Molecular characterization of *Salmonella* Typhi isolates from South Africa 2012-2014

Nomsa Tau
Medical scientist
Centre for Enteric Diseases
National Institute for Communicable Diseases
National Health Laboratory Services
Species and subspecies were originally defined by DNA-DNA hybridisation, confirmed by MLEE and MLST and are currently differentiated by biochemical and serology.

The split in typhoidal and non-typhoidal is based on the disease syndrome. Typhoid and paratyphoid fever is prolonged, whilst extra-intestinal infection is usually acute and metastatic. Gastroenteritis is characterised by diarrhoea.

Differentiation of serovars is by agglutination with specific antisera against LPS (O), two phases of flagella (H1 and H2). There are 46 O, 85 H and 1 capsule (Vi) antigen which have been described in about 1,500 combinations within subspecies I.
Typhoid fever

• A systemic infection caused by bacterium S. Typhi

• NB cause of morbidity and mortality worldwide

• Globally: 26.9 million illnesses and 269 000 deaths annually

• Transmission via faecal-oral route

• S. Typhi is a human restricted pathogen
  • Human carriers - mostly responsible for endemic nature and for community outbreaks of typhoid fever
• Fluoroquinolones are recommended for treatment of typhoid fever
  • Treatment of typhoid fever a challenge

• The emergence and spread of the H58 S. Typhi

• H58 S. Typhi
  • Associated with multi-drug resistance to first-line antimicrobials
  • Reduced susceptibility to fluoroquinolones
  • A public health problem in Africa
  • Little known about the emergence, evolution and transmission of the H58 lineage
Aim

To use molecular techniques for the characterization of S. Typhi isolates from South Africa, 2012-2014.

Objectives:

• Use conventional PCR to screen South African S. Typhi isolates for the presence of the H58 haplotype

• Use multiple-locus variable number tandem repeat analysis (MLVA) assay to study the genetic diversity of S. Typhi isolates from South Africa
Methodology

Screening for H58 S. Typhi

Conventional PCR

- Targeting STY1507 gene present in all S. Typhi isolates
- H58 S. Typhi 107 bp product
- Non-H58 S. Typhi 1100 bp product

Murgia et al. 2016
MLVA assay targeting 5 VNTR loci

<table>
<thead>
<tr>
<th>Strain no</th>
<th>MLVA profile</th>
<th>MLVA Type</th>
</tr>
</thead>
<tbody>
<tr>
<td>Strain 1</td>
<td>197-530-293-187-249</td>
<td>MT1</td>
</tr>
<tr>
<td>Strain 2</td>
<td>197-530-303-170-255</td>
<td>MT2</td>
</tr>
<tr>
<td>Strain 3</td>
<td>197-530-293-187-249</td>
<td>MT1</td>
</tr>
</tbody>
</table>

Tau et al. 2017
Results

195 S. Typhi Isolates

54% (105/195) – H58 S. Typhi Isolates

Number of H58 S. Typhi isolates identified in South Africa from 2012 - 2014.
Geographical distribution of H58 and non-H58 *Salmonella* Typhi within provinces in South Africa for the years 2012 to 2014.

H58 S. Typhi identified in 8 provinces

Most isolated in GA and WC
2012

57 S. Typhi isolates
45 MLVA types
50% (n=28) S. Typhi H58
20 MLVA types

MST calculated for MLVA profiles of S. Typhi isolates from South Africa collected during 2012. Each node represents a different MLVA profile.
MST calculated for MLVA profiles of S. Typhi isolates from South Africa collected during 2013. Each node represents a different MLVA profile.
MST calculated for MLVA profiles of S. Typhi isolates from South Africa collected during 2014. Each node represents a different MLVA profile.

81 S. Typhi isolates
73 MLVA types
64% (52) S. Typhi H58 – 49 MLVA types
• During the study period 155 MLVA types were detected

• No major clusters were identified
  • Small sample size

• MLVA did not indicate predominance of any MLVA type in the country
  • MLVA types STyMT-114 and STyMT-130 present from 2012 to 2014
Summary

• Explored the use of a low-cost conventional PCR for rapid identification of H58 S. Typhi

• Data indicates that H58 S. Typhi is emerging and spreading in SA
  • Replacing the susceptible (Non-H58 S. Typhi) strain

• MLVA assay showed ability to discriminate among H58 S. Typhi isolates
Conclusion

• The dissemination of the H58 S. Typhi within South Africa is concerning
  • threatens successful treatment of typhoid fever

• Continued surveillance of typhoid fever is crucial
  • Monitoring disease spread
  • To inform prevention and control strategies

• MLVA can be very useful molecular characterization tool for the investigations of typhoid fever outbreaks caused by the H58 S. Typhi
Acknowledgements

• National Institute for Communicable Diseases

• Centre for Enteric Diseases