

Sequencing of 10,000 *Salmonella* genomes: a worldwide effort to understand the epidemiology, transmission and virulence of invasive non-typhoidal Salmonellosis

Blanca Perez Sepulveda¹, Siân Owen¹, Caisey Pulford¹, Kate Baker¹, Neil Hall², Nicholas Feasey³, Jay Hinton¹

¹Institute of Integrative Biology, University of Liverpool, Liverpool, UK

²Earlham Institute, Norwich Research Park, Norwich, UK

³Liverpool School of Tropical Medicine, Pembroke Place, Liverpool, UK

Non-typhoidal *Salmonella* (NTS) are typically associated with enterocolitis, often related to the industrialisation of food production. In sub-Saharan Africa (sSA) however, there have been numerous reports of NTS being associated with invasive disease (iNTS disease), causing an estimated 680,000 deaths each year worldwide, the majority of which occur in sSA (Ao *et al.*, 2015). In addition to the high prevalence of immunosuppressive illness which predisposes to iNTS disease in sSA, new clades of *S. Typhimurium* and *S. Enteritidis* have been identified. These clades are characterised by genomic degradation, different prophage repertoires and novel multidrug resistant plasmids.

In order to understand how these clades are contributing to the burden and severity of this disease, it is crucial to expand the molecular surveillance of *Salmonellae* from Africa and other parts of the world, including isolates associated with invasive disease, gastroenteritis and both animals and the environment. The “**10,000 *Salmonella* genomes**” project will generate information relevant to the epidemiology, drug resistance and virulence factors of *Salmonellae* using a whole-genome sequencing approach.

During the first months of the project, we have initiated collaborations with researchers from several African and Latin-American countries, assembling a diverse collection of clinical and environmental *Salmonella* isolates with associated metadata. It is hoped that this enormous dataset will contribute to our understanding of the evolution of iNTS-associated *Salmonella* as well as the zoonotic or environmental reservoir of human disease. Detailed analysis of the accessory genomes of these strains will be performed at the Earlham Institute (Norwich, UK) to identify genes associated with drug resistance and virulence.

We are using a collaborative open-access philosophy to maximise the value of the worldwide *Salmonella*-research community and **we welcome new collaborators**. The resulting genome sequence data will contribute to public health control strategies in developing countries.