TB Slaughter Surveillance in California

- Four of top 40 US adult slaughter plants
- Granuloma submissions to CA lab (FY12-13) = 1,801
- Adults slaughtered in CA (FY11-12) = 819,978
  Rate = 4.4 submissions per 2,000 adults
- “Fat” cattle slaughtered in CA (FY11-12) = 837,083

Live Cattle TB Surveillance

- Private Veterinarians: 125,154 CFTs (1,413 accessions)
  Suspects 1,346 Response Rate 1.08%
- Regulatory Veterinarians: 143,402 CFTs (104 herds)
  Suspects 3,437 Response Rate 2.40%
September 30, 2013: New Slaughter Trace

- Granuloma identified at California plant
- PCR positive *M. tuberculosis* complex
- Culture & genotype pending
- Trace: 12 year-old home raised beef cow
- From San Diego Co. ranch
- Herd quarantined
- TB-testing now
- Wildlife in area
- Herd exposed to “likely” source of April 2013 sample
April 2013 – Slaughter Trace

- Identified at slaughter in California
  Inadequate ID to confidently trace
- Breed DNA analysis: Jersey female
  Most likely: 3 yr old from Pennsylvania
  Entered CA January 2012
  Sold out 500 cow San Diego Co dairy
- *M. bovis* genotype unique to USA
- Most closely resembles Mexican steer in TX in 2001 (26 SNPs difference)
- 5 year traces out; test 24 cattle located
- Investigations continue …
February 2013 Affected Herd

- October 2012 – *M. bovis* culture from slaughter sample
- **No ID collected** in AZ slaughter plant
- Trace 1 of 151 rebranded animals; 117 from CA, 34 from OOS = 72 CA “origin herds”
  
  Breed DNA = Holstein female; 62 possible herds of origin!

- *M. bovis* genotype matched strain from 2002 CA herd
- Test related trace herds = affected herd, Tulare Co
- 2,200 cow dairy under test-and-removal plan
- 14 TB-infected cattle removed to date
- Anticipated release June 2014
Investigation of 2013 Affected Herd

5 years of brand records + sale-yard records + private sales

- 11 dairy herds assoc. at calf ranch
- Trace ~4,400 cattle
- Investigated 99 herds
- Examined 36 herds for “brands from affected herd”
- Test 65 trace herds (approx 106,000 cows)
- No spread of bovine TB detected
- Wildlife surveillance - negative
- Two USDA/APHIS/VS IMT assisted with investigation
- Public Health & OSHA oversight of dairy personnel

How did infection hide for 10 years (only ~1 SNP change)?
11 Affected Dairy Herds in 11 years

- 6 detected by slaughter surveillance
- 5 detected by trace testing (2 were new strains!)
  
  7 different *M. bovis* strain types = 7 introductions of bovine TB in California

- Never found source of introductions
- All were “Mexican strain-types”
- Minimal spread from herds (4 w same strain-type)
- CA is only MAA state in nation

How is *M. bovis* entering State?

- Direct: Cattle (legal/illegal), wildlife, people, etc?
- Fomite: Foodborne, airborne, environment, etc?
**Human M. bovis Cases by County**

(N = 850)

2000-2010

White = No cases
Yellow = 1 - 19 cases
Orange = 20-50 cases
Red = >50 cases
## Spoligotype and 24 MIRU-VNTR Genotyping Results

<table>
<thead>
<tr>
<th>Year</th>
<th>Bovine M. bovis Case</th>
<th># Bovine Isolates Genotyped</th>
<th># CA Human Cases with Genotype</th>
<th>Any Epi Links?</th>
</tr>
</thead>
<tbody>
<tr>
<td>2007</td>
<td>Dairy D: Fresno</td>
<td>6</td>
<td>5</td>
<td>0 reside in affected counties, 2 recent US arrivals, 2/3 interviewed/no link accurate search neg</td>
</tr>
<tr>
<td>2007</td>
<td>Dairy F: Fresno</td>
<td>1</td>
<td>3</td>
<td>0 reside in county, 2 interviewed, no epi link accurate search neg</td>
</tr>
<tr>
<td>2009</td>
<td>Dairy G: San Bernardino</td>
<td>1</td>
<td>4</td>
<td>Accurint search neg^</td>
</tr>
<tr>
<td>2011 (1)</td>
<td>Dairy H: San Bernardino</td>
<td>4</td>
<td>2</td>
<td>0 reside in county Accurint and DMV searches, no links</td>
</tr>
<tr>
<td>2011 (1)</td>
<td>Dairy H: San Bernardino</td>
<td>1*</td>
<td>0</td>
<td>NA</td>
</tr>
<tr>
<td>2011 (2)</td>
<td>Dairy I: San Bernardino</td>
<td>23</td>
<td>0</td>
<td>NA</td>
</tr>
<tr>
<td>2011 (2)</td>
<td>Dairy I: San Bernardino</td>
<td>1*</td>
<td>2</td>
<td>0 reside in county Accurint and DMV searches, no links</td>
</tr>
</tbody>
</table>

* 1-off MIRU-VNTR

16 people infected with strains that match our cow strain