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Publications:

Salmonella: Salmonellosis

Salmonella remains one of the most important zoonotic pathogenic bacteria and is the causative agents of salmonellosis. The aim of this article is to give an overview of Salmonella and salmonellosis, starting by describing the characteristics of the microorganism Salmonella, including biochemical properties, physiology, classification, and nomenclature. Thereafter, the epidemiology of the organism is introduced, including the routes of transmission. Finally, the disease salmonellosis, the virulence mechanisms, and the occurrence in different types of food are described.

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State: Published
Organisations: National Food Institute, Division of Food Microbiology, Federal Institute for Risk Assessment
Authors: Löfström, C. (Intern), Hansen, T. (Intern), Maurischat, S. (Ekstern), Malorny, B. (Ekstern)
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Fluorescence-based real-time quantitative polymerase chain reaction (qPCR) technologies for high throughput screening of pathogens

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Authors: Löfström, C. (Intern), Josefsen, M. H. (Intern), Hansen, T. (Intern), Søndergaard, M. S. R. (Intern), Hoorfar, J. (Intern)
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Animal Botulism Outcomes in the AniBioThreat Project

Botulism disease in both humans and animals is a worldwide concern. Botulinum neurotoxins produced by Clostridium botulinum and other Clostridium species are the most potent biological substances known and are responsible for flaccid paralysis leading to a high mortality rate. Clostridium botulinum and botulinum neurotoxins are considered potential weapons for bioterrorism and have been included in the Australia Group List of Biological Agents. In 2010 the European Commission (DG Justice, Freedom and Security) funded a 3-year project named AniBioThreat to improve the EU's capacity to counter animal bioterrorism threats. A detection portfolio with screening methods for botulism agents and incidents was needed to improve tracking and tracing of accidental and deliberate contamination of the feed and food chain with botulinum neurotoxins and other Clostridia. The complexity of this threat required acquiring new genetic information to better understand the diversity of these Clostridia and develop detection methods targeting both highly specific genetic markers of these Clostridia and the neurotoxins they are able to produce. Several European institutes participating in the AniBioThreat project collaborated on this program to achieve these objectives. Their scientific developments are discussed here.

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Authors: Woudstra, C. (Ekstern), Tevell Åberg, A. (Ekstern), Skarin, H. (Ekstern), Anniballi, F. (Ekstern), De Medici, D. (Ekstern), Bano, L. (Ekstern), Koene, M. (Ekstern), Löfström, C. (Intern), Hansen, T. (Intern), Hedeland, M. (Ekstern), Fach, P. (Ekstern)
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Anthrax

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Organisations: National Food Institute, Division of Food Microbiology, Agence nationale de la sécurité sanitaire, alimentation, environnement et travail, National Institute for Public Health and Environment , CVI, SVA
Authors: Derzelle, S. (Ekstern), Hamidjaja, R. A. (Ekstern), Hansen, T. (Intern), Boene, M. (Ekstern), Löfström, C. (Intern), Thierry, S. (Ekstern), Ågren, J. (Ekstern)
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Evaluation of Direct 16S rDNA Sequencing as a Metagenomics-based Approach to Screening Bacteria in Bottled Water

Deliberate or accidental contamination of food, feed, and water supplies poses a threat to human health worldwide. A rapid and sensitive detection technique that could replace the current labor-intensive and time-consuming culture-based methods is highly desirable. In addition to species-specific assays, such as PCR, there is a need for generic methods to screen for unknown pathogenic microorganisms in samples. This work presents a metagenomics-based direct-sequencing approach for detecting unknown microorganisms, using Bacillus cereus (as a model organism for B. anthracis) in bottled water as an example. Total DNA extraction and 16S rDNA gene sequencing were used in combination with principle component analysis and multicurve resolution to study detection level and possibility for identification. Results showed a detection level of 105 to 106 CFU/L. Using this method, it was possible to separate 2 B. cereus strains by the principal component plot, despite the close sequence resemblance. A linear correlation between the artificial contamination level and the relative amount of the Bacillus artificial contaminant in the metagenome was observed, and a relative amount value above 0.5 confirmed the presence of Bacillus. The analysis also revealed that background flora in the bottled water varied between the different water types that were included in the study. This method has the potential to be adapted to other biological matrices and bacterial pathogens for fast screening of unknown bacterial threats in outbreak situations.

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In silico and in vitro evaluation of PCR-based assays for the detection of Bacillus anthracis chromosomal signature sequences

Bacillus anthracis, the causative agent of anthrax, is a zoonotic pathogen that is relatively common throughout the world and may cause life threatening diseases in animals and humans. There are many PCR-based assays in use for the detection of B. anthracis. While most of the developed assays rely on unique markers present on virulence plasmids pXO1 and pXO2, relatively few assays incorporate chromosomal DNA markers due to the close relatedness of B. anthracis to the B. cereus group strains. For the detection of chromosomal DNA, different genes have been used, such as BA813, rpoB, gyrA, plcR, S-layer, and prophage-lambda. Following a review of the literature, an in silico analysis of all signature sequences reported for identification of B. anthracis was conducted. Published primer and probe sequences were compared for specificity against 134 available Bacillus spp. genomes. Although many of the chromosomal targets evaluated are claimed to be specific to B. anthracis, cross-reactions with closely related B. cereus and B. thuringiensis strains were often observed. Of the 35 investigated PCR assays, only 4 were 100% specific for the B. anthracis chromosome. An interlaboratory ring trial among five European laboratories was then performed to evaluate six assays, including the WHO recommended procedures, using a collection of 90 Bacillus strains. Three assays performed adequately, yielding no false positive or negative results. All three assays target chromosomal markers located within the lambdaBa03 prophage region (PL3, BA5345, and BA5357). Detection limit was further assessed for one of these highly specific assays.

General information

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Organisations: National Food Institute, Division of Food Microbiology, Division of Epidemiology and Microbial Genomics, Lund University, National Institute for Public Health and Environment , Wageningen IMARES, University Paris-Est Anses , National Veterinary Institute

Authors: Ågren, J. (Ekstern), Hamidjaja, R. A. (Ekstern), Hansen, T. (Intern), Ruuls, R. (Ekstern), Thierry, S. (Ekstern), Vigre, H. (Intern), Janse, I. (Ekstern), Sundström, A. (Ekstern), Segerman, B. (Ekstern), Koene, M. (Ekstern), Löfström, C. (Intern), Van Rotterdam, B. (Ekstern), Derzelle, S. (Ekstern)
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Management of Animal Botulism Outbreaks: From Clinical Suspicion to Practical Countermeasures to Prevent or Minimize Outbreaks

Botulism is a severe neuroparalytic disease that affects humans, all warm-blooded animals, and some fishes. The disease is caused by exposure to toxins produced by Clostridium botulinum and other botulinum toxin–producing clostridia. Botulism in animals represents a severe environmental and economic concern because of its high mortality rate. Moreover, meat or other products from affected animals entering the food chain may result in a public health problem. To this end, early diagnosis is crucial to define and apply appropriate veterinary public health measures. Clinical diagnosis is based on clinical findings eliminating other causes of neuromuscular disorders and on the absence of internal lesions observed during postmortem examination. Since clinical signs alone are often insufficient to make a definitive diagnosis, laboratory confirmation is required. Botulinum antitoxin administration and supportive therapies are used to treat sick animals. Once the diagnosis has been made, euthanasia is frequently advisable. Vaccine administration is subject to health authorities' permission, and it is restricted to a small number of animal species. Several measures can be adopted to prevent or minimize outbreaks. In this article we outline all phases of management of animal botulism outbreaks occurring in wet wild birds, poultry, cattle, horses, and fur farm animals.

General information

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Organisations: National Food Institute, Division of Food Microbiology
Authors: Anniballi, F. (Ekstern), Fiore, A. (Ekstern), Löfström, C. (Intern), Skarin, H. (Ekstern), Auricchio, B. (Ekstern), Woudstra, C. (Ekstern), Bano, L. (Ekstern), Segerman, B. (Ekstern), Koene, M. (Ekstern), Båverud, V. (Ekstern), Hansen, T. (Intern), Fach, P. (Ekstern), Åberg, A. T. (Ekstern), Hedeland, M. (Ekstern), Engvall, E. O. (Ekstern), De Medici, D. (Ekstern)
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Metagenomic Detection Methods in Biopreparedness Outbreak Scenarios

In the field of diagnostic microbiology, rapid molecular methods are critically important for detecting pathogens. With rapid and accurate detection, preventive measures can be put in place early, thereby preventing loss of life and further spread of a disease. From a preparedness perspective, early detection and response are important in order to minimize the consequences. During the past 2 decades, advances in next-generation sequencing (NGS) technology have changed the playing field of molecular methods. Today, it is within reach to completely sequence the total microbiological content of a clinical sample, creating a metagenome, in a single week of laboratory work. As new technologies emerge, their dissemination and capacity building must be facilitated, and criteria for use, as well as guidelines on how to report results, must be established. This article focuses on the use of metagenomics, from sample collection to data analysis and to some extent NGS, for the detection of pathogens, the integration of the technique in outbreak response systems, and the risk-based evaluation of sample processing in routine diagnostics labs. The article covers recent advances in the field, current debate, gaps in research, and future directions. Examples of metagenomic detection, as well as possible applications of the methods, are described in various biopreparedness outbreak scenarios.

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Authors: Karlsson, O. E. (Ekstern), Hansen, T. (Intern), Knutsson, R. (Ekstern), Löfström, C. (Intern), Granberg, F. (Ekstern), Berg, M. (Ekstern)

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Molecular diagnostics of foodborne pathogens

Illness caused by foodborne pathogens represents an important economic and public health burden worldwide. In order to minimize the occurrence of foodborne pathogens in the food production chain and thereby increase the food safety, better detection methods and knowledge about the behavior of pathogens are needed. The introduction of the molecular diagnostics methods based on detection of the organisms nucleic acids have made detection, identification and characterization of foodborne pathogens faster and with greater specificity and sensitivity.
The objectives of research in this thesis were to investigate the use of different nucleic acid based methods for molecular diagnostics of foodborne pathogens focusing on Salmonellaand Bacillus cereuswith respect to improve food safety. The work represents two parts of molecular diagnostics; the characterization Salmonellafor better understanding of its behavior in pork processing environments, and detection of B. cereusin food, feed and water samples without prior cultivation.
The persistence of Salmonellain food production chains has been suggested to be a result of bacterial attachment and surface colonization. It was found that the physiological state of Salmonellahas an impact on the ability of Salmonellato attach to a pork meat surface and subsequently the possibility of contributing to cross contamination in the slaughter-line. Cells that were grown immobilized prior application on a pork meat surface were found to be more easily removed. In the pork processing, Salmonellamight appear in an immobilized state on the pork surfaces where low attachment ability might pose a risk for cross contamination. A stronger attachment to a surface makes on the other hand decontamination steps more difficult. The attachment ability of Salmonellacould to some extend be connected to specific genes. Deletion of either of the operons prgor flhDCin S. Typhimurium resulted in lower attachment ability to the pork meat surface. In addition, was it found that a S. Rissen isolate with low attachment ability after immobilized growth lacked two fimbriae genes, safC and

lpfD,important for the adhesion and biofilm formation. It was further found that S. Typhimurium exposed to a heat shock was more resistance to heat and acid inactivation conditions, which might make later decontamination steps more difficult and subsequently lead to a higher risk of contamination of food products.
Deliberate or accidental contamination of food, feed and water supplies pose a threat to human health worldwide and the need for generic detection methods that can screen for many pathogens at the time are highly desirable. A metagenomics based direct 16S rDNA sequencing approach was evaluated as a diagnostic tool for screening of unknown bacteria in bottled water without prior cultivation. B. cereusartificially inoculated in bottled water was used as a model. The results revealed that the method was able to detect B. cereusat levels of 10^5-10^6 CFU/L, a detection level low enough for detection in outbreaks situations. Consequently, the method was found to be a good candidate as a method for detection of B. cereusand for screening of other bacterial contaminants in water samples. The capability of the method was further evaluated on a variety of food and feed model samples. Before the method could be adapted to these types of samples, an optimization of the total DNA extraction step was applied. Five different commercial available DNA extraction kits were evaluated and the MasterPure DNA Purification Kit was found to be suitable for the food and feed samples. The detection of B. cereusin food and feed samples was found to be more complicated and for the method to be used for this type of samples, additional optimizations have to be conducted.
In conclusion, the work present in this thesis contributes to the better understanding of the behavior of Salmonellain the pork processing and which factors that might influence the persistence and adaption. The information can be used for control of Salmonella by contributing to developments of more specific control measures and treatments within the food production-line and thereby improve the food safety. In addition, the method for direct detection of B. cereusin different biological matrices was found promising with the potential to be adapted for screening of bacterial contamination. This makes the method useful in outbreaks situations where the causing agent might be unknown.

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The Workshop on Animal Botulism in Europe
A workshop on animal botulism was held in Uppsala, Sweden, in June 2012. Its purpose was to explore the current status of the disease in Europe by gathering the European experts in animal botulism and to raise awareness of the disease among veterinarians and others involved in biopreparedness. Animal botulism is underreported and underdiagnosed, but an increasing number of reports, as well as the information gathered from this workshop, show that it is an emerging problem in Europe. The workshop was divided into 4 sessions: animal botulism in Europe, the bacteria behind the disease, detection and diagnostics, and European collaboration and surveillance. An electronic survey was conducted before the workshop to identify the 3 most needed discussion points, which were: prevention, preparedness and outbreak response; detection and diagnostics; and European collaboration and surveillance. The main conclusions drawn from these discussions were that there is an urgent need to replace the mouse bioassay for botulinum toxin detection with an in vitro test and that there is a need for a European network to function as a reference laboratory, which could also organize a European supply of botulinum antitoxin and vaccines. The foundation of such a network was discussed, and the proposals are presented here along with the outcome of discussions and a summary of the workshop itself.

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Validation of a real-time PCR based method for detection of Clostridium botulinum types C, D and their mosaic variants C-D and D-C in a multicenter collaborative trial

Two real-time PCR arrays based on the GeneDisc® cycler platform (Pall-GeneDisc Technologies) were evaluated in a multicenter collaborative trial for their capacity to specifically detect and discriminate Clostridium botulinum types C, D and their mosaic variants C-D and D-C that are associated with avian and mammalian botulism. The GeneDisc® arrays developed as part of the DG Home funded European project 'AnibioThreat' were highly sensitive and specific when tested on pure isolates and naturally contaminated samples (mostly clinical specimen from avian origin). Results of the multicenter collaborative trial involving eight laboratories in five European Countries (two laboratories in France, Italy and The Netherlands, one laboratory in Denmark and Sweden), using DNA extracts issued from 33 pure isolates and 48 naturally contaminated samples associated with animal botulism cases, demonstrated the robustness of these tests. Results showed a concordance among the eight laboratories of 99.4%-100% for both arrays. The reproducibility of the tests was high with a relative standard deviation ranging from 1.1% to 7.1%. Considering the high level of agreement achieved between the laboratories these PCR arrays constitute robust and suitable tools for rapid detection of C. botulinum types C, D and mosaic types C-D and D-C. These are the first tests for C. botulinum C and D that have been evaluated in a European multicenter collaborative trial.

General information

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Authors: Woudstra, C. (Ekstern), Skarin, H. (Ekstern), Anniballi, F. (Ekstern), Auricchio, B. (Ekstern), De Medici, D. (Ekstern), Bano, L. (Ekstern), Drigo, I. (Ekstern), Hansen, T. (Intern), Löfström, C. (Intern), Hamidjaja, R. (Ekstern), van Rotterdam, B. J. (Ekstern), Koene, M. (Ekstern), Bäyon-Auboyer, M. (Ekstern), Buffereau, J. (Ekstern), Fach, P. (Ekstern)

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BFI (2013): BFI-level 1
Scopus rating (2013): 1.082 1.077
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): 0.972 0.939
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): 0.888 0.951
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): 0.864 1.066
BFI (2009): BFI-level 1
Scopus rating (2009): 0.669 0.836
BFI (2008): BFI-level 1
Scopus rating (2008): 0.594 0.724
Scopus rating (2007): 0.625 0.737
Scopus rating (2006): 0.387 0.568
Scopus rating (2005): 0.319 0.445
Scopus rating (2004): 0.426 0.524
Scopus rating (2003): 0.344 0.447
Scopus rating (2002): 0.258 0.264
Scopus rating (2001): 0.398 0.375
Scopus rating (2000): 0.484 0.844
Scopus rating (1999): 0.527 0.477
Original language: English
DOIs:
10.1016/j.anaerobe.2013.05.002
Source: dtu
Source-ID: u::7581
Publication: Research - peer-review › Journal article – Annual report year: 2013

Instrumentation and Fluorescent Chemistries Used in qPCR

The polymerase chain reaction has revolutionized the world of scientific research and its broad application has caused a tremendous development of versatile PCR instruments and chemistries to fit its purpose. This chapter provides the reader with a general introduction to the basics of real-time PCR instrumentation, including the thermal and optical systems and the software. Performance parameters such as temperature uniformity, accuracy and ramp speed as well as reaction format, optical systems, calibration of dyes, software and comparison between different real-time PCR platforms will be discussed from a user perspective leading to an instrument selection guide. Differences between fluorescent DNA binding dyes and target-specific fluorescently labeled primers or probes for detection of amplicon accumulation will be discussed, along with the properties and applications of the most frequently applied chemistries. The fluorophores and quenchers used for primer and probe labeling and their compatibility will be presented, and finally the future challenges and trends within the field of qPCR instrumentation will be discussed.

General information

State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment
Authors: Josefsen, M. H. (Intern), Löfström, C. (Intern), Hansen, T. (Intern), Reynisson, E. (Ekstern), Hoorfar, J. (Intern)
Pages: 27-52
Publication date: 2012

Host publication information

Title of host publication: Quantitative Real-time PCR in Applied Microbiology
Publisher: Caister Academic Press
Editor: Filion, M.
ISBN (Print): 978-1-908230-01-0
Chapter: 2
Main Research Area: Technical/natural sciences
Source: dtu
Source-ID: u::3878
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The Transcriptional Heat Shock Response of Salmonella Typhimurium Shows Hysteresis and Heated Cells Show Increased Resistance to Heat and Acid Stress

We investigated if the transcriptional response of Salmonella Typhimurium to temperature and acid variations was hysteretic, i.e. whether the transcriptional regulation caused by environmental stimuli showed memory and remained after the stimuli ceased. The transcriptional activity of non-replicating stationary phase cells of S. Typhimurium caused by the exposure to 45uC and to pH 5 for 30 min was monitored by microarray hybridizations at the end of the treatment period as well as immediately and 30 minutes after conditions were set back to their initial values, 25uC and pH 7. One hundred and two out of 120 up-regulated genes during the heat shock remained up-regulated 30 minutes after the temperature was set back to 25uC, while only 86 out of 293 down regulated genes remained down regulated 30 minutes after the heat shock ceased. Thus, the majority of the induced genes exhibited hysteresis, i.e., they remained up-regulated after the environmental stress ceased. At 25uC the transcriptional regulation of genes encoding for heat shock proteins was determined by the previous environment. Gene networks constructed with up-regulated genes were significantly more modular than those of down-regulated genes, implying that down-regulation was significantly less synchronized than upregulation. The hysteretic transcriptional response to heat shock was accompanied by higher resistance to inactivation at 50uC as well as cross-resistance to inactivation at pH 3; however, growth rates and lag times at 43uC and at pH 4.5 were not
affected. The exposure to pH 5 only caused up-regulation of 12 genes and this response was neither hysteretic nor accompanied of increased resistance to inactivation conditions. Cellular memory at the transcriptional level may represent a mechanism of adaptation to the environment and a deterministic source of variability in gene regulation.

General information

State: Published
Organisations: National Food Institute, Division of Food Microbiology, Institute of Food Research, National Institute for Public Health and Environment , University of Copenhagen
Authors: Pin, C. (Ekstern), Hansen, T. (Intern), Munoz-Cuevas, M. (Ekstern), de Jonge, R. (Ekstern), Rosenkrantz, J. T. (Ekstern), Löfström, C. (Intern), Aarts, H. (Ekstern), Olsen, J. E. (Ekstern)
Number of pages: 10
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Volume: 7
Issue number: 12
ISSN (Print): 1932-6203
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BFI (2015): BFI-level 1

Scopus rating (2015): 1.395 1.044

BFI (2014): BFI-level 1

Scopus rating (2014): 1.518 1.107

BFI (2013): BFI-level 1

Scopus rating (2013): 1.722 1.134

ISI indexed (2013): ISI indexed yes

BFI (2012): BFI-level 1

Scopus rating (2012): 1.931 1.13
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): 2.351 1.218
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
Scopus rating (2010): 2.613 1.154
BFI (2009): BFI-level 1
Scopus rating (2009): 2.453 0.978
BFI (2008): BFI-level 1
Scopus rating (2008): 2.308 0.957
Scopus rating (2007): 1.285 0.521
Original language: English
Electronic versions:

Pin et al 2012 salmonella hysteresis.pdf
Source: dtu
Source-ID: u::6013
Publication: Research - peer-review › Journal article – Annual report year: 2012

Attachment of Salmonella spp. to pork meat

Five strains of Salmonella, one wildtype and four knock-out mutants (the prg, flhDC, yhjH and fliC genes) were investigated based on their probability to attach and subsequently detach from a surface of pork fillet. The attachment followed by detachment was measured and modelled for two different contact times using cells coming from either a planktonic or an immobilized state of growth. The results showed that the probability of detachment generally decreased when the contact time increased and that the highest difference between contact times was achieved when the cells were grown planktonic.

General information

State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment
Authors: Hansen, T. (Intern), Riber, L. (Intern), Löfström, C. (Intern), Hoorfar, J. (Intern)
Pages: 108-108
Publication date: 2011

Host publication information

Title of host publication: Safepork 2011 - Abstract book : 9th International Conference on the Epidemiology and Control of biological, chemical and physical hazards in pigs and pork
Main Research Area: Technical/natural sciences
Conference: 9th International Conference on the Epidemiology and Control of Biological Chemical and Physical Hazards in Pigs and Pork, Maastricht, Netherlands, 09/06/2011 - 09/06/2011
Electronic versions:

ABSTRACT.pdf
Links:

http://www.safepork.org/
Source: orbit
Source-ID: 280757
Publication: Research › Conference abstract in proceedings – Annual report year: 2011

Attachment of Salmonella spp. to pork meat

Five strains of Salmonella, one wildtype and four knock-out mutants (the prg, flhDC, yhjH and fliC genes) were investigated based on their probability to attach and subsequently detach from a surface of pork fillet. The attachment followed by detachment was measured and modelled for two different contact times using cells coming from either a planktonic or an immobilized state of growth. The results showed that the probability of detachment generally decreased when the contact time increased and that the highest difference between contact times was achieved when the cells were grown planktonic.

General information

State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment
Authors: Hansen, T. (Intern), Riber, L. (Intern), Löfström, C. (Intern), Hoorfar, J. (Intern)
Number of pages: 416

Pages: 286-289
Publication date: 2011

Host publication information
Title of host publication: Safepork 2011 Prodeedings Book : 9th International Conference on the Epidemiology and Control of biological, chemical and physical hazards in pigs and pork
Main Research Area: Technical/natural sciences
Conference: 9th International Conference on the Epidemiology and Control of Biological Chemical and Physical Hazards in Pigs and Pork, Maastricht, Netherlands, 09/06/2011 - 09/06/2011
Electronic versions:

PRODEEDINGS.pdf
Source: orbit
Source-ID: 282567
Publication: Research - peer-review › Article in proceedings – Annual report year: 2011

Projects:

AniBioThreat: Bio-preparedness measures concerning prevention, detection and response to animal bioterrorism threats
The aim is to improve the EU's capacity to counter biological animal bioterrorism threats in terms of awareness, prevention and contingency.

National Food Institute

Division of Food Microbiology

Sveriges Veterinärmedicinska Anstalt

Central Veterinary Institute

Lund University

National Police Board

Swedish National Laboratory of Forensic Scioence

MSB Swedish Civil Contingencies Agency

Agence nationale de la sécurité sanitaire, alimentation, environnement et travail

Central Agricultural Office

Swedish University of Agricultural Sciences

Federal Institute for Risk Assessment
Period: 01/10/2010 → 30/09/2013
Number of participants: 5
Acronym: AniBioThreat
Project ID: HOME/2009/ISEC/AG/191
Project participant:

Löfström, Charlotta (Intern)

Hansen, Trine (Intern)

Engelsmann, Pia (Intern)

Skiby, Jeffrey Edward (Intern)

Bang-Berthelsen, Iben (Intern)
Project

Molecular Diagnostics of Foodborne Pathogens

National Food Institute
Period: 01/05/2010 → 18/09/2013
Number of participants: 8
Phd Student:

Hansen, Trine (Intern)
Supervisor:

Löfström, Charlotta (Intern)

Riber, Leise (Intern)

Vigre, Håkan (Intern)
Main Supervisor:
Hoorfar, Jeffrey (Intern)
Examiner:
Pedersen, Karl (Intern)
Rudi, Knut (Ekstern)
Schelin, Jenny Regina (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Anden EU-finansiering
Project: PhD