Subscription and order Prices To buy short-term access, please sign up to your Oxford Academic Account above. You don't have an academic account at Oxford yet? Register Diphtheria in the 21st Century: New Research and Awakening Challenge - 24 Hours of Access Genetic Manipulation of Corynebacterium Diphtheria and other types of corynebacterium. (Article in the Journal) Curr Protoc Microbiol. 2020 09; 58(1): e111. Chang C, Nguyen MT, Ton-What HCPThis article describes several established approaches to the genetic manipulation of Corynebacterium diphtheria, the causal agent of diphtheria, which is known to have provided key evidence for Koch's postulates about the theory of microbes. First, it includes a detailed gene removal method that generates non-polar, in-frame, no marker removal of mutants, using levansucrase SacB as a counter-selectab ... Publisher Full Text (DOI) This article describes several established approaches to the genetic manipulation of Corynebacterium diphtheria, the causal agent of diphtheria, which is known to provide key evidence for Koch's postulates about microbial theory. First, it includes a detailed gene removal method that generates non-polar, in-frame, non-markers removing mutants, using the levansucrase SacB as a counter-chosen marker. Second, it provides a thorough protocol for rescuing mutant removal using Escherichia coli-Corynebacterium shuttle vectors. Finally, the procedure of transposon mutagenese Tn5 is described. In principle, these protocols can be used for other types of corynebacterium, including Corynebacterium glutamicum and Corynebacterium matruchotii. © 2020 Wiley Periodicals LLC Basic Protocol 1: Gene Removal in Corynebacterium diphtheriae Basic Protocol 2: Supplement of mutant strain Basic Protocol 3: Tn5 transposon mutagenesis of Corynebacterium diphtheriae. Toxic coinebaeria ditherium-associated ulcer ulcer. (Article in the Journal) Emerg Infect Dis. 2020 Sep; 26(9):2180-2181.Fuchs F, Marker D, ... Plum GEIIn October 2016, a teenage boy sought medical attention for acute genital ulcers in Cologne, Germany. We assumed a sexually transmitted infection, but initial diagnostic procedures had negative results. He was hospitalized because smear samples from the lesions had grown toxic Corynebacterium diphtheria, which led to the diagnosis of possibly sexually transmitted coquenous diphtheria. FREE Publisher Full TextPMC Free Full TextPMC Free PDFIn October 2016, a teenage boy sought medical attention for acute genital ulcers in Cologne, Germany. We assumed a sexually transmitted infection, but initial diagnostic procedures had negative results. He was because smear samples from the lesions grew toxic Corynebacterium diphtheria, which led to the diagnosis of possibly sexually transmitted coquenous diphtheria. Deadly Deadly diphtheria caused by β-lactam-resistant Diphtheria Corineracteria. (Article in the Journal) Clin Infect Dis. 2020 Aug 09 Online Ahead of Printing Ford BM, Henderson A., ... Beatson SACICONCLUSIONS: We have identified a new mechanism for irresistible antibiotic resistance, in which isolates that appear to be carbapenem susceptible to initial testing may develop in vivo resistance to re-exposure carbapenems. This phenomenon can have significant consequences for the treatment of C. diphtheria infection and can lead to clinical failure. Publisher Full Text (DOI) Respiratory diphtheria, characterized by a firm adherent of pseudomembrane, caused by toxins produced by strains corynebacterium diphtheria, with a similar disease produced sometimes toxified Corynebacterium ulcerans or, rarely, Corynebacterium pseudotuberculosis While laboratory confirmation of diphtheria requires cultural methods to determine toxicity, real-time PCR (RT-PCR) provides a faster method for detecting toxin were described non-toxic toxic toxic (NTTB) isolates Corynebacter but the effect of these isolates on the accuracy of molecular diagnostics is not well characterized. Here we describe a new RT-PCR triplex analysis to detect tox and distinguish C. diphtheria from closely related species C. ulcerans and C. pseudotuberculosis Analytical sensitivity and specificity analysis were evaluated compared to culture using 690 previously characterized microbial isolates. The new triplex analysis accurately characterizes Corynebacterium isolates with 100% analytical sensitivity for all purposes. Analytical specificity with isolates was 94.1%, 100% and 99.5% for toxes, Diph_rpoB and CUP_rpoB targets respectively. Twenty-nine NTTB Corynebacterium isolates representing 5.9% of the 494 non-toxic isolates tested were detected by RT-PCR. Sequencing the entire NTTB isolate genome revealed the various mutations underlying their lack of toxin production, as well as eight isolates without mutations in toxins or promoter areas. This new Corynebacterium RT-PCR provides a quick tool to test isolates and identify probable cases of diphtheria directly from samples. However, the sporadic appearance of NTTB isolates reinforces the view that diagnosing the culture of diphtheria continues to provide the most accurate evidence of the case. Corynebacterium diphtheria Virulence Analyses using the model Caenorhabditis elegans. (Article in the Journal) Curr Protoc Microbiol. 2020 09; 58(1): e109. Chen YW, Ton-To HCPCorynebacterium diphtheria is the leading cause of pharyngeal diphtheria, a respiratory disease characterized by the formation of pseudomembran at the site of infection. Although outbreaks of C. diphtheriae infections are now rare, strains of high-drug- diphtheria C. is one of the most significant public health problems worldwide. Although although Diphtheria was a stud ... The publisher of Full TextCorynebacterium diphtheriae is the main cause of pharyngeal diphtheria, a respiratory disease characterized by the formation of pseudommbration at the site of infection. Although outbreaks of C. diphtheriae infections are now rare, the emergence of strains of glynderia-resistant C. diphtheria is one of the most significant public health problems worldwide. Although C. diphtheria has been studied for over a century and diphtheria toxins and saws have been identified as the main factors of virulence, little is known about the factors associated with bacterial colonization and disease development. Here we describe the use of Caenorhabditis elegans as a cost-effective, universal infection model for assessing the virulence of C. diphtheriae. We provide detailed protocols to synchronize nematodes and to assess the survival of nematodes and the formation of a deformed area caused by C. diphtheria infection. These protocols will allow in the future high bandwidth screening of virulence factors in C. diphtheria and advance our knowledge of C. diphtheria pathogenesis. © 2020 wiley Periodicals LLC. Basic Protocol 1: Synchronization of nematodes Main Protocol 2: Analysis on the survival of nematodes after C. diphtheria infection Basic Protocol 3: Tests for bacterial colonization and the formation of a deformed region. StatPearls: Corinebacteria Diphtheria (BOOK)StatPearls. StatPearls Publishing: Treasure Island (FL) Chaudhary Anmol A Lousiana State Unversity- Monroe Pandey Shivlal S LSU-HSC / Monroe Family Medicine Program BOOKThe term diphtheria comes from the greed of the word diphtheria, which means hide or skin, because of the characteristics of pseudo membrane production. It is a preventable vaccine, but a potentially fatal upper respiratory tract infection. Presentation can be as an imptomatic carrier, a kayaking infection, or as pharyngitis with follo ... The term diphtheria comes from the greedy word diphtheria, which means hide or skin, because of the characteristics of the pseudo membrane produced by the body itself over the place of colonization. It is a preventable vaccine, but a potentially fatal upper respiratory tract infection. Presentation can be as an amptomatic carrier, to a cutaneous infection, or as pharyngitis with the following manifestations such as sore throat, fever, malaise, and cervical lymphadenapathy. A characteristic feature of the disease is the formation of pseudomembrane at the site of colonization. The front pillars of the tonsillary and the rear pharyngal walls are the most common places of participation. Before universal vaccination in the 1940s and 1950s, it was the leading cause of disease and death for children and young adults. However, since the introduction of the immunization, the incidence of this disease has been drastically reduced to almost 5,000 annually worldwide. Due to various factors, including low socio-economic status, insufficient income, inaccessibility to public health, war and population displacement, and ineffective monitoring of immunization schedules have led to frequent sporadic outbreaks worldwide. In this area, we aim to provide advanced courses in Corynebacterium diphtheria. Two cases of imported respiratory diphtheria in Edinburgh, Scotland, October 2019. (article in the journal) Epidemic infect. 2020 May 15; 148:e143. Lee L, Ross D, ... Stevenson JEIWe report two cases of respiratory-toxic diphtheria in fully vaccinated adults born in the UK after travelling to Tunisia in October 2019. Both patients were successfully treated with antibiotics and did not receive diphtheria antitoxin. Contact tracing was carried out after the risk assessment, but no additional cases were identified. This report highlights the importance of ... Publisher Full TextPMC Free Full TextPMC Free PDFWe reports on two cases of respiratory toxic infection with Corinebac dyphteria in fully vaccinated adults born in the UK after a trip to Tunisia in October 2019. Both patients were successfully treated with antibiotics and did not receive diphtheria antitoxin. Contact tracing was carried out after the risk assessment, but no additional cases were identified. This report highlights the importance of maintaining a high index of suspected re-emerging infections in patients with a history of travel to high-risk areas outside Europe.Corynebacterium silvaticum sp. nov., a unique group ntTB corynebacteria in wild boars and roe deer. (Article in the Journal) Int J Syst Evol Microbiol. 2020 June; 70 (6):3614-3624.Dangel A, Berger A, ... Sing AIJA for a total of 34 Corynebacterium sp. Strains have been isolated from the caseous lymph nodes of boar and roe deer abscesses in various regions of Germany. They showed slow growth on the Colombian sheep's blood agar and a rare rise at Hoyle in South Carolina. Analysis of cellular fatty acids isolated them in the group of diphtheria C. genus Corynebacterium. MALDI-TOF MS using specific database extensions and rp... Publisher Full TextA for a total of 34 Corynebacterium sp. Strains have been isolated from caseous lymph nodes of boar and roe deer abscesses in various regions of Germany. They showed slow growth on the Colombian sheep's blood agar and a rare rise at Hoyle in South Carolina. Analysis of cellular fatty acids isolated them in the group of diphtheria C. genus Corynebacterium. MALDI-TOF MS using specific database extensions and rpoB sequencing led to classification as C. ulcerans. Their quinone system is similar to C. ulcerans, with a basic MK-8(H2). Their complex polar lipid profile includes the main lipids of phosphatidyroiditotol, phosphatidinosytol-mannosid, phosphatidylosytol-mannosid, but also unidentified glycolipids, clearly distinguishing them from C ulcers. They showed activity of catalase, urease and phospholipase D, but variable results for alkaline phosphatease and alpha-glucosidease. All were non-toxic, toxic gene bearings and susceptible to clindamycin, penicillin and erythromycin. In 16SrRNA the gene and phylogenies of the RpoB protein strain formed different branches with C. ulcerans as the closest relative. Sequencing of the entire genome revealed a unique sequence of type 578, a distinct brunch in the genome of the pangenomic nucleus MLST, average nucleotide identities of 91%, increased genome sizes (2.55 Mbps) and G/C content (54.4 moles%) compared to related species. These results show that the strains represent a new species for which we use the name Corynebactriumsilvaticum sp. nov., based on their first isolation from forest animals. The strain type is KL0182T (CVUAS 4292T - DSM 109166T - LMG 31313T CIP 111 672T). Pathogenic bacteria of the genus Mycobacterium and Corynebacterium cause severe human diseases such as tuberculosis (Mikobacteria) and diphtheria (Corynebacterium diphtheriae). Cells of these species are surrounded by protective cell walls, rich long chain mycolycs. These fatty acids are conjugated to the disachide trehalosis on the cytoplasmic side of the membrane of bacterial cells. They are then transported through the membrane to periplasma, where they act as donors for other reactions. Previously, we have shown that transitor acetylation of glycolypid trehalose monohydroxycorinomicolate (hTMCM) allows it to be effectively transported to periplasm in corynebacterium glutamicum and that acetylation is mediated by the membrane protein TmaT. Here we show that for optimal transportation hTMCM also requires mint methyltransferase, encoded on the same genetic locus as TmaT. The removal of the C. glutamicum gene NCgl2764 (Rv0224c in M. tuberculosis) abolished the synthesis of monocorinomycolate acetyltralobosay (AcTMCM), which led to the accumulation of hTMCM in the inner membrane and the delay in its conversion into a trigaloous dihydroxycorinocolate (h2TDCM). The NCgl2764 supplement normalized hTMCM to h2TDCM. In contrast, the addition of NCgl2764 derivatives mutated on the residues needed for methyltransferase activity, which failed to correct the defect, suggesting that NCgl2764/Rv0224c encodes methyltransferase, designated here as MtrP. Comprehensive analysis of individual mtrP and tmaT mutants and double mutants have been strikingly similar in several classes of lipid. These findings suggest that both MtrP and TmaT play a non-existent role in regulating synthesis in the regulation of the trialase mycolate transport in Corynebacterineae.Change of diphtheria epidemiology in the United Kingdom, 2009 to 2017. (Article in the journal) Euro Surveill. 2020 March; 25 (11)Gower CM, Scobie A, ... Amirthalingam GESBackgroundDiphtheria is a potentially fatal disease caused by toxic strains of Corynebacterium diphtheria, C. ulcerans or C. pseudotuberculosis. The purpose of our goal was to look at the epidemiology of diphtheria in the United Kingdom (United Kingdom) and the impact of recent changes in public health management and surveillance. Methods Confused human toxy isfleps of diphtheria in the UK are sent for species ... PMC Free PDFBackgroundDiphtheria is a potentially fatal disease caused by toxic strains of Diphtheria Corynebacterium, C. ulcerans or C. pseudotuberculosis. The purpose of our goal was to look at the epidemiology of diphtheria in the United Kingdom (United Kingdom) and the impact of recent changes in public health management and surveillance. Human diphtheria in the UK is sent to confirm species and test for toxicity at the National Reference Laboratory. Clinical, epidemiological and microbiological information on toxic cases between 2009 and 2017 is described in this prospective population-based surveillance study. The result was 33 toxic cases of diphtheria between the ages of 4 and 82. The cause were C. diphtheria (n No. 18) and C. ulcerans (n No. 15). Most cases of C. diphtheria were to cutaneous (14/18), while more than half of cases of C. ulcerans had respiratory representations (8/15). Two thirds (23/33) of cases were under-immunized. Two cases of ulcers have died, both are insufficiently immunized. The main risk factor for acquiring C. diphtheriae was travel to an endemic area and for C. ulcerans, contact with a companion animal. The most confirmed isots are C. diphtheriae or C. ulcerans (441/507; 87%) to test for toxicity were non-toxic, however, the level of toxin positivity was higher (15/23) for C. ulcerans than C. diphtheria (18/469). Ten non-oxygen gene toxins (NTTB) C. diphtheria were also found. ConclusionDifteria is a rare disease in the UK. Milder C. c. Incomplete vaccination status has increased in the last decade. The effect of a tampon type on test points of view. (Article in the Journal) AMB Express. 2020 March 12; 10 (1):46.Ambush A.A., zakharchuk K., ... In the POCT, Malinowska EAEMost uses tampons to sample and/or to use a sample on the test. tampons, differing in the tips of materials, are available on a commercial basis. Different material tips have different chemical and physical characteristics that can affect the collection and release of samples. We investigated the properties of the different types of tampons used Clinical diagnostics with focus... Publisher Full TextPMC Free Full TextPMC Free PDFMost Point Care Test (POCT) use tampons to sample and/or to apply a sample to the test. A variety of tampons at the tips of materials is available commercially. Different material tips have different chemical and physical characteristics that can affect the collection and release of samples. We investigated the properties of different types of tampons used in clinical diagnosis, focusing on two types of analytic, DNA and proteins that are most commonly used by the targets in POCT. As model samples, we used diphtheria toxoid NIBSC 69/017 to study the recovery of protein tests, such as antigens and bacterial strains Escherichia coli ATCC 25922, diphtheria toxin produced by Corynebacterium diphtheria NCTC 10648, and clinical isolate of non-toxic C. diphtheria 5820/15 for the study of nucleic acid recovery. We examined four types of tampons most commonly used in clinical diagnostics in terms of absorption capacity and efficiency in the release of nucleic acids and proteins. Volume absorption was measured in milligrams. Various buffers for washing out were used to release DNA, and the amount of DNA being produced was measured spectrotototically. The amount of protein released from tampons was investigated using Lowry's analysis. We observed statistically significant differences (lt; 0.05) in the average weights of the absorbed liquid, in dna recovery and protein recovery by the four tampon varieties examined. However, the efficiency of releasing DNA and protein was correlated not with the absorbed volume of the sample, but with the properties of tampons. The composition and structure of the tampon can have a significant impact on the collection and the efficiency of the sample production. Thus, checking the POCT for the tampons used for sampling is very important. The use of inappropriate tampons can lead to false negative or misleading analysis results. Corynebacterium rouxii sp. nov., a new member of the diphtheria species complex. (Article in the Journal) Res Microbiol. 2020 Apr - June; 171 (3-4):122-127.Badell E, Hennart M,... The Brisse SRMA group of six clinical isolates previously identified as Coinebacterium biofereria Belfanti, isolated from cutaneous or peritoneum human infections and from one dog, were characterized by genomic sequencing, biochemical analysis and mass spectrometry MALDI-TOF. Six isolates were negative for the diphtheria toxin gene. Philogenetic analyses have shown that six isolates (including FRC ... FREE Publisher Full TextA Group of six clinical isolates previously identified as Corynebacterium diphtheria biovar Belfanti, isolated from humans to cutaneous or peritoneal infections and from one dog, have been genomic sequencing, biochemical analysis and MALDI-TOF mass spectrometry. Six isolates were negative for toxin gene. Philogenetic analyses have shown that six isolates (including FRC0190T) are clearly demarcated from C. diphtheria, Corynebacterium belfantii, Corynebacterium ulcerans and Corynebacterium pseudotuberculosis. The average nucleotide identity of FRC0190T with C. diphtheria NCTC11397T was 92.6%, and was 91.8% with C. belfantii FRC0043T. C. diphtheriae subsp. The lausannense strain of CHUV2995T was later a heterotypic synonym for C. belfantii (ANI, 99.3%). RpoB sequences have shown the identity of atypical, maltious negative C. diphtheria biovar Belfanti isolates previously described from two cats in the U.S. We offer the name Corynebacterium rouxii sp. nov. for a new group, with FRC0190T (Yap. CIP 111752T and DSM 110354T) as a strain of type. Outbreaks of diphtheria in schools in the Central Highlands, Vietnam, 2015-2018. (Article in the Journal) Emerg Infect Dis. 2020 03; 26(3):596-600.Kitamura N, Le TTT, ... Yoshida LMEIDuring 2015-2018, seven schools in rural Vietnam have experienced outbreaks of diphtheria. Multi-location sequence types were the same in schools, but differed between schools. Low vaccination coverage and overcrowded dormitories may have contributed to the outbreaks. The authorities should consider the introduction of regular vaccinations and booster doses for students entering the school system. FREE Publisher Full TextPMC Free Full TextPMC Free PDFDuring 2015-2018, seven schools in rural Vietnam experienced outbreaks of diphtheria. Multi-location sequence types were the same in schools, but differed between schools. Low vaccination coverage and overcrowded dormitories may have contributed to the outbreaks. The authorities should consider the introduction of regular vaccinations and booster doses for students entering the school system. Diphtheria is a terrible disease caused by corynebacterium diphtheria. Lysogenized bacteriophages carrying the toxin gene in C. diphtheria can make the strain toxic. However, such phage spreads the genes of toxins to other strains when it goes through the lithium phase. As little known about the diversity of phages in C. diphtheria in India, this study was conducted to study the promatters integrated into the genome of 29 clinical isolates of C. diphtheria using the entire genome of shotgun sequencing. Among these isolates, 27 were toxic, while 2 had non-toxic strains. Of the 27 toxic strains, all harbored known phages carrying the toxin gene and two other phages with unknown function. However, two strains of non-toxics do not harbor any of the phages in the genome. There is an urgent need to develop prevention that prevent the spread of toxins increased complications of diphtheria after immunization. Corynebacterium diphtheria is a human pathogen that causes diphtheria. In response to oxidative stress caused by the immune system, C. diphtheriae expresses antioxidant enzymes, including sulfoxide reducase sulfoxide (Msr) enzymes, which are crucial for the survival of bacteria under oxidative stress. Although some aspects of the catalytic mechanism of Msr enzymes have been reported, some details are still awaiting full clarification. Here we decided the structure of The Solution C. Diphtheria MsrB (Cd-MsrB) and unraveled its catalytic and oxidative protection mechanisms. Cd-MsrB catalisin sulfoxide reduction involving three redox-active cysteine. Using hetero-nuclear single-quarter-core NMR coherence spectrums, kinetics, biochemical analyses, and MS analyses, we show that the preserved nucleophilic remnants of Cys-122 S-sulfenil is after the reduction of the substrate, which is then solved with canned cysteine, Cys-66, or nonconservative residue Cys Cys-127. We noted that common structural changes during the disulfide cascade expose Cys-122-Cys-66 recycling through thiorodoxin. In the presence of hydrogen peroxide, Cd-MsrB formed reversible intra- and intermolecular disulfides without losing its Cys-coordinated No2, and only the non-conservative Cys-127 reacted with low molecular weight (LMW) thicoticol, protecting it from excessive oxidation. Thus, our analysis of structural and functional functions reveals the critical details of the Cd-MsrB catalytic mechanism, including the major structural permutations that premiere Cys-122-Cys-66 disulfide to reduce thioredoxine and reversible protection against excessive oxidation of catalytic cysteine in Cd-MsrB through intra- and intermolecular disulfide formation and S-mycothiolation. Diphtheria is an infectious disease caused by Coryneberactium. The bacterium primarily infects the throat and upper respiratory tract and produced diphtheria toxin (DT), which binds to elongated factor 2 and blocks protein synthesis, can spread through the bloodstream and affect organs such as the heart and kidneys. For more than 125 years, diphtheria therapy has been based on polyclonal horse sulfur directed against DT (diphtheria antitoxin; DAT). Animal sulfur has many drawbacks, including serum disease, from batch to batch quality change and the use of animals for production. In this work, 400 human recombinant antibodies were created against DT from two different phases display panning strategies using the human immune library. Panning in microtitre plates resulted in 22 unique in vitro neutralization antibodies and panning in the solution combined with functional neutralization screening resulted in 268 in vitro Antibodies. 61 unique antibodies were additionally described as scFv-Fc with 35 produced as all completely IgG1. The best extracorporeal neutralizing antibodies showed a relative potency of 454 IU/mg and a minimum effective dose of 50% (MED50%) 3.0 RM with a constant amount of DT (4x minimum cytopal dose) in IgG format. The target areas of 35 antibodies were analyzed by immunobloo and epitopic mapping using a phage display. All three DT domains (ensimatic domain, translocation domain and receptor binding domain) are targets for neutralizing antibodies. When toxin neutralization analyses were performed at higher levels of the toxin dose, the neutralizing ability of individual antibodies was markedly reduced, but this was largely offset by two or more antibodies in combination, resulting in a potency of 79.4 IU/mg in willo intradermal problem analysis. These recombinant combinations of antibodies are candidates for further clinical and regulatory development to replace the DAT horse. Diphtheria is a acute, highly infectious, toxic and vaccine-preventable disease that usually affects children under the age of 12. The incidence of diphtheria has decreased significantly due to vaccination of diphtheria, whooping coughs, tetani (DPT). Recently, there has been a growing trend in reports of diphtheria around the world and, in particular, from developing countries. According to a report by the World Health Organization (WHO), more than 80% of diphtheria cases in the world during the post-vaccination era were reported in India and Indonesia. This may indicate its re-emergence, which can be explained by several factors that include incomplete immunization. Faringitis caused by the streptococcus group is most common in children and may be clinically similar in the presentation of diphtheria. We share our experience of driving an eight-year-old child who was clinically suffering from diphtheria. Diphthetic angina in the tongue and floor of the mouth: an unusual representation. (Case reports) Br J Oral Maxillofac Surg. 2020 04; 58(3):358-360.Solano N, Gutierrez V, ... Castrillo ABJDiphtheria is an infectious disease caused by Diphtheria Corynebacterium, and is usually characterized by the spread of bacteria in the upper respiratory tract, the formation of pseudomembrane, and the systemic spread of diphtheria toxin throughout the body. Introducing the case of a young man with pseudo-membred plaques on the tongue and floor of the mouth, who received a systemic and... Publisher Full TextDiphtheria is an infectious disease caused by Corynebacterium diphtheria, and is usually characterized by the spread of bacteria in the upper respiratory tract, the formation of pseudomembrane, and the systemic spread of diphtheria toxin throughout the body. Introducing the case of a young man with pseudo-membrane plaques on the tongue and floor of his mouth, who received systemic and lokoregional medical care, with 14 days later. Phenotypic and genotypic correlates of penicillin susceptibility to non-toxic corinecteria diphtheria, British Columbia, Canada, 2015-2018. (Article in the Journal) Emerg Infect Dis. 2020 01; 26 (1): 97-103.Soo J, Chorlton SD, ... Lowe CFEIIn 2015, Institute of Clinical and Laboratory Standards (CLSI) has updated its break points for penicillin susceptibility to corereeecteria species from 1 mg/L to 0.12 mg/L. We evaluated the impact of this change on susceptibility C. diphtheriae reported at the Tertiary Care Center in Vancouver, British Columbia, Canada, during 2015-2018 and carried out sequencing of the entire genome to investiga ... PMC Free PDFIn 2015, Institute of Clinical and Laboratory Standards (CLSI) has updated its break points for penicillin susceptibility in Corynebacterium species from 1 mg/L to 0.12 mg/L. We evaluated the effect of this change on C. diphtheriae susceptibility reported at the Tertiary Care Center in Vancouver, British Columbia, Canada, during 2015-2018 and sequenced the entire genome to study phenotypic and genotypic resistance to penicillin. We identified 44/45 isolates that were intermediately susceptible to penicillin by 2015 break point, despite meeting previous CLSI criteria for susceptibility. Sequencing did not reveal β lactam resistance. Multilocal typing of the sequence revealed a noticeable preponderance of the Type 76 sequence. Overall, we have not seen any evidence of neo-susceptibility to penicillin at phenotypic or genotypic levels in C. diphtheria isolates from our institution. Changing the 2015 CLSI break point could lead to an incorrect classification of penicillin susceptibility to C. diphtheriae isolates, potentially resulting in a suboptimal selection of antimicrobials. Diphtheria. (Review) Nat Rev Dis Primers. 2019 12 05; 5(1):81.Sharma NC, Efstratiou A, ... Ramamurthy TNRDiphtheria is a potentially fatal infection mainly caused by toxic strains of corinecteria diphtheria and sometimes toxice strains of C. ulcerans and C. pseudotuberculosis. Diphtheria, usually an acute respiratory infection, is characterized by the formation of pseudommbration in the throat, but infections are cut through possible. Systemic effects such as myocarditis and neuropathy, ... Publisher Full TextDiphtheria is a potentially fatal infection mainly caused by toxic strains of Corynebacterium diphtheria and sometimes toxic strains of C. ulcerans and C. pseudotuberculosis. Diphtheria, usually an acute respiratory infection, is characterized by the formation of pseudommbration in the throat, but infections are cut through possible. Systemic effects such as myocarditis and neuropathy, which are associated with an increased risk of death, are associated with diphtheria toxin, an exotoxin produced by a pathogen that is produced by a pathogen protein synthesis and causes cell death. Clinical diagnosis confirmed confirmed and the detection of causal Corynebacterium spp., usually

bacterial culture followed by ensimatic and toxin detection tests. Diphtheria can be treated with the timely use of antitoxin diphtheria and antimicrobial therapy. Although effective vaccines are available, the disease may re-emerge in countries where recommended vaccination programmes are not supported and an increasing number of adults are becoming susceptible to diphtheria. Thousands of cases of diphtheria continue to be reported annually from several countries in Asia and Africa, as well as from many outbreaks. Changes in diphtheria epidemiology have been reported worldwide. Prevalence of toxic Corynebacterium spp. stresses the need for appropriate clinical and epidemiological studies to quickly identify and treat affected individuals, as well as public health measures to prevent and contain the spread of the disease. Increased detection of corinebaceria diphtheria in Canada: 2006-2019. (Article in the Journal) Can Commun Dis Republic 2019 November 07; 45 (11):296-301.Bernard KA, Pacheco AL, ... Wiebe DCCCONCLUSIONS: There has been a marked increase in referral to NML for DT testing of Corynebacterium species. This may be due to the increased ability to identify these bacteria using MALDI-TOF systems. Constant monitoring will help to assess whether this increase is solely due to improved diagnostic accuracy or whether it is occurring to cutaneous pathogens. FREE Publisher Full TextPMC Free Full TextPMC Free PDF New Search Next Next