Pathogens in the international food supply – why a broader perspective is needed

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Table 7.4—FDA violations for adulteration of fishery/seafod products by reason for contravention and main products detained, 2001

<table>
<thead>
<tr>
<th>Violation code</th>
<th>No. of violations</th>
<th>Main products detained</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Total violations</strong></td>
<td>5,486</td>
<td>Shrimp/prawns, lobster, milkfish and tilapia, oysters and squid, each 3%</td>
</tr>
<tr>
<td><strong>Adulteration</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Salmonella</td>
<td>1,832</td>
<td>Shrimp/prawns, 58%; lobster, 5%; milkfish and tilapia, each 4%; oysters and squid, each 3%</td>
</tr>
<tr>
<td>Filthy</td>
<td>1,460</td>
<td>Shrimp/prawns, 48%; tuna, 11%; mahi mahi, 7%; crab, 4%; conch/conchmeat, 3%</td>
</tr>
<tr>
<td>No process</td>
<td>683</td>
<td>Sardines, 20%; tuna, 17%; mackerel, 7%; herring, 5%; salmon and shrimp/prawns, each 4%; anchovy, clams, and octopus, each 3%</td>
</tr>
<tr>
<td>Insanitary</td>
<td>351</td>
<td>Shrimp and prawns, 69%; crab, 4%</td>
</tr>
<tr>
<td>Needs acid/Needs fce</td>
<td>336</td>
<td>Tuna, 18%; sardines, 17%; herring, 8%; mackerel, 7%; crab, 6%; anchovy and shrimp/prawns, each 5%; snails, 4%</td>
</tr>
<tr>
<td>Poisonous</td>
<td>231</td>
<td>Swordfish, 87%</td>
</tr>
<tr>
<td><em>Listeria</em></td>
<td>170</td>
<td>Salmon, 17%; fish roe/caviar, 14%; crab and shrimp/prawns, each 11%; pollack, 10%</td>
</tr>
<tr>
<td>Histamine</td>
<td>123</td>
<td>Mahi mahi, 53%; tuna, 32.</td>
</tr>
<tr>
<td>Impthraccp</td>
<td>41</td>
<td>Milkfish, 39%; tuna and groupers, each 17%</td>
</tr>
<tr>
<td>Unsafe col</td>
<td>41</td>
<td>Shrimp/prawns, 29%; seafood salad, 17%; fish roe, 12%</td>
</tr>
<tr>
<td>Mfrhaccp</td>
<td>32</td>
<td>Shrimp/prawns, 41%; tuna, 34%</td>
</tr>
<tr>
<td>Other</td>
<td>56</td>
<td>Shrimp/prawns, 34%; swordfish, 9%; anchovy and milkfish, each 5%</td>
</tr>
<tr>
<td><strong>Insanitary manufacturing, processing, or packing</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Mfr insan</td>
<td>130</td>
<td>Anchovy and clams, oysters, each 12%; mackerel, 7%; mussels and pollack, each 6%</td>
</tr>
</tbody>
</table>

Allshouse et al 2003, USDA Agricultural Economic Report No. 828
Outline

• How do pathogens differ between regions
• Why do we care?
  • Risk assessment
  • Source tracking
  • Validation of detection methods
• Summary and conclusion
How do pathogens differ between regions

• Different taxonomic groups may be found in specific regions
  • Ebola? *Burkholderia pseudomallei*?

• Certain serotypes may be found in some regions and not others or may be more frequent in some regions
  • *Salmonella, E. coli*

• Genotypes of common pathogens may differ between regions
  • Pathogens in some regions may be more likely to be resistant to antibiotics
  • Pathogens in different regions may differ in virulence
Foodborne Illness Acquired in the United States—Major Pathogens

Elaine Scallan,¹ Robert M. Hoekstra, Frederick J. Angulo, Robert V. Tauxe, Marc-Alain Widdowson, Sharon L. Roy, Jeffery L. Jones, and Patricia M. Griffin

Emerging Infectious Diseases • www.cdc.gov/eid • Vol. 17, No. 1, January 2011
Bacteria

*Bacillus cereus*, foodborne
*Brucella* spp.
*Campylobacter* spp.
*Clostridium botulinum*, foodborne
*Clostridium perfringens*, foodborne
STEC O157
STEC non-O157
ETEC, foodborne
Diarrheagenic *E. coli*
other than STEC and ETEC
*Listeria monocytogenes*
*Mycobacterium bovis*
*Salmonella* spp., nontyphoidal
*S. enterica* serotype Typhi
*Shigella* spp.
*Staphylococcus aureus*, foodborne

Parasites

*Cryptosporidium* spp.
*Cyclospora cayetanensis*
*Giardia intestinalis*
*Toxoplasma gondii*
*Trichinella* spp.

Viruses

Astrovirus
Hepatitis A virus
Norovirus
Rotavirus
Sapovirus
- 31 major known pathogens were estimated to cause 9.4 million episodes of foodborne illness.
- Episodes of illness caused by unspecified agents, including known agents with insufficient data to estimate agent-specific illness, known agents not yet recognized as causing foodborne illness, substances known to be in food but of unproven pathogenicity, and unknown agents were estimated to cause 38.4 million episodes of domestically acquired foodborne and 1,686 deaths
Burkholderia pseudomallei

- Causes melioidosis
  - Causes severe disease involving disseminated abscesses
  - Infection can be acquired by inhalation of dust, ingestion of contaminated water, and contact with contaminated soil especially through skin abrasions

- Found in contaminated water and soil and spread to humans and animals through direct contact with the contaminated source.
  - In SE Asia, the organism has been repeatedly isolated from agriculture fields, with infection occurring primarily during the rainy season.

- The distribution of melioidosis is predominantly tropical and subtropical with "hyperendemicity" in the top end of the Northern Territory of Australia and north east Thailand.
How do pathogens differ between regions

• Different taxonomic groups may be found in specific regions
  • Ebola?
• Certain serotypes may be found in some regions and not others
  • *Salmonella*, *E. coli*
• Genotypes of common pathogens may differ between regions
  • Pathogens in some regions may be more likely to be resistant to antibiotics
  • Pathogens in different regions may differ in virulence
**blaNDM-1** “The superbug”

- New Delhi metallobeta-lactamase 1, a transmissible beta-lactamase
- NDM-1 confers resistance to all penicillins, cephalosporins, and carbapenems.
- Most NDM-1 carrying bacteria are resistant to other antibiotics (aminoglycosides and fluoroquinolones)
- First description in 2008: *K. pneumoniae* and *E. coli* in Sweden from a patient transferred from a New Delhi hospital
- In 2010, 50 cases were reported in the UK
- In 2011, a broad range of Gram negative bacteria (*Shigella, Pseudomonas, Vibrio*) were found in samples of sewage and tap water in India
Global distribution of *bla*NDM-1 “The superbug”

Isolates with *bla*NDM-1 reported from:
- Japan
- New Zealand
- Turkey
- Lebanon
- Kuwait
- Moroco
- Algeria
- South Africa
- United Arab Emirates
- Denmark
- Germany
- Slovenia
- Switzerland
- Croatia
- Netherlands
- Guatemala
- France (no travel history)
- China (food-production animal origin)
- United States (*Salmonella Senftenberg*)

Fig. Worldwide distribution of bacteria with NMD-1 as of 1 October 2011

- Potential zoonotic and foodborne transmission
- Important implications for food safety
Why should we care?

- **Risk assessment**: food and commodities from different regions may represent different risk and hence may require different interventions

- **Source tracking**: Strains or subtypes with distinct geographical distributions provide opportunity of source tracking

- **Validation of detection methods**: Detection methods may need to be validated with isolates and strains from source countries
Risk assessment

• Are there unique/unusual pathogens likely to be found in products sourced from different regions

• Are pathogens strains/subtypes unique – do controls that work on domestic strains work on strains that may be introduced from other countries
  – Toxin production of *C. botulinum* strains at refrigeration temperatures
  – *Trichinella nativa* (associated with arctic animals) appears to be more resistant to freezing (a key intervention against *Trichinella*)
Why should we care?

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- **Validation of detection methods**: Detection methods may need to be validated with isolates and strains from source countries
**Salmonella 4,5,12:i:-**

- Closely related to serotype Typhimurium (4,5,12:i:1,2), but lacks the expression of second phase
- Prevalence among humans has been increased in 10 years all over the world
  - First reported in the literature in 1993 (Thailand)
  - Caused multiple outbreaks in Europe
    - In Spain, the 4th most common *Salmonella* serotype in 1998
    - In the US, the 18th and 6th most common serotype in 2002 and 2005, respectively
      - In 2007, caused an outbreak including at least 272 cases
  - Recently linked to multiple outbreaks linked to “feeder rodents”
Deletion Maps for S. 4,5,12:i:- Isolates

S. Typhimurium LT2

S. 4,5,12:i:- from Spain*

S. 4,5,12:i:- from the US, CVM23701+

* Data based on microarray (Garaizar et al. 2002)
+ Data based on genome sequence
PCR screen of 14 Spanish (9 S. 4,5,12:i:-; 5 S. Typhimurium) and 40 North American isolates (31 S. 4,5,12:i:-; 9 S. Typhimurium)

<table>
<thead>
<tr>
<th>Genes</th>
<th>US S. 4,5,12:i:- Clone (N=30)</th>
<th>Spanish S. 4,5,12:i:- Clone (N=10)</th>
<th>Rare S. 4,5,12:i:- GT-1 (N=1)</th>
<th>S. Typhimurium (N=14)</th>
</tr>
</thead>
<tbody>
<tr>
<td>STM2740</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>+</td>
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<tr>
<td>STM2757</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>+</td>
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<td>1053-1997</td>
<td>+</td>
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<td>-</td>
<td>-</td>
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<td>+</td>
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<td>+</td>
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Soyer et al., 2009. JCM.
Summary and conclusions

• Food microbiologists must have an understanding of global diversity of foodborne and zoonotic pathogens
  — ProMed as one resource
• Many “emerging” foodborne pathogens represent zoonotic pathogens
  — Understanding of worldwide trends in animal diseases is important
• Constant changes in agriculture and food production will likely increase challenges associated with, often un(der)recognized pathogens from different regions and sources