The Typhoid Fever Surveillance in Africa Program (TSAP)

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Present global disease burden model for typhoid fever (TF)
- Studies conducted in the period of 1990-2011 covered
- Data available from the below sites:

- Central America: none
- South America: none
- North Africa: 2
- West Africa: 1
- East Africa: 3
- Central Africa: none
- East Asia: 2
- South Asia: 7
- Southeast Asia: 4
- Central Asia: none
Extrapolation of available data to a wider region
Meeting on invasive Salmonelloses convened by the IVI in Kilifi, Kenya in January 2009

Question:
Is there typhoid fever in Africa?
If so, how much?

Outcome:
Recommendation that a sentinel network of field sites be created across Africa that follows similar standards and study procedures.
Objective:

to generate standardized data on incidence of invasive *Salmonella* bloodstream infections in sub-Saharan Africa

**Standardized procedures:**

- Protocol
  1) Inclusion criteria
  2) Clinical procedures
  3) Laboratory procedures

- Logistics incl. sample shipment
- Health care utilization survey (HCUS)
- Database/Data management

**Fig.** Location of TSAP study sites
### TSAP – Outcomes

<table>
<thead>
<tr>
<th>Research Topics</th>
<th>Expected outcomes</th>
</tr>
</thead>
<tbody>
<tr>
<td>Incidences for typhoid/paratyphoid fever and NTS infections</td>
<td>Identification of risk groups/target groups for preventive interventions</td>
</tr>
<tr>
<td>Antimicrobial susceptibility patterns</td>
<td>Adaption of treatment with adequate antibiotics/Re-evaluation of national guidelines/Awareness raising</td>
</tr>
<tr>
<td>Other organisms identified</td>
<td>Information on further causes of febrile diseases (i.e. incidence of viral infections in particular risk groups/per season)</td>
</tr>
<tr>
<td>Co-infection with malaria</td>
<td>Occurrence of <em>P. falciparum</em> on invasive bacterial infections</td>
</tr>
<tr>
<td>Clinical data/risk factor assessment</td>
<td>Determination of risk factors associated with enteric fever</td>
</tr>
<tr>
<td>Information on <em>Salmonella</em> carrier status</td>
<td>Proportion of <em>Salmonella</em> carriers in population</td>
</tr>
</tbody>
</table>
To develop and validate a disease burden prediction model using standardized data

Improvement of the current disease burden model to

• Predict burden of disease at population level and
• Identify populations at higher risk of *Salmonella* infections, using standardized data incl. risk factors collected at TSAP sites.

**Step 1:** Decision on input variables that are transferable and available/or easily determinable

**Step 2:** model to be calibrated against known output variables such as current disease burden estimates and validated in at least three TSAP sites on its ability to predict what it projected.

This model intends to enable the global community to predict the disease burden based on input variables in differing countries or geographical locations and help inform GAVI/country-level decision-making for vaccine introduction.
Active household-level surveillance of fever cases

Rationale:

• **Avoid self-treatment of fever with antibiotics** (leading to reduced microorganism detection rates in blood culture diagnostics)

• Capture patients and perform diagnostics early in the course of the disease (when bacteremia is high)

• **Adjust for the differing health systems**/health-seeking behaviors in TSAP countries, which might lead to incomparable incidence calculations

**Active household-level surveillance** of febrile cases in selected TSAP countries where health-care seeking attendance is hampered due to lack of health-care systems and at sites with considerable antibiotic self-treatment prior to fever diagnostics
Summary

- Standardized surveillance established and running in 10 sites
- Initial data indicate *S. Typhi* and NTS disease burden in study sites
- One year of surveillance data insufficient
- Design/validation of extrapolation model where data feed into
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THANK YOU
### Published S. Typhi incidence: Asia*

<table>
<thead>
<tr>
<th>Site</th>
<th>Hechi, China</th>
<th>Kolkata, India</th>
<th>North Jakarta, Indonesia</th>
<th>Karachi, Pakistan</th>
<th>Hue, Viet Nam</th>
<th>Total</th>
<th>P-value*</th>
</tr>
</thead>
<tbody>
<tr>
<td>Site setting</td>
<td>Urban / rural</td>
<td>Urban slums</td>
<td>Urban slums</td>
<td>Urban slums</td>
<td>Urban</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Surveillance target population (age in years)</td>
<td>5–60</td>
<td>All ages</td>
<td>All ages</td>
<td>2–15</td>
<td>5–18</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Typhoid Incidence (per 100,000/year) By age</td>
<td><strong>15.3</strong></td>
<td><strong>214.2</strong></td>
<td><strong>81.7</strong></td>
<td><strong>451.7</strong></td>
<td><strong>21.3</strong></td>
<td><strong>107.6</strong></td>
<td>&lt; 0.0001</td>
</tr>
<tr>
<td>0–1 years</td>
<td>NA</td>
<td>89.2</td>
<td>0.0</td>
<td>NA</td>
<td>NA</td>
<td>21.6</td>
<td>0.0777</td>
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<tr>
<td>2–4 years</td>
<td>NA</td>
<td>340.1</td>
<td>148.7</td>
<td>573.2</td>
<td>NA</td>
<td>364.8</td>
<td>&lt; 0.0001</td>
</tr>
<tr>
<td>5–15 years</td>
<td>29.3</td>
<td>493.5</td>
<td>180.3</td>
<td>412.9</td>
<td>24.2</td>
<td>170.8</td>
<td>&lt; 0.0001</td>
</tr>
<tr>
<td>≥ 16 years</td>
<td>12.4</td>
<td>119.7</td>
<td>51.2</td>
<td>NA</td>
<td>10.9</td>
<td>46.8</td>
<td>&lt; 0.0001</td>
</tr>
</tbody>
</table>

*Ochiai et al., Bull WHO 2008*