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Infection Control

Current Awareness
Newsletter

SUMMER 2016

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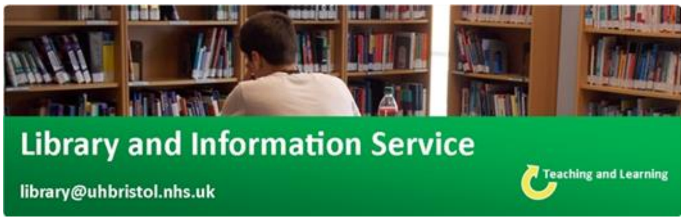
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Journal Tables of Contents

Infection Control & Hospital Epidemiology

July 2016 Vol 37 Iss 7

http://journals.cambridge.org/action/displayIssue?jid=ICE&tab=currentissue

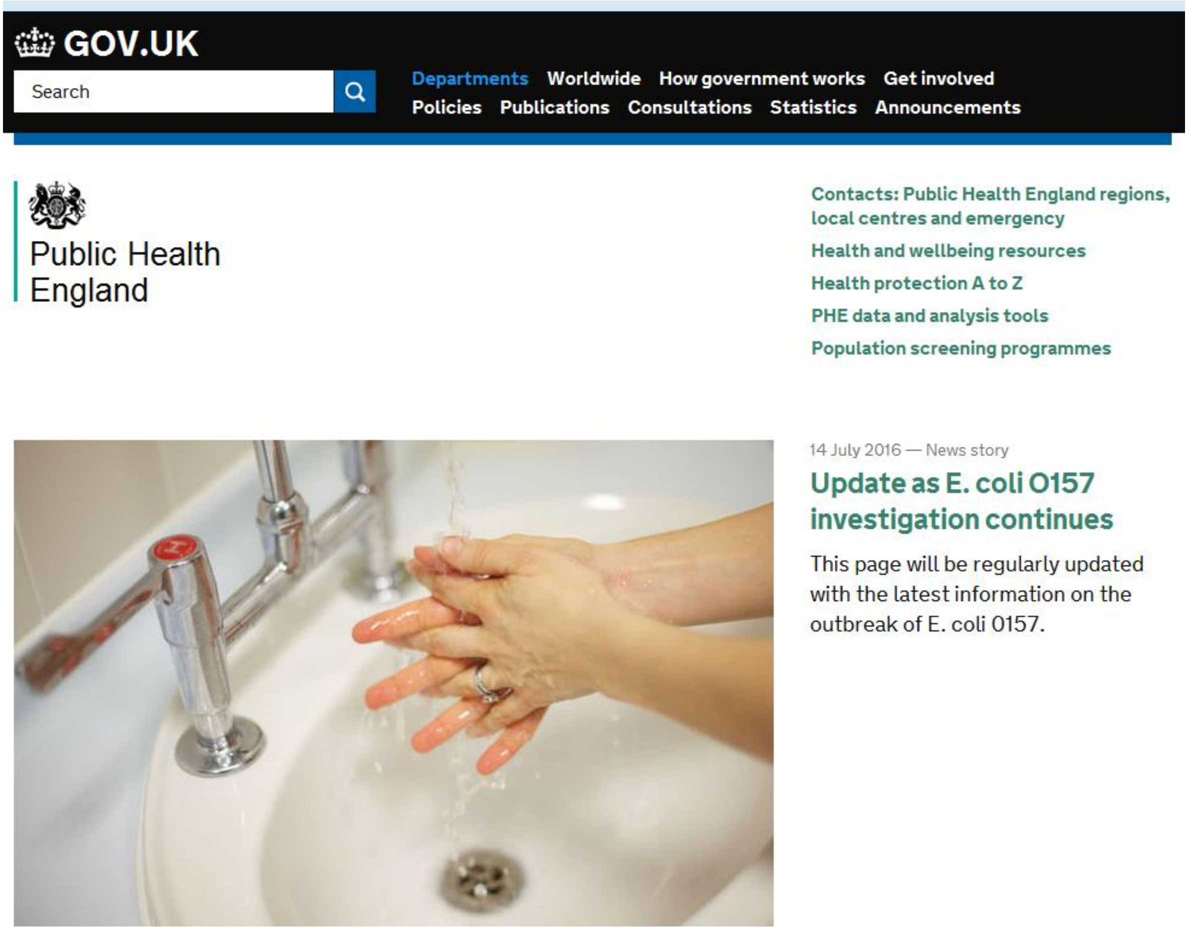
Journal of Infection Prevention

July 2016 Vol 17 Iss 4

http://bji.sagepub.com/content/17/4.toc

Public Health England

https://www.gov.uk/government/organisations/public-health-england



14 July 2016 — News story

Update as E. coli O157 investigation continues

This page will be regularly updated with the latest information on the outbreak of E. coli 0157.

New from the Cochrane Library Systematic Reviews

No new evidence

New from NICE

Signal: Chest physiotherapy for acute bronchiolitis is ineffective and may be harmful

Source: NIHR Dissemination Centre - 10 May 2016

Why was this study needed? Acute bronchiolitis is a common viral infection in children...breathing easier in cases of acute bronchiolitis. The first Cochrane review of the...physiotherapy was ineffective for acute bronchiolitis. However, chest physiotherapy, including...

https://discover.dc.nihr.ac.uk/portal/article/4000316/chest-physiotherapy-for-acute-bronchiolitis-is-ineffective-and-may-be-harmful

Eyes on Evidence : smoke free legislation and respiratory tract infections in children

Source: National Institute for Health and Care Excellence - NICE - 07 March 2016 - Publisher: National Institute for Health and Care Excellence (NICE)

A cohort study reported that the introduction of smoke-free legislation in England resulted in a 3.5% decrease in hospital admissions for acute respiratory tract infections in children.

http://arms.evidence.nhs.uk/resources/hub/1050060/attachment

Fourth external quality assessment scheme for Listeria monocytogenes typing [PDF]

Source: European Centre for Disease Prevention and Control - 09 June 2016

...for the three lots covering typing of Salmonella enterica ssp. enterica, Shiga toxin...selected FWD pathogens were included: Salmonella enterica ssp. enterica, L. monocytogenes, and...participating laboratories could request the Salmonella Braenderup H9812 strain used as molecular...

http://www.ecdc.europa.eu/en/publications/Publications/listeria-eqa-4-2015-2016.pdf

Current Awareness Database

Below is a selection of articles on ecently added to the healthcare databases, grouped in the following categories:

If you would like any of the following articles in full text, or if you would like a more focused search on your own topic, then get in touch: library@uhbristol.nhs.uk

Clostridium difficile

Title: Clostridium difficile ribotype 176 - A predictor for high mortality and risk of nosocomial spread?
Citation: Anaerobe, August 2016, vol./is. 40/(35-40), 1075-9964;1095-8274 (01 Aug 2016)
Author(s): Polivkova S., Krutova M., Petrlova K., Benes J., Nyc O.

Abstract: Purpose: The objective of this survey was to determine the incidence of Clostridium difficile infections (CDI) at the Department of Infectious Diseases, Bulovka Hospital, and to evaluate clinical and epidemiological data on CDI patients together with a detailed molecular characterisation of C. difficile isolates. The patient outcomes were correlated to causative C. difficile PCR-ribotype. **[…]**Methods: The twelve-month study (2013) comprised patients two years of age and older with CDI. CDI severity was estimated using ESCMID criteria and ATLAS scoring. C. difficile isolates were further characterized using ribotyping, **[Abstract shortened]**

Title: A novel method for imaging the pharmacological effects of antibiotic treatment on Clostridium difficile
Citation: Anaerobe, August 2016, vol./is. 40/(10-14), 1075-9964;1095-8274 (01 Aug 2016)
Author(s): Endres B.T., Basseres E., Memariani A., Chang L., Alam M.J., Vickers R.J.,

Abstract: Clostridium difficile is a significant cause of nosocomial-acquired infection that results in severe diarrhea and can lead to mortality. Treatment options for C. difficile infection (CDI) are limited, however, new antibiotics are being developed. Current methods for determining efficacy of experimental antibiotics on C. difficile involve antibiotic killing rates and do not give insight into the drug's pharmacologic effects. Considering this, we hypothesized that by using scanning electron microscopy (SEM) in tandem to drug killing curves, we would be able to determine efficacy and visualize the phenotypic response to drug treatment. To test this hypothesis, supraMIC kill curves were conducted using vancomycin, metronidazole, fidaxomicin, and ridinilazole. Following collection, cells were either plated or imaged using a scanning electron microscope (SEM). Consistent with previous reports, we found that the tested antibiotics had significant bactericidal activity at supraMIC concentrations. By SEM imaging and using a semi-automatic pipeline for image analysis, we were able to determine that vancomycin and to a lesser extent fidaxomicin and ridinilazole significantly affected the cell wall, whereas metronidazole, fidaxomicin, and ridinilazole had significant effects on cell length suggesting a metabolic effect. **[Abstract shortened]**

Title: Determination of the extent of Clostridium difficile colonisation and toxin accumulation in sows and neonatal piglets
Citation: Anaerobe, August 2016, vol./is. 40/(5-9), 1075-9964;1095-8274 (August 01, 2016)
Author(s): Grzeskowiak L., Zentek J., Vahjen W.

Abstract: Clostridium difficile is an important spore-forming, opportunistic pathogen in animal husbandry and health care. In pig farming, only neonatal piglets are affected, and diarrhoea and necrotising lesions are common symptoms leading to dehydration and in some cases death. This study aimed at the assessment of the quantitative development of C. difficile colonisation in neonatal piglets by determining the shedding of spores and C. difficile toxins A (TcdA) and B (TcdB) concentrations in sow (n = 5-6) and piglet pen faeces (n = 5-6) at different time points. Spores were quantified on selective agar plates and toxins using ELISA method. C. difficile was not detected in the faeces of all but one sow during the perinatal period. Faeces of 2- and 4-day-old piglets contained 0.65 log cells/g and 5.88 log cells/g of C. difficile, respectively. Toxins were detected on day 4 at a concentration of 2.13 log ng/g (TcdA) and 2.06 log ng/g (TcdB). On day 6, concentration of C. difficile reached 6.14 log CFU/g and toxins 2.02 log ng/g (TcdA) and 2.20 log ng/g (TcdB). Two-week-old piglets showed 4.72 log CFU/g of C. difficile but toxins could not be detected. At 21 days of age, both C. difficile and toxins were undetectable. The concentration and the prevalence of C. difficile were positively associated with the prevalence of toxins in piglets. A very short time window for colonisation by C. difficile, including toxin-producing strains can be observed in neonatal piglets. The significance for animal health and the risk of a carrier status need to be addressed in future studies.

Title: Clostridium difficile ribotype 027 is not evenly distributed in Hesse, Germany
Citation: Anaerobe, August 2016, vol./is. 40/(1-4), 1075-9964;1095-8274 (August 01, 2016)
Author(s): Arvand M., Bettge-Weller G.

Abstract: Clostridium difficile-isolates associated with CDI in different healthcare facilities in Hesse were analysed. The most common ribotypes were 001 (31.1%) and 027 (27.0%). The proportion of ribotype 027 among regional C. difficile-isolates was 10.8% in North Hesse, 17.2% in Middle Hesse, and 33.5% in the Rhine-Main Metropolitan Area. In the latter region, ribotype 027 was the most prevalent ribotype

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Bronchiolitis

Title: Randomised controlled studies are needed to evaluate the use of high-flow nasal cannula therapy in bronchiolitis.
Citation: Acta paediatrica (Oslo, Norway : 1992), Aug 2016, vol. 105, no. 8, p. 871-873
Author(s): Korppi, Matti, Heikkilä, Paula

Title: Deciphering clinical phenotypes in acute viral lower respiratory tract infection: Bronchiolitis is not an island.

Citation: Thorax, Aug 2016, vol. 71, no. 8, p. 679-680, 1468-3296 (August 2016)
Author(s): Cunningham, Steve, Nair, Harish, Campbell, Harry

Title: A clustering approach to identify severe bronchiolitis profiles in children.
Citation: Thorax, Aug 2016, vol. 71, no. 8, p. 712-718, 1468-3296 (August 2016)
Author(s): Dumas, Orianne, Mansbach, Jonathan M, Jartti, Tuomas, Hasegawa, Kohei,

Abstract: Although bronchiolitis is generally considered a single disease, recent studies suggest heterogeneity. We aimed to identify severe bronchiolitis profiles using a clustering approach. We analysed data from two prospective, multicentre cohorts of children younger than 2 years hospitalised with bronchiolitis, one in the USA (2007-2010 winter seasons, n=2207) and one in Finland (2008-2010 winter seasons, n=408). Severe bronchiolitis profiles were determined by latent class analysis, classifying children based on clinical factors and viral aetiology. In the US study, four profiles were identified. ….. The observed heterogeneity has important implications for future research on the aetiology, management and long-term outcomes of bronchiolitis, such as future risk of childhood asthma. **[Abstract shoretened]**

Title: The severity of acute bronchiolitis in infants was associated with quality of life nine months later
Citation: Acta Paediatrica, International Journal of Paediatrics, July 2016, vol./is. 105/7(834-841)
Author(s): Rolfsjord L.B., Skjerven H.O., Carlsen K.-H., Mowinckel P., Bains K.E.S.,.

Abstract: Aim Acute bronchiolitis in infancy increases the risk of later asthma and reduced health-related quality of life (QoL). We aimed to see whether the severity of acute bronchiolitis in the first year of life was associated with QoL nine months later. Methods The parents of 209 of 404 of children hospitalised for acute bronchiolitis in eight paediatric departments in south-east Norway at a mean four months of age (range 0-12 months) completed the Infant/Toddler Quality of Life Questionnaire sent by mail nine months after the acute illness. …. Conclusion The severity of acute bronchiolitis in infants was associated with reduced QoL nine months later. **[Abstract shortened]**

Title: Acute viral bronchiolitis: Physician perspectives on definition and clinically important outcomes
Citation: Pediatric Pulmonology, July 2016, vol./is. 51/7(724-732), 8755-6863;
Author(s): Fernandes R.M., Andrade M.G., Constant C., Malveiro D., Magalhaes M.

Abstract: Background: Two key limitations hamper intervention research in bronchiolitis: the absence of a clear definition of disease, and the heterogeneous choice of outcome measures in current clinical trials. We assessed how paediatricians and general practitioners (GPs) perceived definition and clinically important outcomes in bronchiolitis. Methods: A nationwide online survey (ABBA study) was conducted through the Portuguese Society of Paediatrics and GPs' mailing lists. We assessed agreement with statements on bronchiolitis definition, and participants were asked to score the relative importance of several outcomes**[….]**Our results highlight the need for a robust standardized definition of acute bronchiolitis in infants and support the development of a core outcome set for future clinical trials. **[Abstract shortened]**

Title: The fecal microbiota profile and bronchiolitis in infants
Citation: Pediatrics, July 2016, vol./is. 138/1(no pagination)
Author(s): Hasegawa K., Linnemann R.W., Mansbach J.M., Ajami N.J., Espinola J.A.,

Abstract: BACKGROUND: Little is known about the association of gut microbiota, a potentially modifiable factor, with bronchiolitis in infants. We aimed to determine the association of fecal microbiota with bronchiolitis in infants. METHODS: We conducted a case-control study. As a part of multicenter prospective study, we collected stool samples from 40 infants hospitalized with bronchiolitis**[….]**CONCLUSIONS: In this case-control study, we identified 4 distinct fecal microbiota profiles in infants. The Bacteroides-dominant profile was associated with a higher likelihood of bronchiolitis. **[Abstract shortened]**

Title: Do bacteria in the gut set the stage for who gets viral bronchiolitis and its severity?
Citation: Pediatrics, July 2016, vol./is. 138/1(no pagination)
Author(s): Seed P.C.

Title: Bronchiolitis and pulse oximetry choosing wisely with a technological pandora's box
Citation: JAMA Pediatrics, June 2016, vol./is. 170/6(531-532), 2168-6203 (June 2016)
Author(s): Bajaj L., Zorc J.J.

Title: Association between hypertonic saline and hospital length of stay in acute viral bronchiolitis: A reanalysis of 2 meta-analyses
Citation: JAMA Pediatrics, June 2016, vol./is. 170/6(577-584), 2168-6203 (June 2016)
Author(s): Brooks C.G., Harrison W.N., Ralston S.L.

Abstract: IMPORTANCE: Two previous meta-analyses of nebulized hypertonic saline (HS) on hospital length of stay (LOS) in acute viral bronchiolitis have suggested benefit. Neither study fully addressed the issue of excessive heterogeneity in the cohort of studies, indicating that it may be inappropriate to combine such dissimilar studies to estimate a common treatment effect. OBJECTIVE: To reanalyze the existing data set for sources of heterogeneity to delineate the population most likely to benefit from HS. DATA SOURCES: We used the previously analyzed cohort of randomized trials from 2 published meta-analyses comparing HS with normal saline (or, in 1 case, with standard of care) in infants hospitalized for bronchiolitis. We also repeated the search strategy used by the most recent Cochrane Review in the Medline database through September 2015**[….]**CONCLUSIONS AND RELEVANCE: Prior analyses were driven by an outlier population and unbalanced treatment groups in positive trials. Once heterogeneity was accounted for, the data did not support the use of HS to decrease LOS in infants hospitalized with bronchiolitis.
[Abstract shortened]

Title: Serum levels of 25(OH) vitamin D and immunoglobulin E in infants with bronchiolitis
Citation: Egyptian Pediatric Association Gazette, June 2016, vol./is. 64/2(86-90),
Author(s): Hassanein B.E.D.M., Soliman D.R., Fayed S.M.A.E., Suleiman M.M.M.

Abstract: Vitamin D status has a great effect on respiratory health throughout the lifespan. The aim of this study was to estimate and find the relationship between both 25(OH) vitamin D and immunoglobulin E serum levels and bronchiolitis in infancy. Methods: We quantified serum 25(OH) D and serum immunoglobulin E using (ELISA) in 50 infants with bronchiolitis and 31 healthy controls of matched age and sex. **[...]**Conclusions: Serum 25(OH) vitamin D was found in decreased quantities in infants with bronchiolitis and it was negatively correlated with serum IgE, suggesting that vitamin D may play a role in the pathogenesis of bronchiolitis. **[Abstract shortened]**

Title: Results of a first-in-man study of mesenchymal stem cell therapy for bronchiolitis obliterans syndrome
Citation: Cytotherapy, June 2016, vol./is. 18/6 SUPPL. 1(S16)
Author(s): Chambers D., Enever D., Lawrence S., Lawson N., Yerkovich S., Sparks L.,

Abstract: Introduction: Bone marrow derived mesenchymal stem cells (MSC) represent an attractive cellular therapeutic target given their immunosuppressive and tolerogenic properties and relative immune privilege. Preclinical studies and human trials in graft versus host disease suggest potential efficacy in bronchiolitis obliterans syndrome (BOS). The purpose of this dual centre, phase 1 study (www.clinicaltrials.gov NCT01175655) was to explore the feasibility and safety of delivery of allogeneic MSC in patients with BOS complicating lung transplantation**[...]**Conclusion: Infusion of allogeneic bone marrow-derived MSC is feasible and appears safe in patients with BOS. As a result of this study, the Australian Lung Transplant Collaborative will be commencing a phase 2 randomised controlled trial to assess the efficacy of MSC therapy in patients with new-onset BOS (total n = 82) in 2016. (Figure presented). **[Abstract shortened]**

Title: Development and validation of a new clinical scale for infants with acute respiratory infection: The resvinet scale
Citation: PLoS ONE, June 2016, vol./is. 11/6(no pagination), 1932-6203 (June 2016)
Author(s): Justicia-Grande A.J., Pardo-Seco J., Cebey-Lopez M., Vilanova-Trillo L.,

Abstract: Background and Aims A properly validated scoring system allowing objective categorization of infants with acute respiratory infections (ARIs), avoiding the need for in-person assessment and that could also be used by non-health professionals is currently not available. We aimed to develop a new clinical assessment scale meeting these specifications**[....]**Conclusions The ReSVinet scale may be useful and reliable in the evaluation of infants with ARI, particularly acute bronchiolitis, even with data obtained from medical records and when employed by parents. Although further studies are necessary, ReSVinet scale already complies with more score validation criteria than the vast majority of the alternatives currently available and used in the clinical practice. **[Abstract shortened]**

Title: Diagnosis and management of bronchiolitis obliterans syndrome following lung or hematopoietic cell transplantation
Citation: Expert Review of Respiratory Medicine, June 2016, vol./is. 10/6(599-602)
Author(s): Meyer K.C.
Language: English

Title: The severity of acute bronchiolitis in infants was associated with quality of life nine months later.
Citation: Acta paediatrica (Oslo, Norway : 1992), Jul 2016, vol. 105, no. 7, p. 834-841,
Author(s): Rolfsjord, Leif Bjarte, Skjerven, Håvard Ove, Carlsen, Kai-Håkon,

Abstract: Acute bronchiolitis in infancy increases the risk of later asthma and reduced health-related quality of life (QoL). We aimed to see whether the severity of acute bronchiolitis in the first year of life was associated with QoL nine months later. The parents of 209 of 404 of children hospitalised for acute bronchiolitis in eight paediatric departments in south-east Norway at a mean four months of age (range 0-12 months) completed the Infant/Toddler Quality of Life Questionnaire sent by mail nine months after the acute illness. **[….]**The severity of acute bronchiolitis in infants was associated with reduced QoL nine months later. **[Abstract shortened**

Title: The Fecal Microbiota Profile and Bronchiolitis in Infants.
Citation: Pediatrics, Jul 2016, vol. 138, no. 1, 1098-4275 (July 2016)
Author(s): Hasegawa, Kohei, Linnemann, Rachel W, Mansbach, Jonathan M, Ajami, Nadim J, Espinola, Janice A, Petrosino, Joseph F, Piedra, Pedro A, Stevenson, Michelle D, Sullivan, Ashley F, Thompson, Amy D, Camargo, Carlos A

Abstract: Little is known about the association of gut microbiota, a potentially modifiable factor, with bronchiolitis in infants. We aimed to determine the association of fecal microbiota with bronchiolitis in infants. We conducted a case-control study. As a part of multicenter prospective study, we collected stool samples from 40 infants hospitalized with bronchiolitis. We concurrently enrolled 115 age-matched healthy controls. By applying 16S rRNA gene sequencing and an unbiased clustering approach to these 155 fecal samples, we identified microbiota profiles and determined the association of microbiota profiles with likelihood of bronchiolitis**[….]**In this case-control study, we identified 4 distinct fecal microbiota profiles in infants. The Bacteroides-dominant profile was associated with a higher likelihood of bronchiolitis. **[Abstract shortened]**

Title: Do Bacteria in the Gut Set the Stage for Who Gets Viral Bronchiolitis and Its Severity?
Citation: Pediatrics, Jul 2016, vol. 138, no. 1, 1098-4275 (July 2016)
Author(s): Seed, Patrick C

Respiratory Syncytial Virus

Title: In Hot Pursuit of the First Vaccine Against Respiratory Syncytial Virus.
Citation: Yonsei medical journal, Jul 2016, vol. 57, no. 4, p. 809-816
Author(s): Kim, Joo Young, Chang, Jun

Abstract: Human respiratory syncytial virus (RSV) is the leading cause of severe lower respiratory tract infection, such as bronchiolitis, bronchitis, or pneumonia, in both infants and the elderly. Despite the global burden of diseases attributable to RSV infection, no

clinically approved vaccine is available, and a humanized monoclonal antibody for prophylaxis is not readily affordable in developing countries. There are several hurdles to the successful development of RSV vaccines: immune-vulnerable target populations such as premature infants, pregnant women, and immunocompromised people; safety concerns associated with vaccine-enhanced diseases; repeated infection; and waning memory. To develop successful strategies for the prevention of RSV infection, it is necessary to understand the protective and pathologic roles of host immune responses to RSV infection. In this review, we will summarize the positive and negative relationship between RSV infection and host immunity and discuss strategies for the development of the first successful RSV vaccine.

Title: Detection of respiratory syncytial virus using direct fluorescent antibody assay in paediatric patients with acute respiratory tract infection
Citation: Journal of Clinical and Diagnostic Research, June 2016, vol./is. 10/6(DC10-DC12),
Author(s): Bhandary R., Boloor R.

Abstract: Introduction: Severe Respiratory Syncytial Virus (RSV) pulmonary disease manifesting as bronchiolitis and pneumonia continues to play a major role in the childhood mortality and morbidity. Hence the present study was undertaken to evaluate the prevalence of RSV among hospitalized children presenting with Acute Respiratory Tract Infection (ARTI) and its correlation with risk factors. Aim: To determine the occurrence of RSV related respiratory tract infection in paediatric patients and to access the risk factors and clinical features associated. .**[.....]**. Conclusion: RSV infection is a significant cause of morbidity among children presenting with ARTI. In resource limited countries DFA can be used as an important tool for rapid detection of RSV and can potentially eliminate prolonged hospitalization and unnecessary use of antibiotics. .**[Abstract shortened]**

Title: Respiratory syncytial virus and rhinovirus severe bronchiolitis are associated with distinct nasopharyngeal microbiota
Citation: Journal of Allergy and Clinical Immunology, June 2016, vol./is. 137/6(1909-1913e4)
Author(s): Mansbach J.M., Hasegawa K., Henke D.M., Ajami N.J., Petrosino J.F.,

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Title: Novel respiratory syncytial virus-like particle vaccine composed of the postfusion and prefusion conformations of the F glycoprotein
Citation: Clinical and Vaccine Immunology, June 2016, vol./is. 23/6(451-459)
Author(s): Cimica V., Boigard H., Bhatia B., Fallon J.T., Alimova A., Gottlieb P.,.

Abstract: Respiratory syncytial virus (RSV) is the leading cause of severe respiratory disease in infants and children and represents an important global health burden for the elderly and the immunocompromised. Despite decades of research efforts, no licensed vaccine for RSV is available. We have developed virus-like particle (VLP)-based RSV vaccines assembled with the human metapneumovirus (hMPV) matrix protein (M) as the structural scaffold and the RSV fusion glycoprotein (F) in either the postfusion or prefusion conformation as its prime surface immunogen. Vaccines were composed of postfusion F, prefusion F, or a combination of the two conformations and formulated with a squalene-based oil emulsion as adjuvant. Immunization with these VLP vaccines afforded full protection against RSV infection and prevented detectable viral replication in the mouse lung after challenge. Analyses of lung

cytokines and chemokines showed that VLP vaccination mostly induced the production of gamma interferon (IFN-gamma), a marker of the Th1-mediated immune response, which is predominantly required for viral protection. Conversely, immunization with a formalin-inactivated RSV (FI-RSV) vaccine induced high levels of inflammatory chemokines and cytokines of the Th2- and Th17-mediated types of immune responses, as well as severe lung inflammation and histopathology. The VLP vaccines showed restricted production of these immune mediators and did not induce severe bronchiolitis or perivascular infiltration as seen with the FI-RSV vaccine. Remarkably, analysis of the serum from immunized mice showed that the VLP vaccine formulated using a combination of postfusion and prefusion F elicited the highest level of neutralizing antibody and enhanced the Th1-mediated immune response.

Group A strep

Title: International circumpolar surveillance interlaboratory quality control program for emm typing of Streptococcus pyogenes, 2011-2015.
Citation: Diagnostic microbiology and infectious disease, Aug 2016, vol. 85, no. 4, p. 398-400, 1879-0070 (August 2016)
Author(s): Rudolph, Karen, Martin, Irene, Demczuk, Walter, Kakulphimp, Jocelyne,

Abstract: In 2011, an interlaboratory quality control (QC) program for emm typing group A streptococci (GAS) was incorporated into existing international circumpolar surveillance QC programs. From 2011 - 2015, 35 GAS isolates were distributed to three laboratories; emm type-level concordance was 100%, while the overall sub-type level concordance was 83%.

Title: Asymptomatic Group A Streptococcus carriage in children with recurrent tonsillitis and tonsillar hypertrophy.
Citation: International journal of pediatric otorhinolaryngology, Jul 2016, vol. 86, p. 57-59,
Author(s): Pontin, Isabela P Olivetti, Sanchez, Daniela Cristina Janolli,

Abstract: Group A Streptococcus (GAS) is the most important bacterial cause of acute tonsillitis in children. Some children are chronic GAS carriers, and this carriage is poorly understood. We determined the frequency of GAS detection using a rapid antigen detection test in pediatric patients with indications for tonsillectomy due to adenotonsillar hypertrophy or recurrent GAS infections. Seventy-two patients underwent a tonsil swab for a rapid antigen detection test. The GAS rapid antigen detection test was positive in 18.1% of children. GAS was not associated with sex, age or previous history of recurrent tonsillitis. Also, the prevalence of GAS was similar between patients with either recurrent tonsillitis or tonsil hypertrophy. In our study, the GAS carriage rate was similar to other reports, and GAS carrier state was not correlated with recurrent tonsillitis.

Title: Patient and Parent-Reported Signs and Symptoms for Group A Streptococcal Pharyngitis.
Citation: Pediatrics, Jul 2016, vol. 138, no. 1, 1098-4275 (July 2016)

Author(s): Lindgren, Christina, Neuman, Mark I, Monuteaux, Michael C,

Abstract: Identifying symptomatic patients who are at low risk for group A streptococcal (GAS) pharyngitis could reduce unnecessary visits and antibiotic use. The accuracy with which patients and parents report signs and symptoms of GAS has not been studied. Our objectives were to measure agreement between patient or parent and physician-reported signs and symptoms of GAS and to evaluate the performance of a modified Centor score, based on patient or parent and physician reports, for identifying patients at low risk for GAS pharyngitis. Children 3 to 21 years old presenting to a single tertiary care emergency department between October 2013 and January 2015 were included if they complained of a sore throat and were tested for GAS. Patients or parents and physicians completed surveys assessing signs and symptoms to determine a modified age-adjusted Centor score for GAS. We evaluated the overall agreement and κ between patient or parent and physician-reported signs and symptoms and compared the performance of the scores based on assessments by patients or parents and physicians and the risk of GAS. Of 320 patients enrolled, 107 (33%) tested GAS positive. Agreement was higher for symptoms (fever [agreement = 82%, κ = 0.64] and cough [72%, 0.45]) than for signs (exudate [80%, 0.41] and tender cervical nodes [73%, 0.18]). Agreement was highest when no signs and symptoms contained in the Centor score were present (94%, κ = 0.61). The proportion of patients testing GAS positive rose as the modified Centor score increased. For identifying GAS pharyngitis, patients or parents and physicians showed moderate to substantial agreement for 3 of 4 key pharyngitis signs and symptoms.

Title: Common Questions About Streptococcal Pharyngitis.
Citation: American family physician, Jul 2016, vol. 94, no. 1, p. 24-31
Author(s): Kalra, Monica G, Higgins, Kim E, Perez, Evan D

Abstract: Group A beta-hemolytic streptococcal (GABHS) infection causes 15% to 30% of sore throats in children and 5% to 15% in adults, and is more common in the late winter and early spring. The strongest independent predictors of GABHS pharyngitis are patient age of five to 15 years, absence of cough, tender anterior cervical adenopathy, tonsillar exudates, and fever. To diagnose GABHS pharyngitis, a rapid antigen detection test should be ordered in patients with a modified Centor or FeverPAIN score of 2 or 3. First-line treatment for GABHS pharyngitis includes a 10-day course of penicillin or amoxicillin. Patients allergic to penicillin can be treated with firstgeneration cephalosporins, clindamycin, or macrolide antibiotics. Nonsteroidal anti-inflammatory drugs are more effective than acetaminophen and placebo for treatment of fever and pain associated with GABHS pharyngitis; medicated throat lozenges used every two hours are also effective. Corticosteroids provide only a small reduction in the duration of symptoms and should not be used routinely.

Title: Whole genome sequencing reveals extensive community-level transmission of group A Streptococcus in remote communities.
Citation: Epidemiology and infection, Jul 2016, vol. 144, no. 9, p. 1991-1998,
Author(s): Bowen, A C, Harris, T, Holt, D C, Giffard, P M, Carapetis, J R, Campbell, P T,

Abstract: Impetigo is common in remote Indigenous children of northern Australia, with the primary driver in this context being Streptococcus pyogenes [or group A Streptococcus

(GAS)]. To reduce the high burden of impetigo, the transmission dynamics of GAS must be more clearly elucidated. We performed whole genome sequencing on 31 GAS isolates collected in a single community from children in 11 households with ⩾2 GAS-infected children. We aimed to determine whether transmission was occurring principally within households or across the community. The 31 isolates were represented by nine multilocus sequence types and isolates within each sequence type differed from one another by only 0-3 single nucleotide polymorphisms. There was evidence of extensive transmission both within households and across the community. Our findings suggest that strategies to reduce the burden of impetigo in this setting will need to extend beyond individual households, and incorporate multi-faceted, community-wide approaches.

Title: Interferon α-Enhanced Clearance of Group A Streptococcus Despite Neutropenia.
Citation: The Journal of infectious diseases, Jul 2016, vol. 214, no. 2, p. 321-328,
Author(s): Uchiyama, Satoshi, Keller, Nadia, Schlaepfer, Erika, Grube, Christina,

Abstract: Neutrophils and monocytes are crucial for controlling bacterial infections. More-frequent bacterial infections are accordingly encountered in neutropenic patients undergoing chemotherapy. This is not the case for pegylated interferon α (IFN-α)-induced neutropenia. We hypothesized that IFN-α induces a compensatory innate antibacterial state that prevents bacterial infections despite the neutropenia. To investigate whether patients with hepatitis C virus infection treated with IFN-α killed group A Streptococcus (GAS) better than before initiating therapy, whole blood was used to perform ex vivo GAS killing assays before, during, and after IFN-α therapy. We found that IFN-α therapy enhanced GAS killing in whole blood ex vivo despite the decreased neutrophil and monocyte numbers during IFN-α therapy. IFN-α also boosted neutrophil- and monocyte-mediated GAS killing in vitro. Underlying mechanisms included increased production of the antibacterial properdin, a regulator of the complement activation, as well as reactive oxygen species. These findings help to explain the rather discrepant facts of neutropenia but preserved antibacterial immune defenses in patients treated with IFN-α.

Title: Structure-activity relationship of lipid core peptide-based Group A Streptococcus vaccine candidates.
Citation: Bioorganic & medicinal chemistry, Jul 2016, vol. 24, no. 14, p. 3095-3101
Author(s): Chan, Amy, Hussein, Waleed M, Ghaffar, Khairunnisa Abdul, Marasini,

Abstract: Infection with Group A Streptococcus (GAS) can result in a range of different illnesses, some of which are fatal. Currently, our efforts to develop a vaccine against GAS focuses on the lipid core peptide (LCP) system, a subunit vaccine containing a lipoamino acid (LAA) moiety which allows the stimulation of systemic antibody activity. In the present study, a peptide (J14) representing the B-cell epitope from the GAS M protein was incorporated alongside a universal T-helper epitope (P25) in four LCP constructs of different spatial orientation or LAA lengths. Through structure-activity studies, it was discovered that while the alteration of the LCP orientation had a weaker effect on immunostimulation, increasing the LAA side chain length within the construct increased antibody responses in murine models. Furthermore, the mice immunised with the lead LCP construct were also able to maintain antibody activity throughout the course of five months. These findings highlight the importance of LAA moieties in the development of intranasal peptide vaccines

and confirmed that its side chain length has an effect on the immunogenicity of the structure.
discoveries.

Salmonella

Title: Assessment of altered binding specificity of bacteriophage for ciprofloxacin-induced antibiotic-resistant Salmonella Typhimurium.
Citation: Archives of microbiology, Aug 2016, vol. 198, no. 6, p. 521-529
Author(s): Kim, Jeongjin, Jo, Ara, Ding, Tian, Lee, Hyeon-Yong, Ahn, Juhee

Abstract: This study describes a new effort toward understanding the interaction mechanisms between antibiotic-resistant Salmonella Typhimurium and phages. The antibiotic susceptibility, β-lactamase activity, bacterial motility, gene expression, and lytic activity were evaluated in ciprofloxacin-induced antibiotic-sensitive Salmonella Typhimurium (ASST(CIP)) and ciprofloxacin-induced antibiotic-resistant S. Typhimurium (ARST(CIP)), which were compared to the wild-type strains (ASST(WT) and ARST(WT)). The MIC values of ampicillin, norfloxacin, chloramphenicol, and tetracycline were significantly increased to > 512, 16, 16, and 256 μg/ml, respectively, in the ARST(CIP). The lowest and highest extracellular lactamase activities were observed in ASST(WT) (6.85 μmol/min/ml) and ARST(CIP) (48.83 μmol/min/ml), respectively. The acrA, lpfE, and hilA genes were significantly upregulated by more than tenfold in both ASST(CIP) and ARST(CIP). The induction of multiple antibiotic resistance resulted from the increased efflux pump activity (AcrAB-TolC). The highest phage adsorption rates were more than 95 % for ASST(WT), ASST(CIP), and ARST(WT), while the lowest adsorption rate was 52 % for ARST(CIP) at 15 min of infection. The least lytic activity of phage was 20 % against the ARST(CIP), followed by ASST(CIP) (30 %). The adsorption rate of phage against ARST(CIP) was 52 % at 15 min of infection, which resulted in the decrease in lytic activity (12 %). Understanding the interaction of phage and bacteria is essential for the practical application of phage to control and detect antibiotic-resistant bacteria. The results provide useful information for understanding the binding specificity of phages for multiple antibiotic-resistant pathogens.

Title: A reduced population of CD103⁺CD11b⁺ dendritic cells has a limited impact on oral Salmonella infection
Citation: Immunology Letters, August 2016, vol./is. 176/(72-80)
Author(s): Fernandez-Santoscoy M., Wenzel U.A., Persson E., Yrlid U., Agace W.,

Abstract: CD103⁺CD11b⁺ dendritic cells (DC) are the major migratory DC subset in the small intestine lamina propria (siLP) and their survival is dependent on the transcription factor interferon regulatory factor 4 (IRF4). Mice with a DC-specific deletion of irf4 (CD11c-cre.Irf4 mice) have reduced mucosal CD103⁺CD11b⁺ DC and altered T cell differentiation to protein antigen. The influence of CD103⁺CD11b⁺ DC on oral infection with the gastrointestinal pathogen Salmonella, however, is poorly understood and is investigated here. We show that, despite being infected with Salmonella, CD11c-cre.Irf4 mice (called Cre⁺ mice) conserve the reduction in CD103⁺CD11b⁺ DC observed in naive Cre⁺ mice, particularly in the mesenteric lymph nodes (MLN) but also in the siLP at day 3 post infection. Moreover, Salmonella-infected Cre⁺ mice have a similar bacterial burden in intestinal tissues (siLP, MLN and Peyer's patches) as well as the spleen compared to infected Cre⁻ controls. The T cell compartment, including the frequency of IFN-gamma and IL-17-producing T cells, is not altered in intestinal tissues of Salmonella-infected Cre⁺ mice relative to infected Cre⁻ controls. In addition, no difference between infected Cre⁺ and Cre⁻ mice was observed in either the concentration of IL-6 or IL-17 in whole tissue lysates of siLP, MLN or Peyer's patches or in the serum concentration of Salmonella-specific IgG and IgM. Overall the data suggest that the reduction of CD103⁺CD11b⁺ DC in Cre⁺ mice has little if any impact on Salmonella burden in infected tissues or eliciting effector functions important in host survival at later stages of the infection.

Title: Whole genome sequencing provides insights into the genetic determinants of invasiveness in Salmonella Dublin.
Citation: Epidemiology and infection, Aug 2016, vol. 144, no. 11, p. 2430-2439
Author(s): Mohammed, M, Cormican, M

Abstract: Salmonella enterica subsp. enterica serovar Dublin (S. Dublin) is one of the non-typhoidal Salmonella (NTS); however, a relatively high proportion of human infections are associated with invasive disease. We applied whole genome sequencing to representative invasive and non-invasive clinical isolates of S. Dublin to determine the genomic variations among them and to investigate the underlying genetic determinants associated with invasiveness in S. Dublin. Although no particular genomic variation was found to differentiate in invasive and non-invasive isolates four virulence factors were detected within the genome of all isolates including two different type VI secretion systems (T6SS) encoded on two Salmonella pathogenicity islands (SPI), including SPI-6 (T6SSSPI-6) and SPI-19 (T6SSSPI-19), an intact lambdoid prophage (Gifsy-2-like prophage) that contributes significantly to the virulence and pathogenesis of Salmonella serotypes in addition to a virulence plasmid. These four virulence factors may all contribute to the potential of S. Dublin to cause invasive disease in humans.

Title: Intranasal Vaccination With Salmonella-Derived Serodominant Secreted Effector Protein B Associated With Gas-Filled Microbubbles Partially Protects Against Gut Infection in Mice.
Citation: The Journal of infectious diseases, Aug 2016, vol. 214, no. 3, p. 438-446,
Author(s): Pigny, Fiona, Lassus, Anne, Terrettaz, Jacques, Tranquart, François, Corthésy, Blaise, Bioley, Gilles

Abstract: Salmonella infection is an increasingly important public health problem owing to the emergence of multidrug resistance and the lack of broadly efficient vaccines. Novel strategies of vaccination are required to induce protective immune responses at mucosal surfaces and in the circulation, to limit bacteria entry and dissemination. To this aim, intranasal anti-Salmonella vaccination with an innovative formulation composed of gas-filled microbubbles and the pathogen-derived protective protein serodominant secreted effector protein B (SseB-MB) was evaluated in a mouse infection model. Intranasal application of SseB-MB induced gut and systemic immunoglobulin A, T-helper type 17 cell (Th17), and Th1 responses, all of which are associated with natural immunity against Salmonella In vaccinated mice, a significant reduction in bacterial load was observed in intestinal tissues and the spleen after an otherwise lethal oral infection. Therefore, MB serve as an efficient carrier for nasal delivery of a Salmonella antigen that results in protection upon activation of the common mucosal immune system.

Title: Implementation of Salmonella serotype determination using pulsed-field gel electrophoresis in a state public health laboratory.
Citation: Diagnostic microbiology and infectious disease, Aug 2016, vol. 85, no. 4, p. 416-418
Author(s): Bopp, Dianna J, Baker, Deborah J, Thompson, Lisa, Saylors, Amy

Abstract: We examined the use of pulsed-field gel electrophoresis (PFGE) to predict serotype for Salmonella isolates. Between 2012 and 2014 we assessed 4481 isolates, resulting in >90% assigned serotypes. PFGE is efficient for determining serotype in the majority of cases and results in expedited serotype determination, as well as cost savings.

Title: Changing Patterns in Enteric Fever Incidence and Increasing Antibiotic Resistance of Enteric Fever Isolates in the United States, 2008-2012.
Citation: Clinical infectious diseases : an official publication of the Infectious Diseases Society of America, Aug 2016, vol. 63, no. 3, p. 322-329
Author(s): Date, Kashmira A, Newton, Anna E, Medalla, Felicita, Blackstock, Anna,

Abstract: Enteric fever in the United States has been primarily associated with travel and with worrisome changes in global patterns of antimicrobial resistance. We present the first comprehensive report of National Typhoid and Paratyphoid Fever Surveillance System (NTPFS) data for a 5-year period (2008-2012). We reviewed data on laboratory-confirmed cases reported to NTPFS, and related antimicrobial susceptibility results of Salmonella Typhi and Paratyphi A isolates sent for testing by participating public health laboratories to the Centers for Disease Control and Prevention's National Antimicrobial Resistance Monitoring System laboratory. During 2008-2012, 2341 enteric fever cases were reported, 80% typhoid and 20% paratyphoid A. The proportion caused by paratyphoid A increased from 16% (2008) to 22% (2012). Foreign travel within 30 days preceding illness onset was reported by 1961 (86%) patients (86% typhoid and 92% paratyphoid A). Travel to southern Asia was common (82% for typhoid, 97% for paratyphoid A). Among 1091 (58%) typhoid and 262 (56%) paratyphoid A isolates tested for antimicrobial susceptibility, the proportion resistant to nalidixic acid (NAL-R) increased from 2008 to 2012 (Typhi, 60% to 68%; Paratyphi A, 91% to 94%). Almost all NAL-R isolates were resistant or showed decreased susceptibility to ciprofloxacin. Resistance to at least ampicillin, chloramphenicol, and trimethoprim-sulfamethoxazole (multidrug resistant [MDR]) was limited to Typhi isolates, primarily acquired in southern Asia (13%). Most MDR isolates were also NAL-R. Enteric fever in the United States is primarily associated with travel to southern Asia, and increasing resistance is adding to treatment challenges. A bivalent typhoid and paratyphoid vaccine is needed. Published by Oxford University Press for the Infectious Diseases Society of America 2016. This work is written by (a) US Government employee(s) and is in the public domain in the

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Title: Functional characterization of glucosamine-6-phosphate synthase (GlmS) in Salmonella enterica serovar Enteritidis.
Citation: Archives of microbiology, Aug 2016, vol. 198, no. 6, p. 541-549,
Author(s): Bennett, Alexis M, Shippy, Daniel C, Eakley, Nicholas, Okwumabua, Ogi,

Abstract: Salmonella is a threat to public health due to consumption of contaminated food. Screening of a transposon library identified a unique mutant that was growth and host cell binding deficient. The objective of this study was to determine the functional role of glucosamine-6-phosphate synthase (GlmS) in the biology and pathogenesis of Salmonella. To examine this, we created a glmS mutant (ΔglmS) of Salmonella and examined the effect on cell envelope integrity, growth, metabolism, and pathogenesis. Our data indicated ΔglmS was defective in growth unless media were supplemented with D-glucosamine (D-GlcN). Examination of the bacterial cell envelope revealed that ΔglmS was highly sensitive to detergents, hydrophobic antibiotics, and bile salts compared to the wild type (WT). A release assay indicated that ΔglmS secreted higher amounts of β-lactamase than the WT in culture supernatant fractions. Furthermore, ΔglmS was attenuated in cell culture models of Salmonella infection. Taken together, this study determined an important role for GlmS in the pathogenesis and biology of Salmonella.

Title: Salmonella Typhimurium and Outbreaks of Egg-Associated Disease in Australia, 2001 to 2011.
Citation: Foodborne pathogens and disease, Jul 2016, vol. 13, no. 7, p. 379-385,
Author(s): Moffatt, Cameron R M, Musto, Jennie, Pingault, Nevada, Miller, Megge,

Abstract: Salmonellosis is a significant public health problem, with eggs frequently identified as a food vehicle during outbreak investigations. Salmonella enterica serovar Typhimurium and Salmonella enterica serovar Enteritidis are the two most frequently identified causes of egg-associated disease in industrialized countries. In Australia, a comprehensive review of egg-associated outbreaks has not been previously undertaken. Using a national register of foodborne outbreaks, we undertook a descriptive review of egg-associated outbreaks between 2001 and 2011. Included in our review was additional detail from the findings of trace back investigations conducted to the farm level. Evidence classifications were developed and applied to each outbreak based on descriptive and analytical epidemiology, food safety investigations, and microbiological testing of clinical, food, and trace back-derived samples. Over the study period, the proportion of foodborne Salmonella outbreaks linked to eggs increased significantly ($p < 0.001$). In total, 166 outbreaks were identified, with 90% caused by Salmonella Typhimurium. The majority of outbreaks were linked to commercial food providers, with raw egg use the major contributing factor. These events resulted in more than 3200 cases, more than 650 hospitalizations, and at least 4 deaths. Fifty-four percent of investigations used analytical epidemiology, food microbiology, and trace back microbiology to demonstrate links between human illness and eggs. Trace back investigations identified S. enterica indistinguishable from outbreak-associated clinical or food samples on 50% of sampled egg farms. Effective control of egg-associated salmonellosis remains a challenge in Australia, with Salmonella Typhimurium dominating as the causative serotype in outbreak events. Although outbreaks predominantly occur in the settings of restaurants, the high recovery rate of indistinguishable Salmonella on epidemiologically implicated egg farms suggests that further efforts to minimize infection pressure at the primary production level are needed in Australia.

Title: Multiple Plasmids Contribute to Antibiotic Resistance and Macrophage Survival In Vitro in CMY2-Bearing Salmonella enterica.
Citation: Foodborne pathogens and disease, Jul 2016, vol. 13, no. 7, p. 398-404
Author(s): Kempf, Allen J, Hulsebus, Holly J, Akbar, Samina

Abstract: Multiple drug resistance (MDR) in bacteria represents a notable problem but if carried on plasmid their spread could become a significant threat to public health. Plasmids in members of the Enterobacteriaceae family and in particular Salmonella and Escherichia coli strains have been implicated in the spread of antibiotic resistance genes. However, the mechanisms involved in the transfer of plasmid-borne resistance genes are not fully understood. Here, we analyzed the ability of Salmonella enterica clinical isolates to transfer plasmid-borne MDR to E. coli. We also determined whether possession of an Inc A/C plasmid by a S. enterica isolate would confer increased fitness compared to an isolate not carrying the plasmid. Sixteen human and animal isolates of S. enterica were screened using a three-panel multiplex PCR assay, and simplex PCR for the blaCMY-2 gene. Using these data we selected a suitable strain as a plasmid donor for the construction of a new Salmonella strain with an Inc A/C plasmid. This allowed us to compare isogenic strains with and without the Inc A/C plasmid in multiple growth, fitness, and invasion assays. The results showed that possession of Inc A/C plasmid confers significant fitness advantage when tested in J774 macrophages as opposed to HEp-2 cells where no significant difference was found. In addition, stress assays performed in vitro showed that the possession of this large plasmid by Salmonella strains tested here does not appear to incur a significant fitness cost. Gaining a better understanding of molecular mechanisms of plasmid transfer between pathogenic bacteria will allow us to characterize the role of MDR in pathogenicity of bacteria and to identify methods to reduce the frequency of dissemination of multiple antibiotic resistance genes.

Title: Higher Storage Temperature Causes Greater Salmonella enterica Serovar Typhimurium Internal Penetration of Artificially Contaminated, Commercially Available, Washed Free Range Eggs.
Citation: Journal of food protection, Jul 2016, vol. 79, no. 7, p. 1247-1251
Author(s): Whiley, Alice, Fallowfield, Howard, Ross, Kirstin, McEvoy, Vanessa,

Abstract: Foodborne salmonellosis is a major public health concern, with contaminated eggs identified as a significant source of infection. In Australia, the most prevalent cause of salmonellosis from eggs is Salmonella enterica subsp. enterica serovar Typhimurium. This study explored the effect of temperature after 1, 7, 14, 21, and 28 days of storage on commercially available washed free range eggs, artificially contaminated with Salmonella Typhimurium on the external surface. At each time point, the external surface of the egg, the crushed eggshell, and the internal egg yolk and albumen were analyzed for Salmonella. After 28 days of storage, 25% of eggs stored at 4°C, 50% of eggs stored at 14°C, and 100% of eggs stored at 23 and 35°C were internally contaminated with Salmonella. After 1 day of storage, more than 50% of all eggs had Salmonella present in the crushed shell after the external surface had been disinfected with ethanol. This is the first study to demonstrate that refrigeration reduced the potential for Salmonella Typhimurium to penetrate the eggshell membrane and internally contaminate table eggs commercially available in Australia. It also suggests that the processes of cracking eggs may be a source of cross-contamination within the kitchen.

Title: Tiny Turtles Purchased at Pet Stores are a Potential High Risk for Salmonella Human Infection in the Valencian Region, Eastern Spain.
Citation: Vector borne and zoonotic diseases (Larchmont, N.Y.), Jul 2016, vol. 16, no. 7, p. 455-460
Author(s): Marin, Clara, Vega, Santiago, Marco-Jiménez, Francisco

Abstract: Turtles may be considered unsafe pets, particularly in households with children. This study aimed to assess Salmonella carriage by turtles in pet stores and in private ownership to inform the public of the potential health risk, enabling informed choices around pet selection. During the period between September and October 2013, 24 pet stores and 96 private owners were sampled in the Valencian Region (Eastern Spain). Salmonella identification procedure was based on ISO 6579: 2002 recommendations (Annex D). Salmonella strains were serotyped in accordance with Kauffman-White-Le-Minor technique. The rate of isolation of Salmonella was very high from pet store samples (75.0% ± 8.8%) and moderate for private owners (29.0% ± 4.6%). Serotyping revealed 18 different serotypes among two Salmonella enterica subspecies: S. enterica subsp. enterica and S. enterica subsp. diarizonae. Most frequently isolated serotypes were Salmonella Typhimurium (39.5%, 17/43) and Salmonella Pomona (9.3%, 4/43). Serotypes identified have previously been reported in turtles, and child Salmonella infections associate with pet turtle exposure. The present study clearly demonstrates that turtles in pet stores, as well as in private owners, could be a direct or indirect source of a high risk of human Salmonella infections. In addition, pet stores should advise their customers of the potential risks associated with reptile ownership.

Title: Around the world in 1,475 Salmonella geo-serotypes
Citation: Emerging Infectious Diseases, July 2016, vol./is. 22/7(1298-1302)
Author(s): Gossner C.M., Le Hello S., De Jong B., Rolfhamre P., Faensen D., Weill F.-X.,

Abstract: It's easy to remember Salmonella serotypes names, isn't it? Surely, this is because the naming system of Salmonella serotypes is by far the most scientist friendly. Traditionally, most Salmonella serotypes have been named after geographic locations. We decided to explore the geographic locations to which Salmonella serotypes refer and describe some unexpected twists in the naming scheme. We found that 93% (n = 1,475) of the 1,585 serotypes could be categorized as geo-serotypes; that is, the name refers to a geographic location. The 3 countries with the most geo-serotypes are Germany, the United Kingdom, and the United States. Other serotype names refer to the name of a person, animal, tribe, or food item or are a composite of symptoms and host. The Salmonella serotypes naming scheme has had a valuable effect on public health microbiology, and in the current era of fast development of whole-genome sequencing, it should remain a reference.

Title: Biofilm Formation and Morphotypes of Salmonella enterica subsp.arizonae Differs from Those of Other Salmonella enterica Subspecies in Isolates from Poultry Houses.
Citation: Journal of food protection, Jul 2016, vol. 79, no. 7, p. 1127-1134
Author(s): Lamas, A, Fernandez-No, I C, Miranda, J M, Vázquez, B, Cepeda, A,

Abstract: Salmonella serovars are responsible for foodborne diseases around the world. The ability to form biofilms allows microorganisms to survive in the environment. In this study, 73 Salmonella strains, belonging to four different subspecies, were isolated from poultry houses and foodstuffs and tested. Biofilm formation was measured at four different temperatures and two nutrient concentrations. Morphotypes and cellulose production were evaluated at three different temperatures. The presence of several genes related to biofilm production was also examined. All strains and subspecies of Salmonella had the ability to form biofilms, and 46.57% of strains produced biofilms under all conditions tested. Biofilm formation was strain dependent and varied according to the conditions. This is the first study to analyze biofilm formation in a wide number of Salmonella enterica subsp. arizonae strains, and no direct relationship between the high prevalence of Salmonella enterica subsp. arizonae strains and their ability to form biofilm was established. Morphotypes and cellulose production varied as the temperature changed, with 20°C being the optimum temperature for expression of the red, dry, and rough morphotype and cellulose. Salmonella enterica subsp. arizonae, whose morphotype is poorly studied, only showed a smooth and white morphotype and lacked the csgD and gcpA genes that are implicated in biofilm production. Thus, Salmonella biofilm formation under different environmental conditions is a public health problem because it can survive and advance through the food chain to reach the consumer.

Title: Extended-spectrum cephalosporin- resistant Salmonella enterica serovar heidelberg strains, the Netherlands
Citation: Emerging Infectious Diseases, July 2016, vol./is. 22/7(1257-1261)
Author(s): Liakopoulos A., Geurts Y., Dierikx C.M., Brouwer M.S.M., Kant A., Wit B.,

Abstract: Extended-spectrum cephalosporin-resistant Salmonella enterica serovar Heidelberg strains (JF6X01.0022/XbaI.0251, JF6X01.0326/XbaI.1966, JF6X01.0258/XbaI.1968, and JF6X01.0045/XbaI.1970) have been identified in the United States with pulsed-field gel electrophoresis. Our examination of isolates showed introduction of these strains in the Netherlands and highlight the need for active surveillance and intervention strategies by public health organizations.

Title: Evaluation of potential public health risk associated with waste water treatment in some halal abattoirs of Malaysia
Citation: Indian Journal of Public Health Research and Development, July 2016, vol./is. 7/3(256-261)
Author(s): Adamu M.T., Shamsul B.M.T., Desa M.N., Khairani-Bejo S.

Abstract: Background: Abattoir waste can be detrimental to humans and the environment if proper precautions are put in place. In general, the major environmental problem is linked to abattoir liquid wastes which serve as vehicle for dissemination of pathogenic microorganisms. Epidemiological investigations have implicated food and water as most common vehicle for infections cause by pathogens such as E.coli O157:H7. **[…]**Conclusion: Effectiveness of waste water treatment was found to be very low in most of the abattoirs from the assessment. .**[Abstract shortened]**

Title: The differential effects of 1,25-dihydroxyvitamin D3 on Salmonella-induced interleukin-8 and human beta-defensin-2 in intestinal epithelial cells.
Citation: Clinical and experimental immunology, Jul 2016, vol. 185, no. 1, p. 98-106
Author(s): Huang, F-C

Abstract: Salmonellosis or Salmonella, one of the most common food-borne diseases, remains a major public health problem worldwide. Intestinal epithelial cells (IECs) play an essential role in the mucosal innate immunity of the host to defend against the invasion of Salmonella by interleukin (IL)-8 and human β-defensin-2 (hBD-2). Accumulated research has unravelled important roles of vitamin D in the regulation of innate immunity. Therefore, we investigated the effects of 1,25-dihydroxyvitamin D3 (1,25D3) on Salmonella-induced innate immunity in IECs. We demonstrate that pretreatment of 1,25D3 results in suppression of Salmonella-induced IL-8 but enhancement of hBD-2, either protein secretion and mRNA expression, in IECs. Furthermore, 1,25D3 enhanced Salmonella-induced membranous recruitment of nucleotide oligomerization domain (NOD2) and its mRNA expression and activation of protein kinase B (Akt), a downstream effector of phosphoinositide 3-kinase (PI3K). Inhibition of the PI3K/Akt signal counteracted the suppressive effect of 1,25D3 on Salmonella-induced IL-8 expression, while knock-down of NOD2 by siRNA diminished the enhanced hBD-2 expression. These data suggest differential regulation of 1,25D3 on Salmonella-induced IL-8 and hBD-2 expression in IECs via PI3K/Akt signal and NOD2 protein expression, respectively. Active vitamin D-enhanced anti-microbial peptide in Salmonella-infected IECs protected the host against infection, while modulation of proinflammatory responses by active vitamin D prevented the host from the detrimental effects of overwhelming inflammation. Thus, active vitamin D-induced innate immunity in IECs enhances the host's protective mechanism, which may provide an alternative therapy for invasive Salmonella infection

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Title: Ciprofloxacin and ceftriaxone alter cytokine responses, but not Toll-like receptors, to Salmonella infection in vitro.
Citation: The Journal of antimicrobial chemotherapy, Jul 2016, vol. 71, no. 7, p. 1826-1833
Author(s): Anuforom, Olachi, Wallace, Graham R, Buckner, Michelle M C, Piddock,

Abstract: Antibiotics that enhance host natural defences to infection offer an alternative approach to treating infections. However, mechanisms underlying such processes are poorly understood. The aim of this study was to investigate the effects of clinically relevant concentrations of two antibiotics on bacterial interactions with murine macrophages. Adhesion of Salmonella Typhimurium SL1344 to and invasion by Salmonella Typhimurium SL1344 of antibiotic-treated or untreated J774 murine macrophages were measured using a tissue culture infection model. Expression of genes central to the Toll-like receptor (TLR) signalling pathway of macrophages infected with Salmonella was analysed using the RT(2) Profiler PCR Array. Cytokine production was measured by ELISA. Adhesion of Salmonella Typhimurium SL1344 to J774 macrophage monolayers was increased when macrophages were exposed to ciprofloxacin and ceftriaxone, while invasion was decreased by ciprofloxacin. Expression of IL-1β and TNF-α mRNA was greater in SL1344-infected macrophages that had been treated with ciprofloxacin or ceftriaxone than in macrophages exposed to antibiotics alone or SL1344 alone. TLR mRNA was down-regulated by SL1344 infection, a response that was not altered by antibiotic pretreatment. Clinically relevant concentrations of two antibiotics differentially enhanced the response of immune cells and their interaction with bacteria, increasing bacterial adhesion to macrophages and increasing cytokine production. As increased expression of IL-1β fosters apoptosis of Salmonella-infected macrophages and clearance by neutrophils, the immunomodulatory potential of these antibiotics may explain, in part, why these two drugs continue to be used to treat salmonellosis successfully.

Title: Protein turnover analysis in Salmonella Typhimurium during infection by dynamic SILAC, Topograph, and quantitative proteomics.
Citation: Journal of basic microbiology, Jul 2016, vol. 56, no. 7, p. 801-811
Author(s): Wang, Zhe, Han, Qiang-Qiang, Zhou, Mao-Tian, Chen, Xi, Guo, Lin

Abstract: Protein turnover affects protein abundance and phenotypes. Comprehensive investigation of protein turnover dynamics has the potential to provide substantial information about gene expression. Here we report a large-scale protein turnover study in Salmonella Typhimurium during infection by quantitative proteomics. Murine macrophage-like RAW 264.7 cells were infected with SILAC labeled Salmonella. Bacterial cells were extracted after 0, 30, 60, 120, and 240 min. Mass spectrometry analyses yielded information about Salmonella protein turnover dynamics and a software program named Topograph was used for the calculation of protein half lives. The half lives of 311 proteins from intracellular Salmonella were obtained. For bacteria cultured in control medium (DMEM), the half lives for 870 proteins were obtained. The calculated median of protein half lives was 69.13 and 99.30 min for the infection group and the DMEM group, respectively, indicating an elevated protein turnover at the initial stage of infection. Gene ontology analyses revealed that a number of protein functional groups were significantly regulated by infection, including proteins involved in ribosome, periplasmic space, cellular amino acid metabolic process, ion binding, and catalytic activity. The half lives of proteins involved in purine metabolism pathway were found to be significantly shortened during infection

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Title: Use of Attenuated but Metabolically Competent Salmonella as a Probiotic To Prevent or Treat Salmonella Infection.
Citation: Infection and immunity, Jul 2016, vol. 84, no. 7, p. 2131-2140
Author(s): Sabag-Daigle, Anice, Blunk, Henry M, Gonzalez, Juan F, Steidley, Brandi L,

Abstract: Salmonella enterica is among the most burdensome of foodborne disease agents. There are over 2,600 serovars that cause a range of disease manifestations ranging from enterocolitis to typhoid fever. While there are two vaccines in use in humans to protect against typhoid fever, there are none that prevent enterocolitis. If vaccines preventing enterocolitis were to be developed, they would likely protect against only one or a few serovars. In this report, we tested the hypothesis that probiotic organisms could compete for the preferred nutrient sources of Salmonella and thus prevent or treat infection. To this end, we added the fra locus, which encodes a utilization pathway for the Salmonella-specific nutrient source fructose-asparagine (F-Asn), to the probiotic bacterium Escherichia coli Nissle 1917 (Nissle) to increase its ability to compete with Salmonella in mouse models. We also tested a metabolically competent, but avirulent, Salmonella enterica serovar Typhimurium mutant for its ability to compete with wild-type Salmonella The modified Nissle strain became more virulent and less able to protect against Salmonella in some instances. On the other hand, the modified Salmonella strain was safe and effective in preventing infection with wild-type Salmonella While we tested for efficacy only against Salmonella Typhimurium, the modified Salmonella strain may be able to compete metabolically with most, if not all, Salmonella serovars, representing a novel approach to control of this pathogen.

Title: The differential effects of 1,25-dihydroxyvitamin D3 on Salmonella-induced interleukin-8 and human beta-defensin-2 in intestinal epithelial cells.
Citation: Clinical and experimental immunology, Jul 2016, vol. 185, no. 1, p. 98-106
Author(s): Huang, F-C

Abstract: Salmonellosis or Salmonella, one of the most common food-borne diseases, remains a major public health problem worldwide. Intestinal epithelial cells (IECs) play an essential role in the mucosal innate immunity of the host to defend against the invasion of Salmonella by interleukin (IL)-8 and human β-defensin-2 (hBD-2). Accumulated research has unravelled important roles of vitamin D in the regulation of innate immunity. Therefore, we investigated the effects of 1,25-dihydroxyvitamin D3 (1,25D3) on Salmonella-induced innate immunity in IECs. We demonstrate that pretreatment of 1,25D3 results in suppression of Salmonella-induced IL-8 but enhancement of hBD-2, either protein secretion and mRNA expression, in IECs. Furthermore, 1,25D3 enhanced Salmonella-induced membranous recruitment of nucleotide oligomerization domain (NOD2) and its mRNA expression and activation of protein kinase B (Akt), a downstream effector of phosphoinositide 3-kinase (PI3K). Inhibition of the PI3K/Akt signal counteracted the suppressive effect of 1,25D3 on Salmonella-induced IL-8 expression, while knock-down of NOD2 by siRNA diminished the enhanced hBD-2 expression. These data suggest differential regulation of 1,25D3 on Salmonella-induced IL-8 and hBD-2 expression in IECs via PI3K/Akt signal and NOD2 protein expression, respectively. Active vitamin D-enhanced anti-microbial peptide in Salmonella-infected IECs protected the host against infection, while modulation of proinflammatory responses by active vitamin D prevented the host from the detrimental effects of overwhelming inflammation. Thus, active vitamin D-induced innate immunity in IECs enhances the host's protective mechanism, which may provide an alternative therapy for invasive Salmonella infection

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Title: Assessing the probability of infection by Salmonella due to sewage sludge use in agriculture under several exposure scenarios for crops and soil ingestion
Citation: Science of the Total Environment, October 2016, vol./is. 568/(66-74)
Author(s): Krzyzanowski F., de Souza Lauretto M., Nardocci A.C., Sato M.I.Z.

Abstract: A deeper understanding about the risks involved in sewage sludge practice in agriculture is required. The aims of the present study were to determine the annual risk of infection of consuming lettuce, carrots and tomatoes cultivated in soil amended with sewage sludge. The risk to agricultural workers of accidental ingestion of sludge or amended soil was also investigated.A Quantitative Microbial Risk Assessment was conducted based on Salmonella concentrations from five WWTPs were used to estimate the probability of annual infection associated with crops and soil ingestion. The risk of infection was estimated for nine exposure scenarios considering concentration of the pathogen, sewage sludge dilution in soil, variation of Salmonella concentration in soil, soil attachment to crops, seasonal average temperatures, hours of post-harvesting exposure, Salmonella regrowth in lettuce and tomatoes, Salmonella inhibition factor in carrots, crop ingestion and frequency of exposure, sludge/soil ingestion by agricultural workers and frequency of exposure. Annual risks values varied across the scenarios evaluated. Highest values of annual risk were found for scenarios in which the variation in the concentration of Salmonella spp. in both soil and crops (scenario 1) and without variation in the concentration of Salmonella spp. in soil and variation in crops (scenario 3) ranging from 10⁻³ to 10⁻² for all groups considered. For agricultural workers, the highest annual risks of infection were found when workers applied sewage sludge to agricultural soils (2.26 x 10⁻²). Sensitivity analysis suggests that the main drivers for the estimated risks are Salmonella concentration and ingestion rate. These risk values resulted from conservative scenarios since some assumptions were derived from local or general studies. Although these scenarios can be considered conservative, the sensitivity analysis yielded the drivers of the risks, which can be useful for managing risks from the fresh products chain with stakeholders' involvement.

Title: Presence of animal feeding operations and community socioeconomic factors impact salmonellosis incidence rates: An ecological analysis using data from the Foodborne Diseases Active Surveillance Network (FoodNet), 2004-2010
Citation: Environmental Research, October 2016, vol./is. 150/(166-172)
Author(s): Shaw K.S., Cruz-Cano R., Jiang C., Malayil L., Blythe D., Ryan P., Sapkota A.R.

Abstract: Nontyphoidal Salmonella spp. are a leading cause of foodborne illness. Risk factors for salmonellosis include the consumption of contaminated chicken, eggs, pork and beef. Agricultural, environmental and socioeconomic factors also have been associated with rates of Salmonella infection. However, to our knowledge, these factors have not been modeled together at the community-level to improve our understanding of whether rates of salmonellosis are variable across communities defined by differing factors. To address this knowledge gap, we obtained data on culture-confirmed Salmonella Typhimurium, S. Enteritidis, S. Newport and S. Javiana cases (2004-2010; n=14,297) from the Foodborne Diseases Active Surveillance Network (FoodNet), and socioeconomic, environmental and agricultural data from the 2010 Census of Population and Housing, the 2011 American Community Survey, and the 2007 U.S. Census of Agriculture. We linked data by zip code and derived incidence rate ratios using negative binomial regressions. Multiple community-level factors were associated with salmonellosis rates; however, our findings varied by state. For example, in Georgia (Incidence Rate Ratio (IRR)=1.01; 95% Confidence Interval (CI)=1.005-1.015) Maryland (IRR=1.01; 95% CI=1.003-1.015) and Tennessee (IRR=1.01; 95% CI=1.002-1.012), zip codes characterized by greater rurality had higher rates of S. Newport infections. The presence of broiler chicken operations, dairy operations and cattle operations in a zip code also was associated with significantly higher rates of infection with at least one serotype in states that are leading producers of these animal products. For instance, in Georgia and Tennessee, rates of S. Enteritidis infection were 48% (IRR=1.48; 95% CI=1.12-

1.95) and 46% (IRR=1.46; 95% CI=1.17-1.81) higher in zip codes with broiler chicken operations compared to those without these operations. In Maryland, New Mexico and Tennessee, higher poverty levels in zip codes were associated with higher rates of infection with one or more Salmonella serotypes. In Georgia and Tennessee, zip codes with higher percentages of the population composed of African Americans had significantly higher rates of infection with one or more Salmonella serotypes. In summary, our findings show that community-level agricultural, environmental and socioeconomic factors may be important with regard to rates of infection with Salmonella Typhimurium, Enteritidis, Newport and Javiana.

Title: The differential effects of 1,25-dihydroxyvitamin D3 on Salmonella-induced interleukin-8 and human beta-defensin-2 in intestinal epithelial cells
Citation: Clinical and Experimental Immunology, July 2016, vol./is. 185/1(98-106)
Author(s): Huang F.-C.

Abstract: Salmonellosis or Salmonella, one of the most common food-borne diseases, remains a major public health problem worldwide. Intestinal epithelial cells (IECs) play an essential role in the mucosal innate immunity of the host to defend against the invasion of Salmonella by interleukin (IL)-8 and human beta-defensin-2 (hBD-2). Accumulated research has unravelled important roles of vitamin D in the regulation of innate immunity. Therefore, we investigated the effects of 1,25-dihydroxyvitamin D3 (1,25D3) on Salmonella-induced innate immunity in IECs. We demonstrate that pretreatment of 1,25D3 results in suppression of Salmonella-induced IL-8 but enhancement of hBD-2, either protein secretion and mRNA expression, in IECs. Furthermore, 1,25D3 enhanced Salmonella-induced membranous recruitment of nucleotide oligomerization domain (NOD2) and its mRNA expression and activation of protein kinase B (Akt), a downstream effector of phosphoinositide 3-kinase (PI3K). Inhibition of the PI3K/Akt signal counteracted the suppressive effect of 1,25D3 on Salmonella-induced IL-8 expression, while knock-down of NOD2 by siRNA diminished the enhanced hBD-2 expression. These data suggest differential regulation of 1,25D3 on Salmonella-induced IL-8 and hBD-2 expression in IECs via PI3K/Akt signal and NOD2 protein expression, respectively. Active vitamin D-enhanced anti-microbial peptide in Salmonella-infected IECs protected the host against infection, while modulation of proinflammatory responses by active vitamin D prevented the host from the detrimental effects of overwhelming inflammation. Thus, active vitamin D-induced innate immunity in IECs enhances the host's protective mechanism, which may provide an alternative therapy for invasive Salmonella infection.

Title: The Salmonella effector SteA binds phosphatidylinositol 4-phosphate for subcellular targeting within host cells.
Citation: Cellular microbiology, Jul 2016, vol. 18, no. 7, p. 949-969,

Author(s): Domingues, Lia, Ismail, Ahmad, Charro, Nuno, Rodríguez-Escudero, Isabel,

Abstract: Many bacterial pathogens use specialized secretion systems to deliver virulence effector proteins into eukaryotic host cells. The function of these effectors depends on their localization within infected cells, but the mechanisms determining subcellular targeting of each effector are mostly elusive. Here, we show that the Salmonella type III secretion effector SteA binds specifically to phosphatidylinositol 4-phosphate [PI(4)P]. Ectopically expressed SteA localized at the plasma membrane (PM) of eukaryotic cells. However, SteA was displaced from the PM of Saccharomyces cerevisiae in mutants unable to synthesize the local pool of PI(4)P and from the PM of HeLa cells after localized depletion of PI(4)P. Moreover, in infected cells, bacterially translocated or ectopically expressed SteA localized at the membrane of the Salmonella-containing vacuole (SCV) and to Salmonella-induced tubules; using the PI(4)P-binding domain of the Legionella type IV secretion effector SidC as probe, we found PI(4)P at the SCV membrane and associated tubules throughout Salmonella infection of HeLa cells. Both binding of SteA to PI(4)P and the subcellular localization of ectopically expressed or bacterially translocated SteA were dependent on a lysine residue near the N-terminus of the protein. Overall, this indicates that binding of SteA to PI(4)P is necessary for its localization within host cells

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Title: Higher Storage Temperature Causes Greater Salmonella enterica Serovar Typhimurium Internal Penetration of Artificially Contaminated, Commercially Available, Washed Free Range Eggs.
Citation: Journal of food protection, Jul 2016, vol. 79, no. 7, p. 1247-1251,
Author(s): Whiley, Alice, Fallowfield, Howard, Ross, Kirstin, McEvoy, Vanessa,

Abstract: Foodborne salmonellosis is a major public health concern, with contaminated eggs identified as a significant source of infection. In Australia, the most prevalent cause of salmonellosis from eggs is Salmonella enterica subsp. enterica serovar Typhimurium. This study explored the effect of temperature after 1, 7, 14, 21, and 28 days of storage on commercially available washed free range eggs, artificially contaminated with Salmonella Typhimurium on the external surface. At each time point, the external surface of the egg, the crushed eggshell, and the internal egg yolk and albumen were analyzed for Salmonella. After 28 days of storage, 25% of eggs stored at 4°C, 50% of eggs stored at 14°C, and 100% of eggs stored at 23 and 35°C were internally contaminated with Salmonella. After 1 day of storage, more than 50% of all eggs had Salmonella present in the crushed shell after the external surface had been disinfected with ethanol. This is the first study to demonstrate that refrigeration reduced the potential for Salmonella Typhimurium to penetrate the eggshell membrane and internally contaminate table eggs commercially available in Australia. It also suggests that the processes of cracking eggs may be a source of cross-contamination within the kitchen.

Title: Clustered Intracellular Salmonella enterica Serovar Typhimurium Blocks Host Cell Cytokinesis.
Citation: Infection and immunity, Jul 2016, vol. 84, no. 7, p. 2149-2158
Author(s): Santos, António J M, Durkin, Charlotte H, Helaine, Sophie, Boucrot, Emmanuel,

Abstract: Several bacterial pathogens and viruses interfere with the cell cycle of their host cells to enhance virulence. This is especially apparent in bacteria that colonize the gut epithelium, where inhibition of the cell cycle of infected cells enhances the intestinal colonization. We found that intracellular Salmonella enterica serovar Typhimurium induced the binucleation of a large proportion of epithelial cells by 14 h postinvasion and that the effect was dependent on an intact Salmonella pathogenicity island 2 (SPI-2) type 3 secretion system. The SPI-2 effectors SseF and SseG were required to induce binucleation. SseF and SseG are known to maintain microcolonies of Salmonella-containing vacuoles close to the microtubule organizing center of infected epithelial cells. During host cell division, these clustered microcolonies prevented the correct localization of members of the chromosomal passenger complex and mitotic kinesin-like protein 1 and consequently prevented cytokinesis. Tetraploidy, arising from a cytokinesis defect, is known to have a deleterious effect on subsequent cell divisions, resulting in either chromosomal instabilities or cell cycle arrest. In infected mice, proliferation of small intestinal epithelial cells was compromised in an SseF/SseG-dependent manner, suggesting that cytokinesis failure caused by S Typhimurium delays epithelial cell turnover in the intestine.

Title: A Salmonella Toxin Promotes Persister Formation through Acetylation of tRNA.
Citation: Molecular cell, Jul 2016, vol. 63, no. 1, p. 86-96
Author(s): Cheverton, Angela M, Gollan, Bridget, Przydacz, Michal, Wong, Chi T,

Abstract: The recalcitrance of many bacterial infections to antibiotic treatment is thought to be due to the presence of persisters that are non-growing, antibiotic-insensitive cells. Eventually, persisters resume growth, accounting for relapses of infection. Salmonella is an important pathogen that causes disease through its ability to survive inside macrophages. After macrophage phagocytosis, a significant proportion of the Salmonella population forms non-growing persisters through the action of toxin-antitoxin modules. Here we reveal that one such toxin, TacT, is an acetyltransferase that blocks the primary amine group of amino acids on charged tRNA molecules, thereby inhibiting translation and promoting persister formation. Furthermore, we report the crystal structure of TacT and note unique structural features, including two positively charged surface patches that are essential for toxicity. Finally, we identify a detoxifying mechanism in Salmonella wherein peptidyl-tRNA hydrolase counteracts TacT-dependent growth arrest, explaining how bacterial persisters can resume growth.

Title: Genetically Similar Isolates of Salmonella enterica Serotype Enteritidis Persistent in China for a Long-Term Period.
Citation: Journal of food science, Jul 2016, vol. 81, no. 7, p. M1778.
Author(s): Song, Qifa, Shen, Xuanyi, Yang, Yuanbin, Zhang, Danyang, Gao, Hong

Abstract: Salmonella enterica serotype Enteritidis (S. Enteritidis) is an important causative agent of nontyphoidal salmonellosis in human populations. In this study, we collected 72 S. Enteritidis strains from 2004 to 2014 in Ningbo, mid-east China. Of the 72 strains, we identified a dominant clone of 58 strains recovered from patient's feces (n = 48), blood (n = 1), pleural effusion (n = 1), chickens (n = 3), and dessert cakes (n = 5) by pulsed-field gel electrophoresis (PFGE) and variable-number of tandem repeat analysis (MLVA). The profile arrangements of MLVA were SE1-SE2-SE3-SE5-SE6-SE8-SE9: 4-4-3-11-10-1-3. These dominant strains were susceptible to ampicillin, chloramphenicol, tetracycline, ciprofloxacin, gentamicin, cefotaxime and trimethoprim-sulfamethoxazole, and resistant to nalidixic acid. Additionally, all isolates harboured virulence genes invA, sipA, sopE, and spvB when tested by PCR. Our results reveal that genetically similar S. Enteritidis strains which accounted for several outbreaks as well as blood infection and pleural cavity infection are prevalent in China for a long-term period. This situation calls for further attention in the prevention and control of foodborne disease caused by Salmonella species

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Title: Emergence of blaCTX-M-15, blaTEM-169 and blaPER-1 extended-spectrum β-lactamase genes among different Salmonella enterica serovars from human faecal samples.
Citation: Infectious diseases (London, England), Jul 2016, vol. 48, no. 7, p. 550-556
Author(s): Tajbakhsh, Mercedeh, Avini, Mohammad Yaghoobi, Alikhajeh, Jahan, Tajeddin,

Abstract: Broad-spectrum β-lactams are used for empirical therapy of severe infections with non-typhoid Salmonella serotypes; however, activities of these drugs against the strains producing different β-lactamase is not so clear. This study investigated the prevalence of β-lactamase genes among isolates of S. enterica serovars from human faecal samples and determined their diversity in activity against different β-lactams. Antimicrobial resistance of faecal isolates of S. enterica to extended-spectrum cephalosporins was analysed and MIC values were determined for the strains presenting extended-spectrum β-lactamases (ESBLs) phenotypes. The β-lactamase genes were identified by PCR and sequencing. β-lactamase activity of the Salmonella strains exhibiting ESBL phenotype was detected by biological, iodometric, spectrophotometry and nitrocefin assays. Out of 202 S. enterica isolates, ESBLs phenotype was detected among 3.4% (7/202) of the strains. blaTEM-1 and blaCTX-M-15 were among the frequent β-lactamase genes. Detection of blaTEM-169 in S. enterica serovar Typhimurium and S. enterica serovar Bredeney and blaPER-1 in S. enterica serovar Infantis was a new finding in this experiment. Location of blaCTX-M-15/blaTEM-169/blaPER-1 genes on plasmid was confirmed in a transformation experiment. While crude extracts of the enzymes from each strain showed higher activity against cephalothin and cefotaxime, the lowest activity was detected against ceftazidime. The greatest synergistic activity was seen in a strain of S. enterica that carried blaCTX-M-15 and blaPER-1 genes compared with those presenting blaCTX-M-15/blaTEM-169 or blaCTX-M-15/blaTEM-1 genotypes. The results show dissemination of ESBLs encoding genes and their combined activity among different serovars of S. enterica that are a threat for future treatment options.

Title: Attribution of Salmonella enterica serotype Hadar infections using antimicrobial resistance data from two points in the food supply system.
Citation: Epidemiology and infection, Jul 2016, vol. 144, no. 9, p. 1983-1990
Author(s): Vieira, A R, Grass, J, Fedorka-Cray, P J, Plumblee, J R, Tate, H, Cole, D J

Abstract: A challenge to the development of foodborne illness prevention measures is determining the sources of enteric illness. Microbial subtyping source-attribution models attribute illnesses to various sources, requiring data characterizing bacterial isolate subtypes collected from human and food sources. We evaluated the use of antimicrobial resistance data on isolates of Salmonella enterica serotype Hadar, collected from ill humans, food animals, and from retail meats, in two microbial subtyping attribution models. We also compared model results when either antimicrobial resistance or pulsed-field gel electrophoresis (PFGE) patterns were used to subtype isolates. Depending on the subtyping model used, 68-96% of the human infections were attributed to meat and poultry food products. All models yielded similar outcomes, with 86% [95% confidence interval (CI) 80-91] to 91% (95% CI 88-96) of the attributable infections attributed to turkey, and 6% (95% CI 2-10) to 14% (95% CI 8-20) to chicken. Few illnesses (<3%) were attributed to cattle or swine. Results were similar whether the isolates were obtained from food animals during processing or from retail meat products. Our results support the view that microbial subtyping models are a flexible and robust approach for attributing Salmonella Hadar.

Title: Resilience of the intestinal microbiota following pathogenic bacterial infection is independent of innate immunity mediated by NOD1 or NOD2.
Citation: Microbes and infection / Institut Pasteur, Jul 2016, vol. 18, no. 7-8, p. 460-471,

Author(s): Robertson, Susan J, Geddes, Kaoru, Maisonneuve, Charles

Abstract: The innate immune receptors, NOD1 and NOD2, are key regulators of intestinal homeostasis. NOD2 deficiency is linked to increased risk for Crohn's disease, a type of inflammatory bowel disease characterized by chronic inflammatory pathology and dysbiosis within resident microbial communities. However, the relationship between NOD protein-regulated immune functions and dysbiosis remains unclear. We hypothesized that the relationship between NOD1 or NOD2 deficiency and altered community structure during chronic disease may arise via NOD-dependent impairment of community resilience over time. Using the Salmonella ΔaroA model of chronic colitis with littermate mice to control for environmental influences on the microbiota, we show that NOD proteins exert a relatively minor impact on the chronic inflammatory environment and do not significantly contribute to bacterial abundance or community resilience following infection. Rather, temporal shifts in relative abundance of targeted bacterial groups correlated with inflammatory phenotype driven by presence of the pathogen and the ensuing complex immune response.

Campylobacter

Title: Role of matrix metalloproteinases in the pathogenesis of childhood gastroenteritis
Citation: Journal of Medical Virology, August 2016, vol./is. 88/8(1341-1346)
Author(s): Kawamura Y., Gotoh K., Takeuchi N., Miura H., Nishimura N., Ozaki T.,
Abstract: Matrix metalloproteinases (MMPs) and tissue inhibitors of metalloproteinases (TIMPs) have been implicated in the pathogenesis of gastrointestinal diseases, such as rotavirus gastroenteritis (GE). Kinetics of these biomarkers were examined in paired serum samples collected from bacterial enteritis patients with Campylobacter (n=2) and Salmonella (n=4) and viral GE patients with rotavirus (n=27), norovirus (n=25), and adenovirus (n=11). At the time of hospital admission, all viral GE patients demonstrated increased MMP-9 and decreased MMP-2 and TIMP-2 serum levels. In contrast to viral GE patients, serum MMP-9 levels were not elevated at the time of hospital admission but elevated at the time of discharge; serum MMP-2 and TIMP-2 levels were decreased both at the time of admission and discharge in bacterial enteritis patients. Interestingly, the kinetics of serum MMP-2, MMP-9, and TIMP-2 levels were similar among the viral GE patients but distinct from bacterial enteritis patients. Thus, the involvement of MMPs and TIMPs in the pathophysiology of gastrointestinal symptoms likely varies depending on the etiological agent. Further studies are required to verify whether the extent of the bacterial enteritis or age of the patients influences these serum biomarkers.

Title: Evaluation of Various Campylobacter-Specific Quantitative PCR (qPCR) Assays for Detection and Enumeration of Campylobacteraceae in Irrigation Water and Wastewater via a Miniaturized Most-Probable-Number-qPCR Assay.

Citation: Applied and environmental microbiology, Aug 2016, vol. 82, no. 15, p. 4743-4756,
Author(s): Banting, Graham S, Braithwaite, Shannon, Scott, Candis, Kim, Jinyong, Jeon,

Abstract: Campylobacter spp. are the leading cause of bacterial gastroenteritis worldwide, and water is increasingly seen as a risk factor in transmission. Here we describe a most-probable-number (MPN)-quantitative PCR (qPCR) assay in which water samples are centrifuged and aliquoted into microtiter plates and the bacteria are enumerated by qPCR. We observed that commonly used Campylobacter molecular assays produced vastly different detection rates. ……..The results of this study demonstrate the importance of assay validation upon data interpretation of environmental monitoring for Campylobacter when using molecular biology-based assays. Previous studies describing Campylobacter prevalence in Canada utilized primers that we have determined to be nonspecific due to their cross-amplification of Arcobacter spp. As such, Campylobacter prevalence may have been vastly overestimated in other studies. Additionally, the development of a quantitative assay described in this study will allow accurate determination of Campylobacter concentrations in environmental water samples, allowing more informed decisions to be made about water usage based on quantitative microbial risk assessment.
[Abstract shortened]

Title: Variation in the limit-of-detection of the ProSpecT Campylobacter microplate enzyme immunoassay in stools spiked with emerging Campylobacter species.
Citation: Journal of microbiological methods, Aug 2016, vol. 127, p. 236-241
Author(s): Bojanić, Krunoslav, Midwinter, Anne Camilla, Marshall, Jonathan Craig,

Abstract: Campylobacter enteritis in humans is primarily associated with C. jejuni/coli infection. The impact of other Campylobacter spp. is likely to be underestimated due to the bias of culture methods towards Campylobacter jejuni/coli diagnosis. Stool antigen tests are becoming increasingly popular and appear generally less species-specific. A review of independent studies of the ProSpecT® Campylobacter Microplate enzyme immunoassay (EIA) developed for C. jejuni/coli showed comparable diagnostic results to culture methods but the examination of non-jejuni/coli Campylobacter spp. was limited and the limit-of-detection (LOD), where reported, varied between studies. This study investigated LOD of EIA for Campylobacter upsaliensis, Campylobacter hyointestinalis and Campylobacter helveticus spiked in human stools. Multiple stools and Campylobacter isolates were used in three different concentrations (10(4)-10(9)CFU/ml) to reflect sample heterogeneity. All Campylobacter species evaluated were detectable by EIA. Multivariate analysis showed LOD varied between Campylobacter spp. and faecal consistency as fixed effects and individual faecal samples as random effects. EIA showed excellent performance in replicate testing for both within and between batches of reagents, in agreement between visual and spectrophotometric reading of results, and returned no discordance between the bacterial concentrations within independent dilution test runs (positive results with lower but not higher concentrations). This study shows how limitations in experimental procedures lead to an overestimation of consistency and uniformity of LOD for EIA that may not hold under routine use in diagnostic laboratories. Benefits and limitations for clinical practice and the influence on estimates of performance characteristics from detection of multiple Campylobacter spp. by EIA are discussed.

Title: Adaptation of Campylobacter jejuni to biocides used in the food industry affects biofilm structure, adhesion strength, and cross-resistance to clinical antimicrobial compounds.
Citation: Biofouling, Aug 2016, vol. 32, no. 7, p. 827-839, 1029-2454 (August 2016)
Author(s): Techaruvichit, Punnida, Takahashi, Hajime, Kuda, Takashi, Miya, Satoko,

Abstract: The emergence of biocide-adapted Campylobacter jejuni strains that developed into biofilms and their potential to develop clinical resistance to antimicrobial compounds was studied. C. jejuni was grown in sub-lethal concentrations of five biocides used in the food industry. C. jejuni exhibited adaptation to these biocides with increased minimum inhibitory concentrations. The 3-D structures of the biofilms produced by the biocide-adapted cells were investigated by atomic force microscopy (AFM). The results revealed marked variability in biofilm architecture, including ice-crystal-like structures. Adaptation to the biocides enhanced biofilm formation, with significant increases in biovolume, surface coverage, roughness, and the surface adhesion force of the biofilms. Adaptation to commercial biocides induced resistance to kanamycin and streptomycin. This study suggests that the inappropriate use of biocides may lead to cells being exposed to them at sub-lethal concentrations, which can result in adaptation of the pathogens to the biocides and a subsequent risk to public health.

Title: Extreme precipitation events and increased risk of campylobacteriosis in Maryland, U.S.A
Citation: Environmental Research, August 2016, vol./is. 149/(216-221)
Author(s): Soneja S., Jiang C., Romeo Upperman C., Murtugudde R., Mitchell C.S.

Abstract: Consumption of contaminated poultry, raw milk and water are significant risk factors for Campylobacter infection. Previous studies also have investigated the association between weather (temperature and precipitation) and increased risk of campylobacteriosis, but limited information exists regarding the impacts of extreme heat and precipitation events on campylobacteriosis risk, and how such risk may differentially impact coastal communities. We obtained Campylobacter case data 2002-2012; n=4804) from the Maryland Foodborne Diseases Active Surveillance Network (FoodNet). We identified extreme heat and extreme precipitation events during this time (2002-2012) using location and calendar day specific thresholds (95th percentile for extreme heat and 90th percentile for extreme precipitation) that were computed based on a 30-year baseline (1960-1989). We linked these datasets using GIS and used negative binomial generalized estimating equations adjusted for demographic confounders to calculate the association between exposure to extreme events and risk of campylobacteriosis in Maryland. We observed that a one-day increase in exposure to extreme precipitation events was associated with a 3% increase in risk of campylobacteriosis in coastal areas of Maryland (Incidence Rate Ratio (IRR): 1.03, 95% confidence interval (CI): 1.01, 1.05), but such an association was not observed in noncoastal areas. Furthermore, the risk associated with extreme precipitation events was considerably higher during La Nina periods (IRR: 1.09, 95% CI: 1.05, 1.13), while there was no evidence of elevated risk during El Nino or ENSO Neutral periods. Exposure to extreme heat events was not associated with an increased risk of campylobacteriosis, except during La Nina periods (IRR: 1.04, 95% CI: 1.01, 1.08). Extreme precipitation events could result in flooding within coastal areas that may bring water contaminated with bacterial pathogens (originating from sources such as septic systems, municipal wastewater treatment plants and concentrated animal feeding operations) into close proximity with individuals, where frequency of contact may be higher.

Title: Discussing State-of-the-Art Spatial Visualization Techniques Applicable for the Epidemiological Surveillance Data on the Example of Campylobacter spp. in Raw Chicken Meat.
Citation: Zoonoses and public health, Aug 2016, vol. 63, no. 5, p. 358-369,
Author(s): Plaza-Rodríguez, C, Appel, B, Kaesbohrer, A, Filter, M

Abstract: Within the European activities for the 'Monitoring and Collection of Information on Zoonoses', annually EFSA publishes a European report, including information related to the prevalence of Campylobacter spp. in Germany. Spatial epidemiology becomes here a fundamental tool for the generation of these reports, including the representation of prevalence as an essential element. Until now, choropleth maps are the default visualization technique applied in epidemiological monitoring and surveillance reports made by EFSA and German authorities. However, due to its limitations, it seems to be reasonable to explore alternative chart type. Four maps including choropleth, cartogram, graduated symbols and dot-density maps were created to visualize real-world sample data on the prevalence of Campylobacter spp. in raw chicken meat samples in Germany in 2011. In addition, adjacent and coincident maps were created to visualize also the associated uncertainty. As an outcome, we found that there is not a single data visualization technique that encompasses all the necessary features to visualize prevalence data alone or prevalence data together with their associated uncertainty. All the visualization techniques contemplated in this study demonstrated to have both advantages and disadvantages. To determine which visualization technique should be used for future reports, we recommend to create a dialogue between end-users and epidemiologists on the basis of sample data and charts. The final decision should also consider the knowledge and experience of end-users as well as the specific objective to be achieved with the charts.

Title: Molecular Epidemiology of Campylobacter coli Strains Isolated from Different Sources in New Zealand between 2005 and 2014.
Citation: Applied and environmental microbiology, Jul 2016, vol. 82, no. 14, p. 4363-4370
Author(s): Nohra, Antoine, Grinberg, Alex, Midwinter, Anne C, Marshall, Jonathan C,

Abstract: Campylobacteriosis is one of the most important foodborne diseases worldwide and a significant health burden in New Zealand. Campylobacter jejuni is the predominant species worldwide, accounting for approximately 90% of human cases, followed by Campylobacter coli Most studies in New Zealand have focused on C. jejuni; hence, the impact of C. coli strains on human health is not well understood. The aim of this study was to genotype C. coli isolates collected in the Manawatu region of New Zealand from clinical cases, fresh poultry meat, ruminant feces, and environmental water sources, between 2005 and 2014, to study their population structure and estimate the contribution of each source to the burden of human disease. Campylobacter isolates were identified by PCR and typed by multilocus sequence typing. C. coli accounted for 2.9% (n = 47/1,601) of Campylobacter isolates from human clinical cases, 9.6% (n = 108/1,123) from poultry, 13.4% (n = 49/364) from ruminants, and 6.4% (n = 11/171) from water. Molecular subtyping revealed 27 different sequence types (STs), of which 18 belonged to clonal complex ST-828. ST-1581 was the most prevalent C. coli sequence type isolated from both human cases (n = 12/47) and poultry (n = 44/110). When classified using cladistics, all sequence types belonged to clade 1 except ST-7774, which belonged to clade 2. ST-854, ST-1590, and ST-4009 were isolated only from human cases and fresh poultry, while ST-3232 was isolated only from human cases and ruminant sources. Modeling indicated ruminants and poultry as the main sources of C. coli human infection. We performed a molecular epidemiological study of Campylobacter coli infection in New Zealand, one of few such studies globally. This study analyzed the population genetic structure of the bacterium and included a probabilistic source attribution model covering different animal and water sources. The results are discussed in a global context.

Title: Comparing characteristics of sporadic and outbreak-associated foodborne Illnesses, United States, 2004-2011
Citation: Emerging Infectious Diseases, July 2016, vol./is. 22/7(1193-1200)
Author(s): Ebel E.D., Williams M.S., Cole D., Travis C.C., Klontz K.C., Golden N.J.,

Abstract: Outbreak data have been used to estimate the proportion of illnesses attributable to different foods. Applying outbreak-based attribution estimates to nonoutbreak foodborne illnesses requires an assumption of similar exposure pathways for outbreak and sporadic illnesses. This assumption cannot be tested, but other comparisons can assess its veracity. Our study compares demographic, clinical, temporal, and geographic characteristics of outbreak and sporadic illnesses from Campylobacter, Escherichia coli O157, Listeria, and Salmonella bacteria ascertained by the Foodborne Diseases Active Surveillance Network (FoodNet). Differences among FoodNet sites in outbreak and sporadic illnesses might reflect differences in surveillance practices. For Campylobacter, Listeria, and Escherichia coli O157, outbreak and sporadic illnesses are similar for severity, sex, and age. For Salmonella, outbreak and sporadic illnesses are similar for severity and sex. Nevertheless, the percentage of outbreak illnesses in the youngest age category was lower. Therefore, we do not reject the assumption that outbreak and sporadic illnesses are similar.

Title: Clinical relevance of infections with zoonotic and human oral species of Campylobacter.
Citation: Journal of microbiology (Seoul, Korea), Jul 2016, vol. 54, no. 7, p. 459-467
Author(s): Lee, Soomin, Lee, Jeeyeon, Ha, Jimyeong, Choi, Yukyung, Kim, Sejeong, Lee, Heeyoung, Yoon, Yohan, Choi, Kyoung-Hee

Abstract: Genus Campylobacter has been recognized as a causative bacterial agent of animal and human diseases. Human Campylobacter infections have caused more concern. Campylobacters can be classified into two groups in terms of their original host: zoonotic and human oral species. The major zoonotic species are Campylobacter jejuni and Campylobacter coli, which mostly reside in the intestines of avian species and are transmitted to humans via consumption of contaminated poultry products, thus causing human gastroenteritis and other diseases as sequelae. The other campylobacters, human oral species, include C. concisus, C. showae, C. gracilis, C. ureolyticus, C. curvus, and C. rectus. These species are isolated from the oral cavity, natural colonization site, but have potential clinical relevance in the periodontal region to varying extent. Two species, C. jejuni and C. coli, are believed to be mainly associated with intestinal diseases, but recent studies suggested that oral Campylobacter species also play a significant role in intestinal diseases. This review offers an outline of the two Campylobacter groups (zoonotic and human oral), their virulence traits, and the associated illnesses including gastroenteritis.

Title: Campylobacter in broiler slaughter samples assessed by direct count on mCCDA and Campy-Cefex agar.
Citation: Brazilian journal of microbiology : [publication of the Brazilian Society for Microbiology], Jul 2016, vol. 47, no. 3, p. 764-769, 1678-4405 (2016 Jul-Sep)
Author(s): Gonsalves, Camila Cristina, Borsoi, Anderlise, Perdoncini, Gustavo, Rodrigues,

Abstract: Campylobacter spp. cause foodborne illnesses in humans primarily through the consumption of contaminated chicken. The aim of this study was to evaluate the United States Department of Agriculture's (USDA) recommended methodology, protocol MLG 41.02, for the isolation, identification and direct plate counting of Campylobacter jejuni and C. coli samples from the broiler slaughtering process. A plating method using both mCCDA and Campy-Cefex agars is recommended to recover Campylobacter cells. It is also possible to use this method in different matrices (cloacal swabs and water samples). Cloacal swabs, samples from pre-chiller and post-chiller carcasses and samples of pre-chiller, chiller and direct supply water were collected each week for four weeks from the same flock at a slaughterhouse located in an abattoir in southern Brazil. Samples were analyzed to directly count Campylobacter spp., and the results showed a high frequency of Campylobacter spp. on Campy-Cefex agar. For the isolated species, 72% were identified as Campylobacter jejuni and 38% as Campylobacter coli. It was possible to count Campylobacter jejuni and Campylobacter coli from different samples, including the water supply samples, using the two-agar method. These results suggest that slaughterhouses can use direct counting methods with both agars and different matrices as a monitoring tool to assess the presence of Campylobacter bacteria in their products.

Title: Potential Use of Fosfomycin-Tromethamine for Treatment of Recurrent Campylobacter Species Enteritis.
Citation: Antimicrobial agents and chemotherapy, Jul 2016, vol. 60, no. 7, p. 4398-4400,
Author(s): Aguilar-Company, Juan, Los-Arcos, Ibai, Pigrau, Carles, Rodríguez-Pardo, Dolors,

Abstract: We report 2 cases of recurrent Campylobacter coli enteritis caused by macrolide- and fluoroquinolone-resistant strains in 2 patients with hypogammaglobulinemia, successfully treated with a prolonged course of fosfomycin-tromethamine with no side effects. Fosfomycin-tromethamine may be a feasible alternative therapy for recurrent enteritis caused by Campylobacter species resistant to first-line drugs.

Title: Restaurant Cooking Trends and Increased Risk for Campylobacter Infection.
Citation: Emerging infectious diseases, Jul 2016, vol. 22, no. 7, p. 1208-1215
Author(s): Jones, Anna K, Rigby, Dan, Burton, Michael, Millman, Caroline, Williams, Nicola J,

Abstract: In the United Kingdom, outbreaks of Campylobacter infection are increasingly attributed to undercooked chicken livers, yet many recipes, including those of top chefs, advocate short cooking times and serving livers pink. During 2015, we studied preferences of chefs and the public in the United Kingdom and investigated the link between liver rareness and survival of Campylobacter. We used photographs to assess chefs' ability to identify chicken livers meeting safe cooking guidelines. To investigate the microbiological safety of livers chefs preferred to serve, we modeled Campylobacter survival in infected chicken livers cooked to various temperatures. Most chefs correctly identified safely cooked livers but overestimated the public's preference for rareness and thus preferred to serve them more rare. We estimated that 19%-52% of livers served commercially in the United Kingdom fail to reach 70°C and that predicted Campylobacter survival rates are 48%-98%. These findings indicate that cooking trends are linked to increasing Campylobacter infections.

Title: Characterization of Antimicrobial Susceptibility and Its Association with Virulence Genes Related to Adherence, Invasion, and Cytotoxicity in Campylobacter jejuni and Campylobacter coli Isolates from Animals, Meat, and Humans.
Citation: Microbial drug resistance (Larchmont, N.Y.), Jul 2016, vol. 22, no. 5, p. 432-444,

Author(s): Lapierre, Lisette, Gatica, María A, Riquelme, Víctor, Vergara, Constanza,
Abstract: The aim of this research was to statistically analyze the association between antimicrobial susceptibility/resistance to erythromycine, gentamicin, ciprofloxacin, and tetracycline and 11 virulence genes associated with adherence, invasion, and cytotoxicity in 528 isolates of Campylobacter coli and Campylobacter jejuni obtained from retail meat and fecal samples from food-producing animals and human patients. A high percentage of Campylobacter strains were resistant to antimicrobials, specifically ciprofloxacin and tetracycline. Moreover, we observed a wide distribution of virulence genes within the analyzed strains. C. jejuni strains were more susceptible to antimicrobials, and showed greater number of virulence genes than C. coli strains. Genes related to invasion capability, such as racR, ciaB, and pldA, were associated with antimicrobial-susceptible strains in both species. The genes cdtA and dnaJ, a citotoxin unit and an adherence-related gene, respectively, were associated with antimicrobial-resistant strains in both species. In conclusion, Campylobacter strains show a statistically significant association between antimicrobial susceptibility and the presence of virulence genes.

Title: Resistance of Campylobacter jejuni Isolated from Layer Farms in Northern Jordan Using Microbroth Dilution and Disc Diffusion Techniques.
Citation: Journal of food science, Jul 2016, vol. 81, no. 7, p. M1749.
Author(s): Al-Natour, Mohammad Q, Alaboudi, Akram R, Osaili, Tareq M, Obaidat,

Abstract: Campylobacter jejuni is an important pathogen of significant public health importance. This pathogen is associated with human infection and has been isolated from mammals and birds. Ninety-two cloacal C. jejuni isolates were identified from 35 layer farms in Northern Jordan. Antimicrobial susceptibility was determined using minimal inhibitory concentration (MIC) and disc diffusion techniques with variable suggested breakpoints. Using MIC and EUCAST cut-off values, the study revealed a significantly high resistance level (100%) among the layers' isolates against ciprofloxacin and tetracycline. A relatively high resistance (41%) toward gentamicin and amoxicillin and low resistance to nalidixic acid (21%), erythromycin (14%), and florfenicol (6.5%) were also found. This high level of resistance may indicate abuses in the handling of antibiotics, which may require stricter control in the local layer industry. A good agreement between the 2 techniques used was demonstrated and the disc diffusion technique could be used as a rapid screening test for antimicrobial susceptibility of C. jejuni to many antibiotics using specific Campylobacter breakpoints.

Clostridium difficile

Title: Fecal microbiota transplantation for the intestinal decolonization of extensively antimicrobial-resistant opportunistic pathogens: a review.
Citation: Infectious diseases (London, England), Aug 2016, vol. 48, no. 8, p. 587-592
Author(s): Manges, Amee R, Steiner, Theodore S, Wright, Alissa J

Abstract: Treatment options for multidrug-resistant (MDR) bacterial infections are limited and often less effective. Non-pharmacologic approaches to preventing or treating MDR infections are currently restricted to improved antimicrobial stewardship and infection control practices. Fecal microbiota transplantation (FMT), a highly effective treatment for recurrent Clostridium difficile infection, has emerged as a promising therapy for intestinal MDR bacterial decolonization. A total of eight case reports have been published showing FMT resulted in intestinal decolonization of extended spectrum β-lactamase (ESBL)-producing and carbapenemase-producing Enterobacteriaceae, vancomycin-resistant Enterococci, or methicillin-resistant Staphylococcus aureus. The procedure has been shown to work even in immunocompromised patients and those experiencing medical crises without any adverse events. Five trials are currently underway to further investigate the use of FMT for MDR bacterial decolonization. FMT is a completely novel way to eradicate drug-resistant bacteria from the intestinal reservoir and should be further investigated to address the global problem of difficult-to-treat, MDR bacterial infections.

Title: Infectious Diarrhea: Norovirus and Clostridium difficile in Older Adults.
Citation: Clinics in geriatric medicine, Aug 2016, vol. 32, no. 3, p. 509-522
Author(s): White, Mary B, Rajagopalan, Shobita, Yoshikawa, Thomas T

Abstract: Norovirus infection usually results in acute gastroenteritis, often with incapacitating nausea, vomiting, and diarrhea. It is highly contagious and resistant to eradication with alcohol-based hand sanitizer. Appropriate preventative and infection control measures can mitigate the morbidity and mortality associated with norovirus infection. Clostridium difficile infection is the leading cause of health care-associated diarrhea in the United States. Antibiotic use is by far the most common risk factor for C difficile colonization and infection. Appropriate preventive measures and judicious use of antibiotics can help mitigate the morbidity and mortality associated with C difficile infection.

Title: Hospital Clostridium difficile infection (CDI) incidence as a risk factor for hospital-associated CDI.
Citation: American journal of infection control, Jul 2016, vol. 44, no. 7, p. 825-829
Author(s): Miller, Aaron C, Polgreen, Linnea A, Cavanaugh, Joseph E, Polgreen, Philip M

Abstract: Environmental risk factors for Clostridium difficile infections (CDIs) have been described at the room or unit level but not the hospital level. To understand the environmental risk factors for CDI, we investigated the association between institutional- and individual-level CDI. We performed a retrospective cohort study using the Healthcare Cost and Utilization Project state inpatient databases for California (2005-2011). For each patient's hospital stay, we calculated the hospital CDI incidence rate corresponding to the patient's quarter of discharge, while excluding each patient's own CDI status. Adjusting for patient and hospital characteristics, we ran a pooled logistic regression to determine individual CDI risk attributable to the hospital's CDI rate. There were 10,329,988 patients (26,086 cases and 10,303,902 noncases) who were analyzed. We found that a percentage point increase in the CDI incidence rate a patient encountered increased the odds of CDI by a factor of 1.182. As a point of comparison, a 1-percentage point increase in the CDI incidence rate that the patient encountered had roughly the same impact on their odds of acquiring CDI as a 55.8-day increase in their length of stay or a 60-year increase in age. Patients treated in hospitals with a higher CDI rate are more likely to acquire CDI.

Title: Epidemiology of Clostridium difficile Infection-Associated Reactive Arthritis in Children: An Underdiagnosed, Potentially Morbid Condition.
Citation: JAMA pediatrics, Jul 2016, vol. 170, no. 7, p. e160217.
Author(s): Horton, Daniel B, Strom, Brian L, Putt, Mary E, Rose, Carlos D, Sherry, David D,

Abstract: The incidence of Clostridium difficile infection has increased among children. The epidemiology of pediatric C difficile infection-associated reactive arthritis is poorly understood. To characterize the incidence, recognition, and distinguishing clinical features of pediatric C difficile infection-associated reactive arthritis among children with C difficile infection. In this cohort and nested case-control study using electronic health records from January 1, 2004, to December 31, 2013, across 3 geographically diverse pediatric health care networks, we screened for reactive arthritis among 148 children between ages 2 and 21 years with diagnostic or procedural codes suggesting musculoskeletal disease associated with C difficile diagnosis or positive testing. We identified 26 cases with acute arthritis or tenosynovitis within 4 weeks before to 12 weeks after confirmed C difficile infection with (1) no alternative explanation for arthritis and (2) negative synovial cultures (if obtained). Network-matched C difficile-infected controls without arthritis were randomly selected at the time of cohort member C difficile infections. Incidence of C difficile infection-associated reactive arthritis was calculated based on (1) pediatric source population and (2) children with C difficile infection. Characteristics of cases and controls were compared using conditional logistic regression. Based on the cases identified within the source population of the 3 hospital networks, we estimated that C difficile infection-associated reactive arthritis incidence was 5.0 cases per million person-years (95% CI, 3.0-7.8). Reactive arthritis affected 1.4% of children with C difficile infection yearly (95% CI 0.8%-2.3%). Joint symptoms began a median of 10.5 days after initial gastrointestinal symptoms, often accompanied by fever (n = 15 [58%]) or rash (n = 14 [54%]). Only 35% of cases of C difficile infection-associated reactive arthritis were correctly diagnosed by treating health care professionals (range across centers, 0%-64%). Five affected children (19%) were treated for presumed culture-negative septic hip arthritis despite having prior postantibiotic diarrhea and/or other involved joints. Compared with controls, cases of C difficile infection-associated reactive arthritis were less likely to have underlying chronic conditions (odds ratio [OR], 0.3; 95% CI, 0.1-0.8). Although

all cases had community-onset C difficile infection and fewer comorbidities, they were more likely to be treated in emergency departments and/or hospitalized (OR, 7.1; 95% CI, 1.6-31.7). C difficile infection-associated reactive arthritis is an underdiagnosed, potentially morbid reactive arthritis associated with C difficile infection occasionally misdiagnosed as septic arthritis. Given the rising incidence of pediatric C difficile infections, better recognition of its associated reactive arthritis is needed.

Title: [Infection control and safety culture in German hospitals].
Citation: Bundesgesundheitsblatt, Gesundheitsforschung, Gesundheitsschutz, Jul 2016, vol. 59, no. 7, p. 908-915
Author(s): Hansen, Sonja, Schwab, Frank, Gropmann, Alexander, Behnke, Michael, Gastmeier, Petra, PROHIBIT Consortium

Abstract: Healthcare-associated infections (HAI) are the most frequent adverse events in the healthcare setting and their prevention is an important contribution to patient safety in hospitals. To analyse to what extent safety cultural aspects with relevance to infection control are implemented in German hospitals. Safety cultural aspects of infection control were surveyed with an online questionnaire; data were analysed descriptively. Data from 543 hospitals with a median of [IQR] 275 [157; 453] beds were analysed. Almost all hospitals (96.6 %) had internal guidelines for infection control (IC) in place; 82 % defined IC objectives, most often regarding hand hygiene (HH) (93 %) and multidrug resistant organisms (72 %) and less frequently for antibiotic stewardship (48 %) or prevention of specific HAI. In 94 % of hospitals, a reporting system for adverse events was in place, which was also used to report low compliance with HH, outbreaks and Clostridium difficile-associated infections. Members of the IC team were most often seen to hold daily responsibility for IC in the hospital, but rarely other hospital staff (94 versus 19 %). Safety cultural aspects are not fully implemented in German hospitals. IC should be more strongly implemented in healthcare workers' daily routine and more visibly supported by hospital management.

Title: Choosing Wisely in Healthcare Epidemiology and Antimicrobial Stewardship.
Citation: Infection control and hospital epidemiology, Jul 2016, vol. 37, no. 7, p. 755-760,
Author(s): Morgan, Daniel J, Croft, Lindsay D, Deloney, Valerie, Popovich, Kyle J,

Abstract: OBJECTIVE To identify Choosing Wisely items for the American Board of Internal Medicine Foundation. METHODS The Society for Healthcare Epidemiology of America (SHEA) elicited potential items from a hospital epidemiology listserv, SHEA committee members, and a SHEA-Infectious Diseases Society of America compendium with SHEA Research Network members ranking items by Delphi method voting. The SHEA Guidelines Committee reviewed the top 10 items for appropriateness for Choosing Wisely. Five final recommendations were approved via individual member vote by committees and the SHEA Board. RESULTS Ninety-six items were proposed by 87 listserv members and 99 SHEA committee members. Top 40 items were ranked by 24 committee members and 64 of 226 SHEA Research Network members. The 5 final recommendations follow: 1. Don't continue antibiotics beyond 72 hours in hospitalized patients unless patient has clear evidence of infection. 2. Avoid invasive devices (including central venous catheters, endotracheal tubes, and urinary catheters)and, if required, use no longer than necessary. They pose a major risk for infections. 3. Don't perform urinalysis, urine culture, blood culture, or Clostridium difficile testing unless patients have signs or symptoms of infection. Tests can be falsely positive leading to overdiagnosis and overtreatment. 4. Do not use antibiotics in patients with recent C. difficile without convincing evidence of need. Antibiotics pose a high risk of C. difficile recurrence. 5. Don't continue surgical prophylactic antibiotics after the patient has left the operating room. Five runner-up recommendations are included. CONCLUSIONS These 5 SHEA Choosing Wisely and 5 runner-up items limit medical overuse. Infect Control Hosp Epidemiol 2016;37:755-760.

Title: Point-prevalence survey of healthcare-associated infections in Beijing, China: a survey and analysis in 2014.
Citation: The Journal of hospital infection, Jul 2016, vol. 93, no. 3, p. 271-279
Author(s): Liu, J Y, Wu, Y H, Cai, M, Zhou, C L

Abstract: Point-prevalence studies can identify priorities for infection control. In May 2014, the Beijing Nosocomial Infection Control and Quality Improvement Centre organized a point-prevalence survey in 124 acute care hospitals in Beijing province. By analysing the survey results and factors affecting the point prevalence of healthcare-associated infections (HCAIs) in secondary and tertiary acute care hospitals in a certain area of China, this study provides evidence and reference to monitor HCAIs in a wide variety of hospitals. An epidemiological cross-sectional survey conducted by infection control practitioners was used to assess the point-prevalence rate of HCAIs by reviewing cases and performing bedside surveys. In total, 124 hospitals and 61,990 patients were surveyed, and 1389 (2.2%) HCAIs were diagnosed in 1294 (2.1%) patients. Respiratory tract infections were the most common HCAIs (54.4%, 51.7-56.9%), followed by urinary tract infections (15.0%, 13.2-16.9%), gastrointestinal tract infections (7.7%, 6.3-9.1%), surgical site infections (6.3%, 5.1-7.6%) and bloodstream infections (5.5%, 4.3-6.8%). In this survey, the top three pathogens were Pseudomonas aeruginosa, Acinetobacter baumannii and Escherichia coli. Rates of central vein catheter insertion, urethral catheterization and mechanical ventilation were 9.9%, 12.4% and 3.8%, respectively. Overall, 23.7% of the patients underwent surgery on or before the date of the survey. HCAIs were present in 14.5% of intensive care unit patients, 2.3% of medical patients and 2% of surgical patients. Diarrhoea was found in 0.8% of the assessed cases; however, tests for Clostridium difficile are not routinely available in China. In areas with limited personnel and resources, regular investigation of the point prevalence of HCAIs can be performed in lieu of comprehensive monitoring to elucidate risk factors and disease burdens of HCAIs.

Title: Reproducible elimination of Clostridium difficile spores using a clinical area washer disinfector in 3 different health care sites.
Citation: American journal of infection control, Jul 2016, vol. 44, no. 7, p. e107.
Author(s): MacDonald, Kelly, Bishop, Jane, Dobbyn, Bev, Kibsey, Pamela, Alfa, Michelle J

Abstract: Following a Clostridium difficile infection outbreak, the Infection Prevention and Control team at our institution queried the risk of transmission via bedpans reprocessed in washer disinfectors (WDs). This study's objective was to determine the effectiveness of the mechanical action, detergent, and temperature on the eradication of C difficile spores in 1 type of WD model. Three types of reusable bedpans/pots were inoculated with sterile human feces that contained 1 × 10(7) CFU/mL C difficile spores. The 0.3 mL fecal-spore suspension was inoculated in sealed cryovials. These items were reprocessed using the longest wash cycle of WDs in 9 clinical units, and then tested for residual C difficile spores. The number of colonies on each replicate organism detection and counting plate was recorded after anaerobic incubation at 35°C for 48 hours, and the log reduction was calculated. All 9 WDs met the manufacturer's operational specifications. Forty-three (96%) of 45 bedpans had no viable spores (>5.9 log10C difficile spore reduction). Two bedpans had 1 to 2 spores remaining. Viable C difficile spores were isolated from all 9 cryovials. Results demonstrated that when operating the WD as stipulated, C difficile spores were satisfactorily eliminated from bedpan surfaces. Temperature alone was insufficient to kill C difficile spores. It also suggested the importance of staff training, machine maintenance, and WD purchase specifications.

Title: Rising Vancomycin-Resistant Enterococcus Infections in Hospitalized Children in the United States.
Citation: Hospital pediatrics, Jul 2016, vol. 6, no. 7, p. 404-411,
Author(s): Adams, Daniel J, Eberly, Matthew D, Goudie, Anthony, Nylund, Cade M

Abstract: Vancomycin-resistant Enterococcus (VRE) is an emerging drug-resistant organism responsible for increasing numbers of nosocomial infections in adults. Few data are available on the epidemiology and impact of VRE infections in children. We hypothesized a significant increase in VRE infections among hospitalized children. Additionally, we predicted that VRE infection would be associated with certain comorbid conditions and increased duration and cost of hospitalization. A retrospective study of inpatient pediatric patients was performed using data on hospitalizations for VRE from the Healthcare Cost and Utilization Project Kids' Inpatient Database from 1997 to 2012. We used a multivariable logistic regression model to establish factors associated with VRE infection and a high-dimensional propensity score match to evaluate death, length of stay, and cost of hospitalization. Hospitalizations for VRE infection showed an increasing trend, from 53 hospitalizations per million in 1997 to 120 in 2012 (P < .001). Conditions associated with VRE included Clostridium difficile infection and other diagnoses involving immunosuppression and significant antibiotic and health care exposure. Patients with VRE infection had a significantly longer length of stay (attributable difference [AD] 2.1 days, P < .001) and higher hospitalization costs (AD $8233, P = .004). VRE infection was not associated with an increased risk of death (odds ratio 1.03; 95% confidence interval 0.73-1.47). VRE infections among hospitalized children are increasing at a substantial rate. This study demonstrates the significant impact of VRE on the health of pediatric patients and highlights the importance of strict adherence to existing infection control policies and VRE surveillance in certain high-risk pediatric populations. Copyright © 2016 by the American Academy of

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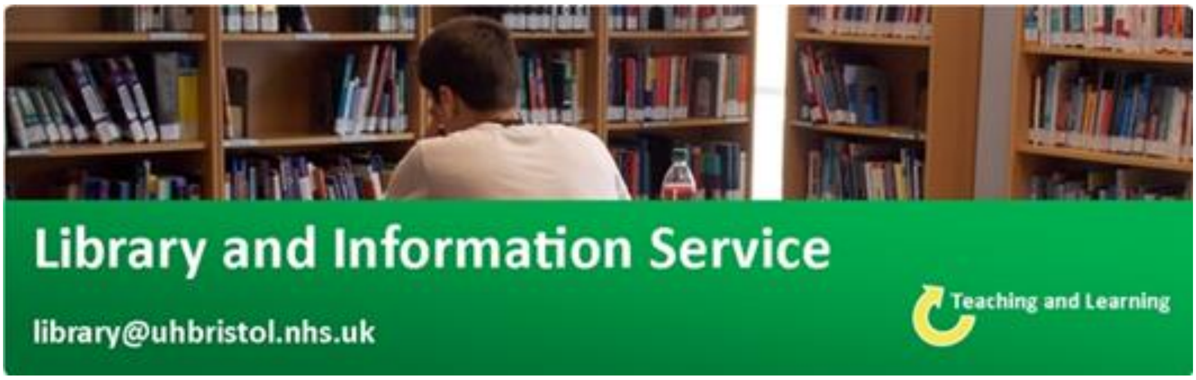
Title: Point-prevalence survey of healthcare-associated infections in Beijing, China: A survey and analysis in 2014
Citation: Journal of Hospital Infection, July 2016, vol./is. 93/3(271-279)
Author(s): Liu J.Y., Wu Y.H., Cai M., Zhou C.L.

Abstract: Background: Point-prevalence studies can identify priorities for infection control. Aim: In May 2014, the Beijing Nosocomial Infection Control and Quality Improvement Centre organized a point-prevalence survey in 124 acute care hospitals in Beijing province.

By analysing the survey results and factors affecting the point prevalence of healthcare-associated infections (HCAIs) in secondary and tertiary acute care hospitals in a certain area of China, this study provides evidence and reference to monitor HCAIs in a wide variety of hospitals. Methods: An epidemiological cross-sectional survey conducted by infection control practitioners was used to assess the point-prevalence rate of HCAIs by reviewing cases and performing bedside surveys. Findings: In total, 124 hospitals and 61,990 patients were surveyed, and 1389 (2.2%) HCAIs were diagnosed in 1294 (2.1%) patients. Respiratory tract infections were the most common HCAIs (54.4%, 51.7-56.9%), followed by urinary tract infections (15.0%, 13.2-16.9%), gastrointestinal tract infections (7.7%, 6.3-9.1%), surgical site infections (6.3%, 5.1-7.6%) and bloodstream infections (5.5%, 4.3-6.8%). In this survey, the top three pathogens were Pseudomonas aeruginosa, Acinetobacter baumannii and Escherichia coli. Rates of central vein catheter insertion, urethral catheterization and mechanical ventilation were 9.9%, 12.4% and 3.8%, respectively. Overall, 23.7% of the patients underwent surgery on or before the date of the survey. HCAIs were present in 14.5% of intensive care unit patients, 2.3% of medical patients and 2% of surgical patients. Diarrhoea was found in 0.8% of the assessed cases; however, tests for Clostridium difficile are not routinely available in China. Conclusion: In areas with limited personnel and resources, regular investigation of the point prevalence of HCAIs can be performed in lieu of comprehensive monitoring to elucidate risk factors and disease burdens of HCAIs.



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