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Defining a stable strain taxonomy in *N. gonorrhoeae* using LIN codes

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Background

Defining a stable strain taxonomy in *N. gonorrhoeae* has proved challenging, in part due to high levels of recombination disrupting phylogenetic signals. A core genome MLST scheme (cgMLST) has previously been constructed, providing key insights into gonococcal population structure (Harrison, 2020). However, because this grouping system used single linkage clustering, group fusion has become an issue as more gonococcal genomes are acquired. In this work a stable cgMLST-based Life Identification Number (LIN) code classification for the gonococcus was developed.

Aim/Methods

The gonococcal core genome was reassessed and strict thresholds for inclusion in a new core genome scheme chosen. Following this, genetic discontinuities in the population structure were detected, in order to partition similarity in cgMLST profile into a series of ordered bins. Based on this system each isolate was assigned a multi-position integer-based LIN code, reflecting the level of similarity across the core genome. This LIN code classification will be implemented in the PubMLST.org *Neisseria* database.

Results

The gonococcal LIN code classification system provides a rigorous and stable nomenclature for the categorisation and exploration of gonococcal population structure. Comparison to previous typing methods demonstrates the improvements made through this approach, and characterises how previously defined cgMLST groups relate to the new LIN code system.

Conclusions

The stability of the gonococcal LIN code will facilitate future analyses of gonococcal population structure, ensuring that the nomenclature used across research projects and publications to refer to various lineages remains consistent.