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Variation of *Neisseria gonorrhoeae* strain types identified within 2,805 isolates from the U.S. Gonococcal Isolate Surveillance Project across 13 jurisdictions, 2018 -2021

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## Background

CDC provides annual reporting of *Neisseria gonorrhoeae* (NG) strains and common antimicrobial resistant (AR) markers prevalent within the U.S. identified through CDC's Gonococcal Isolate Surveillance Project (GISP) and regional AR Laboratory Network. During the COVID-19 pandemic with temporary closures of STD clinics, there was a reduced volume of NG monitoring in 2020-2021. This study compares NG strains present in the U.S. prior to and after the start of the COVID-19 pandemic. This study coincides with the updated CDC treatment recommendation for uncomplicated gonorrhea with ceftriaxone only, removing azithromycin from dual treatment (12/2020).

## Aim/Methods

GISP collects urethral specimens from the first 25 men with symptomatic urethritis per month attending participating STD clinics across 32-33 jurisdictions; the first 5 specimens were whole genome sequenced by the regional AR Laboratory Network. CDC performed genomic analysis to identify common strain types (MLST) and AR markers. From January-March, 2020, 33 jurisdictions provided NG specimens. Post March, 2020 only 13 jurisdictions provided specimens of which >80% expected sequences were available for 2020-2021. This study reports the comparison of MLST frequency from those 13 sites from 2018–2021 (n=2805 sequences).

## Results

Of the 10 predominant MLSTs in 2018 only 6 MLSTs were represented in the top 10 of 2021. Several MLSTs significantly increased in frequency across this time. ST10314 (carrying ciprofloxacin resistance, GyrA S91F) increased from 3.4% (23/669) in 2018 to 11.0% (77/700) in 2021; and was represented in all jurisdictions (2021). ST8134 and ST11982 (predominately carried mosaic mtr operon, associated with elevated azithromycin MIC (~1.0-2.0 ug/ml)) were underrepresented (< 0.1%) in 2018, but increased to 8.0% (56/700) and 4.6% (32/700), respectively, in 2021. In 2021, ST8134 was highly abundant (>10%) in three jurisdictions in the Midwest, and ST11982 was abundant (>10%) in two jurisdictions in the West Coast.

## Conclusions

Monitoring of national *Neisseria gonorrhoeae* strain types and AR markers was performed through surveillance and genomic analyses. Temporal comparison across GISP jurisdictions identified differential expansion of strain types, which coincided with the pandemic and updated treatment recommendations. Understanding the variance within local regions may provide support for public health action and reduction of transmission.