

(1) Submission ID#1526689

25 years of Multi Locus Sequence Typing

Author(s)

Martin C. J. Maiden, PhD

Professor

Department of Biology, University of Oxford

Background

Multilocus sequence typing (MLST), a product of the IPNC, is 25 years old. Initiated in Baltimore at the 10th meeting in 1996 the first MLST scheme was presented in Nice at the 11th in 1998. It has since been widely implemented applied across microbiology: a 'textbook' technique that has accompanied and complemented the rapid expansion of genomics, both enabled by increasingly high-throughput nucleotide sequencing at decreasing costs. This is an apposite moment to reflect on the success of MLST and to review its future.

Aim/Methods

MLST was conceived as a 'public good' to facilitate global health and related research: it was therefore not commercialised, and a crucial component is curated nomenclature schemes delivered free via the Internet. There are now over 160 schemes for different organisms, most hosted on the successor of the original MLST site, PubMLST.org. The IPNC community plays a continuing role in ensuring and assuring the integrity and usefulness of the Neisseria databases. Advanced data querying, display, analysis and export have been implemented.

Results

At the time of writing, public data from nearly 94,000 Neisseria isolates, including almost 50,000 whole genomes are available. Further, the databases have the capacity for 'private data': unpublished data or that which has commercial or other sensitivities. Although the original scheme was based on seven gene fragments, other schemes have been developed up to and including whole genome MLST (wgMLST). The database enables 'population annotation' a fusion of epidemiology, population biology, evolution and functional studies and has placed a major role in the development, implementation, and post-licensure surveillance of vaccines.

Conclusions

The terms sequence type (ST) and clonal complex (cc) are widely used and understood. It is unlikely that they will be replaced soon; indeed, in applications such as the characterisation of clinical specimens conventional MLST remains important. MLST has always had much wider implications than simply epidemiology in rationalising provenance and phenotype information for basic understanding. Finally, a principal motivation for MLST was preventing a 'descent into chaos' by the implementation of multiple competing and incompatible nomenclature schemes: a role as important now as it was 25 years ago.