

# What have we learned from the **10,000** *Salmonella* **GENOMES PROJECT** ABOUT THE WORLDWIDE EPIDEMIOLOGY, TRANSMISSION AND VIRULENCE OF INTS?

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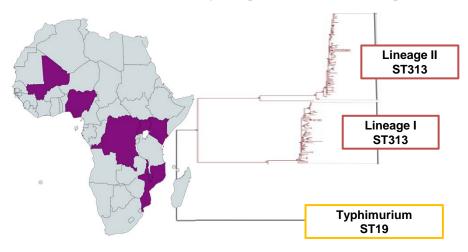
11<sup>th</sup> International Conference on Typhoid & Other Invasive Salmonelloses March 26-28, 2019 - Hanoi, Vietnam



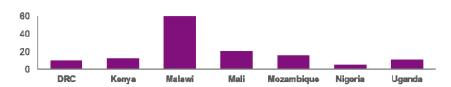


#### iNTS cause systemic disease in sub-Saharan Africa

### S. Typhimurium:2 distinct phylogenetic lineages

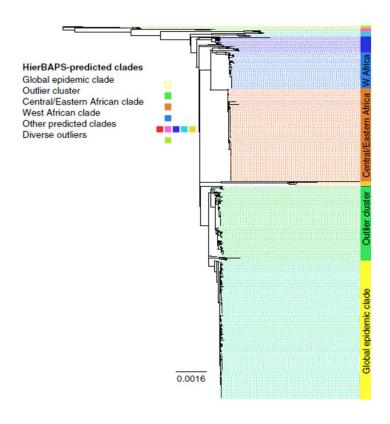


Okoro et al. (2012) Nature Genetics



129 iNTS genomes sequenced from 7 countries in sub-Saharan Africa

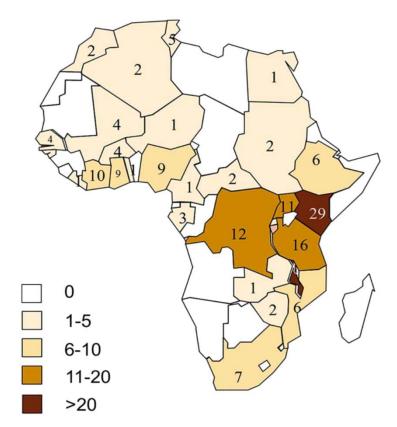
#### S. Enteritidis: African clades



Feasey et al. (2016) Nature Genetics



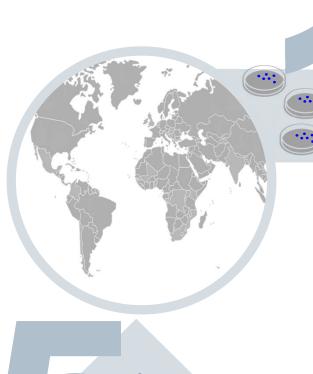




Number of publications from countries reporting iNTS blood culture isolates (Uche et al. 2017)

- More genomic data needed
- Most iNTS studies from 5 African countries
- Source and transmission?
- Antibiotic sensitive strains
- Evolution in action (previous studies were time-limited snapshots)

What is the situation in the rest of the world?

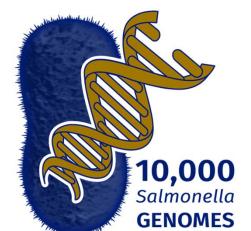


Salmonella isolated from different sources: clinical, animal and environmental













- Live bacteria
- Thermolysates
- > DNA







DNA extraction and sequencing was performed at the **Earlham Institute** 

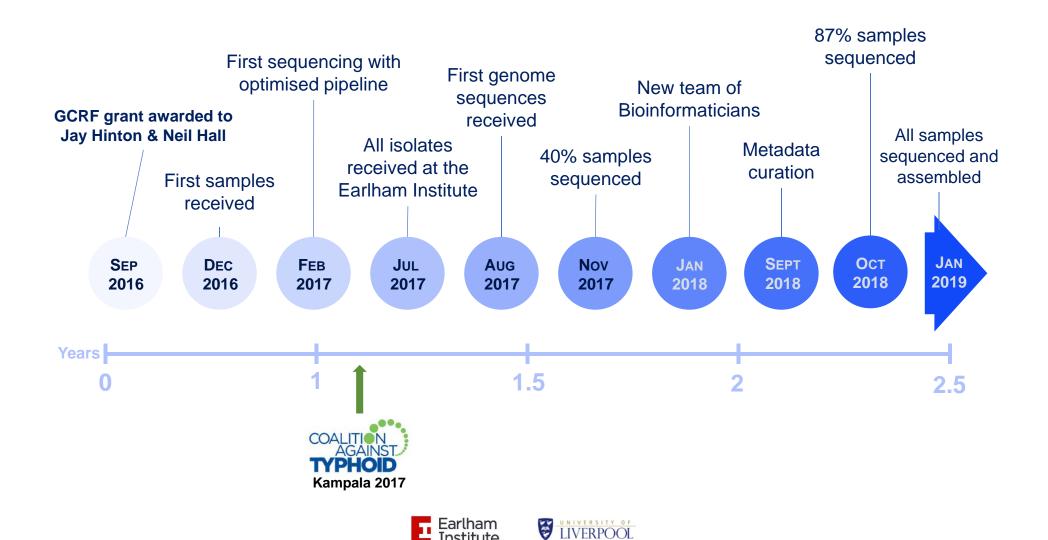


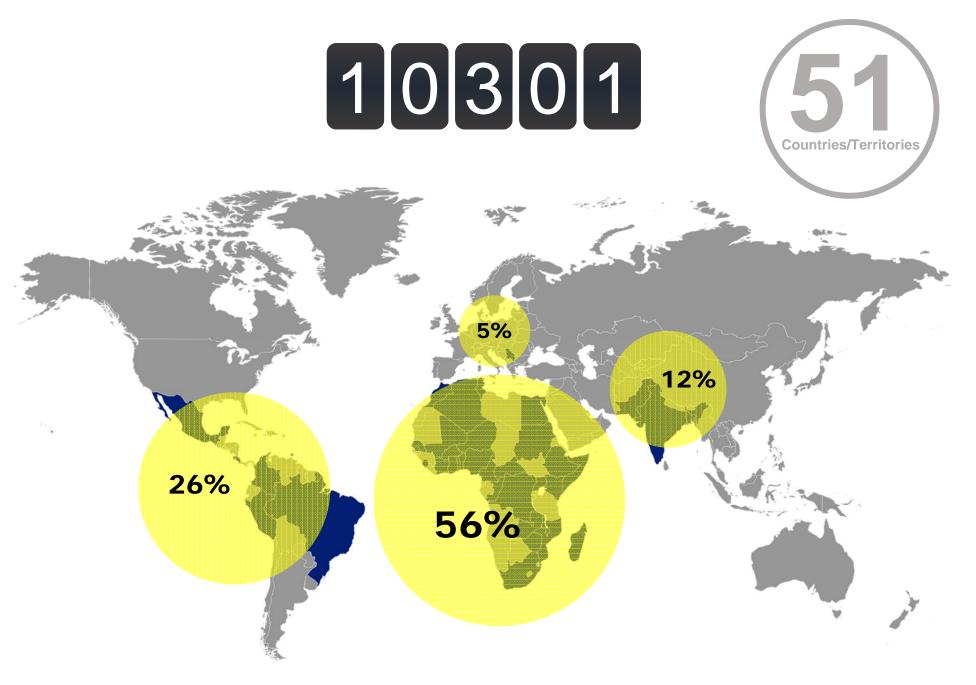






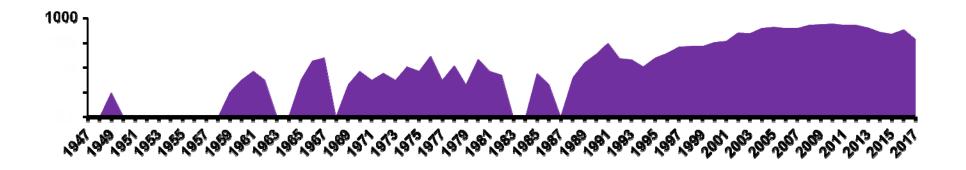
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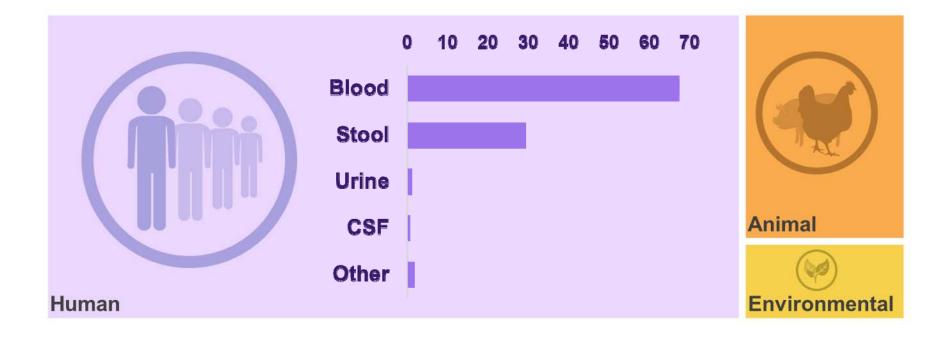






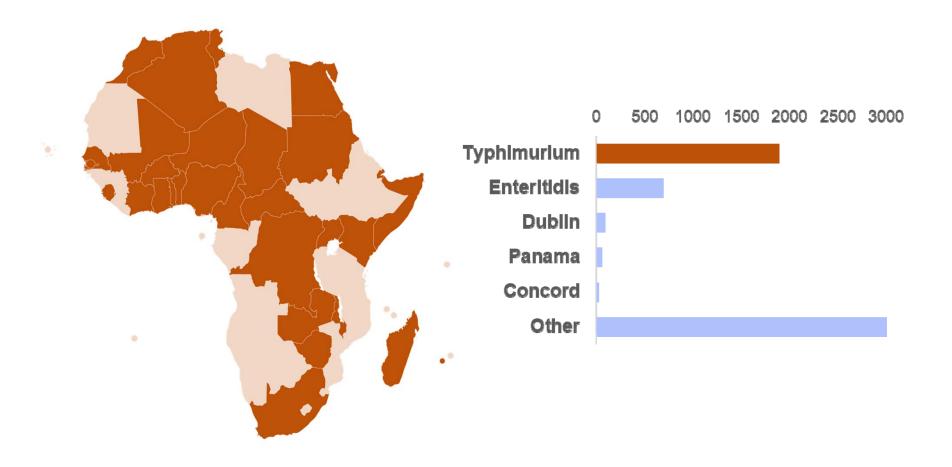






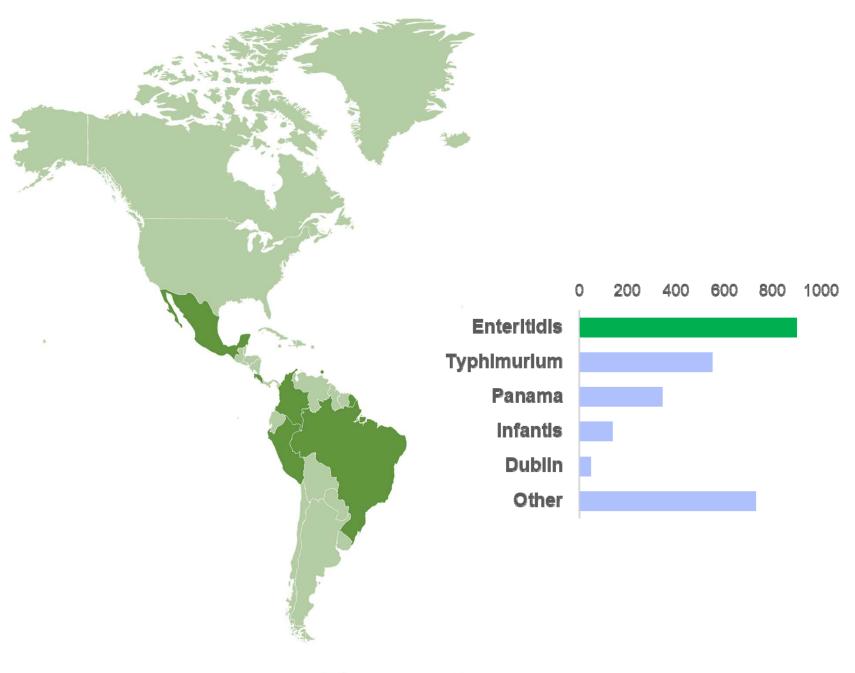










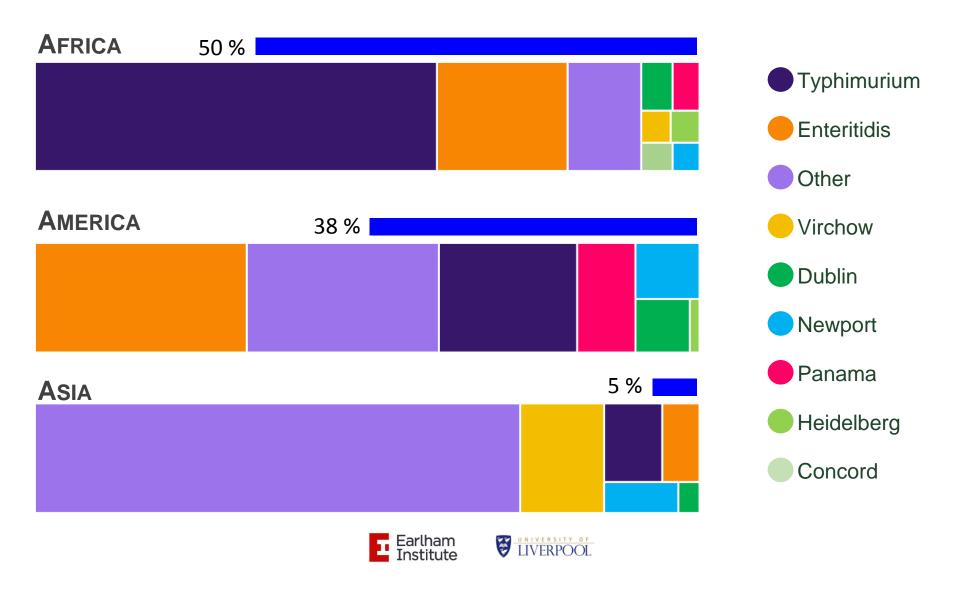


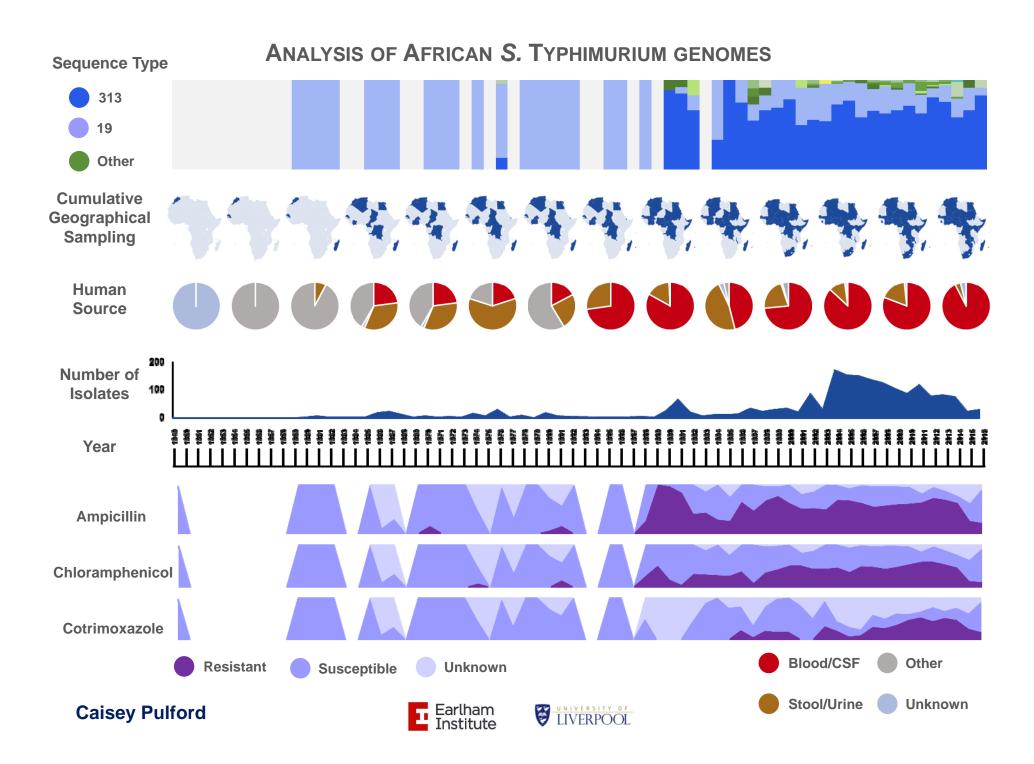




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Salmonella genomes that passed QC







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## All our collaborators!



Hinton Lab members Nick Feasey



Neil Hall Ross Low



**Global Challenges Research Fund (GCRF)**