



The research commercialisation office of the University of Oxford, previously called **Isis Innovation**, has been renamed **Oxford University Innovation**

All documents and other materials will be updated accordingly.
In the meantime the remaining content of this Isis Innovation document is still valid.

URLs beginning www.isis-innovation.com/... are automatically redirected to our new domain, www.innovation.ox.ac.uk/...

Phone numbers and email addresses for individual members of staff are unchanged

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Ribosomal MLST –

Rapid, efficient identification of all bacterial species and strains

Ribosomal Multilocus Sequence Typing (rMLST) indexes the DNA sequences of bacterial ribosomal protein genes to provide a universal typing method that covers the entire bacterial domain.

The method works at every taxonomic level, from species identification down to sub-strain level typing.

Ribosomal Multilocus Sequence Typing (rMLST) offers a universal method of speciation and bacterial typing that works at every taxonomic level (Figures 1-3). The approach indexes the variation of the 53 ribosomal protein subunit (rps) genes, assigning allele numbers to each unique sequence at each of the loci. This is analogous to conventional MLST which usually uses the sequences of 6-8 species or genus specific gene fragments.

The availability of whole genome sequence (WGS) data for thousands of bacterial isolates representing known bacterial diversity has provided an opportunity to develop a universal typing scheme that does not suffer from the practical constraints of designing universal primers inherent in conventional MLST. The loci chosen for rMLST represent a coherent set that, almost uniquely, are universally present throughout members of the bacterial domain. These are distributed around the chromosome and encode proteins under stabilising selection for functional conservation.

A web-accessible database has been developed at <http://rmlst.org/> containing allele definitions for over 325,000 unique allele sequences. A linked genome database has WGS data for about 118,000 isolates representing more than 3400 bacterial species. The rps gene variation catalogued in this database permits rapid speciation and typing of any bacterial isolate for which WGS data are available.

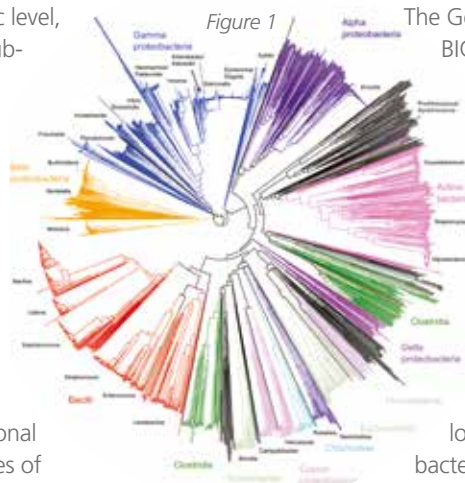


Figure 1

The Genome Comparator module of our BIGSdb platform allows genomic data from hundreds of isolates to be compared using gene-by-gene analysis at any taxonomic level. As rMLST uses 53 loci it is able to resolve down to the level of strain type, comparable, and often better, than conventional MLST.

Ribosomal sequence types (rSTs) are defined based on unique combination of alleles at the 53 rps loci. rSTs have been defined for 14 bacterial genera that include many human pathogenic species and work is on-going to scale-up the process to encompass all bacterial species.

References:

- Jolley & Maiden 2010. BIGSdb: Scalable analysis of bacterial genome variation at the population level. BMC Bioinformatics 11:595.
- Jolley et al. 2012. Ribosomal multilocus sequence typing: universal characterisation of bacteria from domain to strain. Microbiology 158:1005-15.

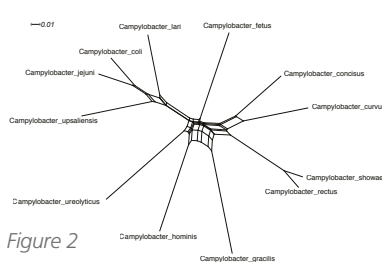


Figure 2

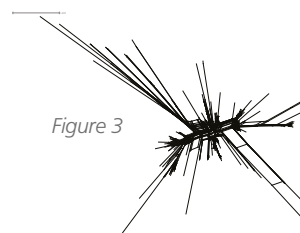


Figure 3: Isolates within a single clonal complex of a species: NeighborNet diagram from rMLST allelic profiles of 186 *Campylobacter jejuni* isolates from within the ST-21 clonal complex.



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