MOLECULAR EPIDEMIOLOGY OF NEISSERIA GONORRHOEAE ISOLATES PRE- AND POST-COVID (2017-2022): SASKATCHEWAN

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Background:
Gonorrhea is the second most prevalent bacterial sexually transmitted infection in Canada and the incidence of gonorrhoea in Saskatchewan has been increasing. The COVID-19 pandemic has had considerable impact on public health related infections, for example, the extinction of the B/Yamagata/16/1988 lineage of influenza. Decreases in gonococcal strain type (ST) diversity during the pandemic have been reported. The purpose of this study was to ascertain trends in gonococcal susceptibility to antibiotics and strain types in Saskatchewan before and after the COVID pandemic (2017-2022).

Methods:
Neisseria gonorrhoeae isolates (n = 427) from Saskatchewan, Canada, were collected from 2017-2022. DNA was sequenced using Illumina and genomes were assembled with the Gen2Epi pipeline. NG-MLST, NG-MAST and NG-STAR STs were determined using Gen2Epi and PathogenWatch. Phenotypic susceptibilities to 10 antibiotics were determined using CLSI guidelines.

Results:
A marked shift in STs for NG-MLST, NG-MAST and NG-STAR was observed. NG-MLST STs1584, 1901 and 12462 were most common from 2017-2020. Between 2021-2022, these STs became less dominant and STs 14610, 7822 and 16674 represented a larger percentage of the isolates. For MG-MAST, STs 10451, 11933, and 5985 predominated between 2017-2020, and STs 19760 and 14994 dominated in 2021-2022. For NG-STAR, pre-pandemic STs 1061, 160 and 90 were most prevalent and STs 1493 and 4486 prevailed between 2021 and 2022. All isolates were susceptible to ceftriaxone and cefixime and under 5% of the isolates were resistant to azithromycin. Resistance to erythromycin and ciprofloxacin increased during this period and 27.7 % of the isolates, overall, carried plasmid-mediated resistance to tetracycline (TRNG).

Conclusion:
Surveillance of antimicrobial susceptibilities between 2017-2022 in Saskatchewan indicated that, despite the shift in strain types of *N. gonorrhoeae* post-pandemic, all isolates remained susceptible to antibiotics recommended for treatment. An outbreak

of TRNG isolates was undetected because tetracycline resistance is no longer actively reported.

Disclosure of Interest Statement:
The authors declare no competing interests.