Global Data

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International Symposium ” Principles and measures: How to overcome a life-threatening crisis in the food chain
14-15 November 2013, BfR, Berlin
European Union
- Data and sampling information requirements


• Ensure effective monitoring
  – zoonoses and zoonotic agents
  – antimicrobial resistance
  – investigation of foodborne outbreaks

• Provides the necessary information to evaluate the trends and sources of zoonoses and zoonotic agents

• Identifies hazards, assesses exposures, and risks
Outbreak data investigations
Directive 2003/99/EC

• Mandatory epidemiological investigation of food-borne outbreaks
  – Epidemiological profile
  – Foodstuffs potentially implicated and potential causes

• Missing of information Possible exclusion of data

National Food Institute, Technical University of Denmark
Reporting
Directive 2003/99/EC

Member States

Animal, food and feed monitoring & Foodborne outbreaks

Communicable human diseases

European Food Safety Authority

ECDC

National Food Institute, Technical University of Denmark
Salmonella in human cases, eggs and laying hens and the number of *Salmonella* outbreaks caused by eggs, 2007–2011
Causative agent in outbreaks related to food products in EU, 2011

Egg and egg products

Fish and fish products

Vegetables

Output examples

- European Union summary report on Zoonoses, zoonotic agents and foodborne outbreaks
- European Union summary report on AMR
- Scientific opinions
- Technical reports
- Risk assessment.
- EFSA journals
- + 2500 scientific outputs
  500th opinion – 2007
  1000th opinion – 2009
  1.837 opinions in 2012
Joint ECDC-EFSA rapid outbreak assessment

ECDC + EFSA performed a joint assessment of the outbreak and report about investigative activities in the four affected countries including consumption advices given to consumers

The Commission have asked EFSA and ECDC to elaborate a Standard Operation Procedure (SOP) for joint risk assessments in the event of outbreaks

Main conclusions and recommendations
Between 1 October 2012 and 8 April 2013, 16 confirmed cases of hepatitis A virus (HAV) infections with subgenotype IB and identical RNA sequence were reported in four Nordic countries.

As none of the cases have a travel history outside the EU within their period of potential exposure, this represents a multicountry outbreak, with exposure currently taking place in the EU. The descriptive epidemiology indicates foodborne transmission originating from a persistent common source in the EU with possibly multiple vehicles of infection that are contaminated with viruses sharing an identical sequence.

Epidemiological investigations in affected countries strongly point towards frozen berries as the vehicle of infection. This hypothesis is being further investigated. RNA sequencing, interviews of cases in affected countries, food investigations, and purchase history research should provide additional evidence.

According to the available information, it is likely that additional cases will be identified and reported. ECDC encourages Member States to report case awareness about a possible increase in HAV subgenotype IB cases, report all new cases in EPIs-PWD, and use the common case definition and questionnaire to interview recent cases (available in EPIs-PWD and upon request).

ECDC, EFSA and the European Commission, in cooperation with the affected countries, will continue to closely monitor this event and will update the outbreak assessment as soon as new relevant information becomes available.

Public health issue
Multicountry outbreak of hepatitis A (HAV) subgenotype IB in Denmark, Finland, Norway and Sweden.
EU has 28 Member States

Different
• Climate, wild animal populations
• Structure and size
• Food consumption patterns
• Occurrence of the pathogens
• Organisation of competent authorities

Different attitudes and perceptions of risk:
• Chemicals, pesticides
• Antimicrobial, hormones
• Cloning of animals
• Bacterial pathogens
• Nutrition, health

Source: Nations Online Project
Go Global
- Historical data versus real-time data
WHO Global influenza surveillance and response system (GISRS) FluNet

Geographic spread of influenza activity
(geographic spread reflects the number and distribution of regions within a country reporting influenza activity.)

Status as of Week 51
14 Dec - 20 Dec 2009

Risk assessment and management

The boundaries and names shown and the designations used on this map do not imply the expression of any opinion whatsoever on the part of the World Health Organization concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. Dotted lines on maps represent approximate border lines for which there may not yet be full agreement.

Map produced: 14 January 2010, 09:00 GMT

Data Source: World Health Organization
Map Production: Public Health Information and Geographic Information Systems (GIS)
World Health Organization

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WHO Global Salm Surv (GSS) country data bank 2002

103 countries have signed up to enter data to the database
WHO Global Foodborne Infections Network (GFN) country data bank, 2012

Members from 185 countries

- In total by August 2013
  - 2,247,754 isolates
  - 1,746,601 are from humans
  - 359 different serotypes are reported
    - 1,146,037 are S. Enteritidis
    - 410,452 are S. Typhimurium
WHO GFN

• A network of institutions and individuals committed to enhancing the capacity of countries to detect, respond and prevent foodborne and other enteric infections

• Capacity-building program that promotes
  – integrated, laboratory based surveillance
  – intersectoral collaboration among human health, veterinary and food-related disciplines
Upcoming: GFN WHONET database

- Include more data
- Other pathogens
- AMR profiles
Whole genome sequencing – the next generation?
Past or Future

• Old school
  – Isolation of pure culture
  – One to several weeks to perform full typing
  – Very different typing systems for microorganisms (different labs)
  – Very specialized knowledge base for different microorganisms

• New school
  – Isolation of pure culture (although might not be needed)
  – Hours to perform full sequencing
  – Minutes to get typing result
  – One test fits all (virus, bacteria, parasites)
  – Same-Same for all microbiology (human, animal, environment)
Global Microbial identifier (GMI)

Informal global, visionary taskforce of scientists and other stakeholders who share the aim of making novel genomic technologies and informatics tools available.
Global Microbial Identifier

Vision

GMI is committed to a world where high quality microbiological genomic information from human, animal and plant domains is freely shared among all nations for the use of research and to improve (public) healthcare and a healthy environment for all
Global Microbial Identifier

Mission

GMI mission is to build a global platform linked to an open and interactive worldwide network of DB for standardized identification, characterization and comparison of microorganisms through the storing of whole genome sequences of microorganisms, the connected metadata, and the provision of analytical facilities and shared standards.
Global Microbial Identifier

A global system will enable two major lines of action:

• Simple identification of all microorganisms in clinical (or other) settings, making redundant existing systems, and enabling reduction of total time for characterization down to typical time needed to obtain the original isolate.

• A total database of sequences of all relevant microbiological strains globally, enabling real-time global surveillance of disease and pathogen developments.
"Building a global system sharing often sensitive data will create barriers, one of which might be the willingness of sharing sequence data and the associated metadata.

In the future, sequence data-bases need to have open access to serve as an early warning system...

It should be realized that relevant sequence data might also be attractive for any industry ....However, important privacy issues concerning future data mining potential clearly exist."

*Statement from international expert meeting on microbiological genomic identification systems 1-2 September 2011 in Bruxelles, Belgium.*
Burden of Foodborne Disease
What is "Foodborne Disease Burden"?

- Diseases *commonly transmitted through food*
- All causes - pathogens, chemicals, parasites
- Acute and chronic diseases
- Long-term complications

% foodborne?

- Diarrhoea
- Cancers
- Epilepsy
- Arthritis
- Hepatitis
- Peptic ulcer
- Multi-organ failure
- Meningitis
2006 WHO Consultation to Develop a Strategy for the Global Burden of Foodborne Diseases

Recommended establishment of Foodborne Disease Burden Epidemiology Reference Group (FERG) to execute strategy
What do we mean by 'burden'?
Which approach to use when?

- Incidence, Prevalence, Mortality, DALYs, HALE & others
- Surveillance systems
- Intervention impact
- $ Costs (DALYs)
Completing the 'burden' picture

Disease model
Campylobacter spp

Infection → Gastroenteritis (No GP) → Hospitalization (GP) → Reactive arthritis (No GP) → Recovery

- Irritable bowel syndrome
- Guillain-Barré syndrome
- Long term sequelae
- Death
Thank you for your attention

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