GENOTYPES OF PENICILLIN SUSCEPTIBLE ISOLATES IN SASKATCHEWAN, CANADA INDICATE THAT SUSCEPTIBILITY TO PENICILLIN MAY BE PREDICTABLE

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Background:
Neisseria gonorrhoeae isolates have developed resistance to every class of antimicrobial introduced for therapy, including ceftriaxone. As treatment options become limited, re-introduction of previously recommended antimicrobials, such as penicillin, may be a viable option if susceptibility can be predicted. In several world regions, including Canada and the USA, over 80% gonococcal isolates are reported to be susceptible to penicillin. The purpose of this study was to establish the molecular characteristics of penicillin susceptible isolates to ascertain whether the development of a diagnostic test for penicillin susceptibility is feasible.

Methods:
416 isolates (2017-2022) from Saskatchewan, Canada were sequenced using Illumina and genomes were assembled with the Gen2Epi pipeline. NG-STAR sequence types were obtained using PathogenWatch and PAARSNP. MICs were determined using CLSI guidelines. PPNG were excluded from the analysis.

Results:
1104 *N. gonorrhoeae* isolates were analyzed for penicillin susceptibility retrospectively (2003-2022). The percentage of susceptible isolates ranged from 72.46%-100% in any given year and averaged at 93.57%. Only 71 (6.43%) isolates were chromosomally resistant to penicillin and 6 were PPNG. In examining the NG-STAR strain types of 416 isolates (2017-2022), predominant PBP2 PenA types were 14.001, 14.002, 34.001, 2.001, and 5.001, and carried various mutations in PorB1b and MtrR. Several isolates in all PBP2 types carried a 364D penA insertion and a L421P ponA substitution. None of the isolates contained an insertion at codon 345 and Mosaic penA type 34.001 (n= 78) contained I312M, G545S and V316T substitutions. Most of the susceptible and intermediate isolates were non-mosaic.

Conclusion:
Gonococcal susceptibility to penicillin has remained high in Saskatchewan for 19 years. None of the isolates (2017-2022) contained the penA 345 insertion predictive of resistance (Mortimer et al., 2022) consistent with our findings of over 93%

susceptibility. The introduction of a molecular test to predict chromosomal susceptibility to penicillin remains promising.

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