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Modelling the distribution of antimicrobial resistance genes and defence genes in *N. gonorrhoeae* genomes

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Background

Neisseria gonorrhoeae (Ng) is the causative agent of gonorrhoea and responsible for a significant global disease burden. Known to be a highly mutable pathogen, Ng has acquired and retained antimicrobial resistance (AMR) mechanisms to all known classes of antimicrobials, which have been extensively categorised by various typing systems. Despite its prevalence and impacts to human health, we know little about the bacterial defence systems which enable Ng to thrive.

Aim/Methods

This study applies a newly constructed bioinformatics pipeline to ~38,000 Ng whole genome sequences from available data sets, to identify and model trends across phylogroups, geographic regions, AMR genes, and genes involved in bacterial defence systems.

Results

Analyses are underway to investigate the relationship between these genes in a phylogenetic context, which may provide insight regarding the evolutionary pathways of Ng as well as appropriate targets for novel therapeutics.

Conclusions

Findings from the use of this novel bioinformatics pipeline can serve to inform future therapeutic research and deepen our understanding of Ng pathogenesis. Given that Ng is widely considered an urgent threat to human health due to its extensive arsenal of AMR mechanisms, the outcomes of this research may significantly accelerate the development of innovative therapeutic approaches or revitalise existing ones.