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Neisseria gonorrhoeae Sequence Typing for Antimicrobial Resistance (NG-STAR) for identification and surveillance of high-level ceftriaxone resistant isolates

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### Background

The spread of antimicrobial resistant *Neisseria gonorrhoeae* has become a worldwide concern, with many countries reporting resistance to azithromycin and cephalosporins, the current recommended therapies. *N. gonorrhoeae* Sequence Typing for Antimicrobial Resistance (NG-STAR) is an internationally available curated database and a valuable tool for tracking the spread of antimicrobial resistance (AMR) in gonorrhea worldwide by providing consistent nomenclature for antimicrobial resistance determinants. The *penA* gene contains several cephalosporin resistance determinants and with the emergence of highly resistant strains containing *penA*-60.001, often associated with NG-STAR type-233, NG-STAR has become instrumental in monitoring the worldwide dissemination of highly resistant *N. gonorrhoeae* strains.

### Aim/Methods

NG-STAR was used to assign allele numbers to unique DNA sequences of 7 genes (penA, mtrR, porB, ponA, gyrA, parC and 23S rRNA) that are associated with AMR. The combination of allele numbers for all genes produced profiles corresponding to unique NG-STAR types. New alleles and sequence types (STs) were submitted to the database by users worldwide and used to monitor the spread of highly resistant *N. gonorrhoeae* strains.

## Results

From 2019-2023, 5218 NG-STAR STs were assigned, consisting of 603 penA, 577 mtrR, 71 porB, 20 ponA, 61 gyrA, 186 parC, and 81 23S rRNA alleles. Alleles and STs were submitted from 36 countries across all continents, with the majority of submissions from Canada, Sweden, and USA. Isolation year was known for 1624/5218 (31.1%) submitted STs, 70% of which were isolated between 2017-19 (n=1136). The most common penA types were penA-2 (found in 1276/5218 STs), penA-14 (n=447/5218), penA-19 (n=404/5218) and the most common mosaic penA was type 34 (n=229/5218). penA-60 was found in 49 STs, 40 of which had unknown origin, with the remaining from China, Canada, Australia, and Sweden.

## Conclusions

NG-STAR is a valuable resource for monitoring the spread of AMR *N. gonorrhoeae* strains. The database is internationally standardized and contains data submitted from all continents. Global use of NG-STAR enables worldwide monitoring of high-level AMR-associated alleles such as penA-60.001 using standardized nomenclature. This enables a more timely response and improved monitoring of emerging drug resistant clones to help prevent the further spread of AMR gonorrhea isolates.