

## A genomic overview of the population structure of Salmonella.

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### ABSTRACT

### AUTHORS

### FUNDING INFORMATION

For many decades, *Salmonella enterica* has been subdivided by serological properties into serovars or further subdivided for epidemiological tracing by a variety of diagnostic tests with higher resolution. Recently, it has been proposed that so-called eBurst groups (eBGs) based on the alleles of seven housekeeping genes (legacy multilocus sequence typing [MLST]) corresponded to natural populations and could replace serotyping. However, this approach lacks the resolution needed for epidemiological tracing and the existence of natural populations had not been independently validated by independent criteria. Here, we describe EnteroBase, a web-based platform that assembles draft genomes from Illumina short reads in the public domain or that are uploaded by users. EnteroBase implements legacy MLST as well as ribosomal gene MLST (rMLST), core genome MLST (cgMLST), and whole genome MLST (wgMLST) and currently contains over 100,000 assembled genomes from *Salmonella*. It also provides graphical tools for visual interrogation of these genotypes and those based on core single nucleotide polymorphisms (SNPs). eBGs based on legacy MLST are largely consistent with eBGs based on rMLST, thus demonstrating that these correspond to natural populations. rMLST also facilitated the selection of representative genotypes for SNP analyses of the entire breadth of diversity within *Salmonella*. In contrast, cgMLST provides the resolution needed for epidemiological investigations. These observations show that genomic genotyping, with the assistance of EnteroBase, can be applied at all levels of diversity within the *Salmonella* genus.

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