

## **WGSA.net: A Flexible Global Resource for Genomic Predictions of Antimicrobial Resistance and Surveillance of *Salmonella* Typhi.**

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**Background:** Whole genome sequencing has the ability to transform the way in which we manage the emergence of microbes that pose a direct threat to human health, in real time. However, there is a need for tools to make microbial genome data broadly and rapidly accessible to those who are not expert in genomics, thus linking the genome sciences to public health utility globally. The treatment of typhoid is being compromised by the emergence of strains with resistance to multiple antibiotics (MDR), including those currently used for treatment. The emergence of MDR typhoid has been driven by the global spread of an MDR *Salmonella* Typhi lineage known as H58 or haplotype 4.3.1. Thus, typhoid represents an exemplar of how MDR is threatening treatment at a global level.

**Methods:** We have developed WGSA.net, a web application that maps over 2,400 *S. Typhi* public genomes onto geographical space and predicts their antimicrobial resistance profile, with the ability to add new data rapidly. Users can analyse their own genomes or browse existing public collections.

**Results:** WGSA performs two essential tasks for surveillance and epidemiological investigations of *S. Typhi*, i.e., i) placing isolates into lineages and the recently established genotyping scheme, identifying their closest relatives and linking to their geographic distribution, and ii) detecting the presence of genes and mutations associated with antimicrobial resistance, a fundamental phenotype to assess the risk that the isolates pose to public health. Over 50 percent of the genome data currently available in WGSA belongs to the MDR lineage H58.

**Conclusions:** The data made easily accessible in WGSA can help the local investigator rapidly identify the potential source of their isolate and to predict likely resistance phenotype. This approach could be used to underpin the surveillance of typhoid and MDR, both locally and globally.