## Destexposure Prophylaxis Could Induc to Other Classes of Antimicrobials Neisseria gonorrhoeae: An In Silico Analysis

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Abstract: We found to genes in Neisseria gone g resistan to other antimicrobials SECURIOR S prophylax is may select

hree randomized controlled trials have now established that doxycycline postex posure prophylax is (PEP) can reduce the incidence of chlamydia and syphilis in men who have sex with men (MSM).1-3 The Doxycycline Postexposure Prophylaxis (Doxy PEP) study, the largest and most rigorous of these found that doxycycline also reduced the incident gonorhoeae.3 As a result of these findings, ce San Francisco are now offering doxy cycline PEP to of MSM attending their clinics.

A major concern about the widespread use of doxycycline PEP is that it will induce resistance to tetracyclines in N. gonorrhoeae and other bacterial species. Two doxycycline PEP

or other species, such as Streptococcus pyogenes. pothesis, we assessed the e-associated mutations norrhoeae and if these tance-conferring mutations to other classes of antimicrobials.

We tested the 2 major determinants of reduced susceptibility to tetracyclines-tetM and rps.J V 57M. High-level tetracycline resistance (>16 mg/L) is typically due to the plasmid-mediated acuisition of the tetM gene. The rps/ V57M substitution reduces of the 30S ribosome subunit for tetracyclines and re--level resistance.9

MATERIALS AND METHODS

N. gonorrhoeae Collection

(YCYCLINE POSTEXPOSURE PROPHYLAXIS COULD INDUCE CROSS-RESISTANCE 1

OTHER CLASSES OF ANTIMICROBIALS IN NEISSERIA GONORRHOEAE:

microbials has been frequently associated with the state of the state

In the direct pathway, tetracyclines have been noted to induce mutations that confer cross-resistance to fluoroguinolones, β-lactams, and

linked to markers of resistance to other antimicrobials, then the use of doxycycline may indirectly select for resistance to these other DATA ANALYSIS

All known RAMs were grouped per gene to construct a binary variable per gene that indicated if any RAM was present in Thibaut Vanbaelen, Sheeba Santhini Manoharan-Basil, and Chris Kenyon used to construct the variables are as follows: gwA (S91F, D95A, D95G, D95N), parC (D86N, S88P, E91K), penA (A311V, V316T, 1312M, ins346D, T483S, P551S, G542S, G545S), pon4 (L421P),

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Authors' Contributions: C.K., T.V., and S.S.M.-B. conceptualized the study. C.K. was responsible for the statistical analyses. All authors read and approved the final draft.

Ethics Statement: This analysis involved a secondary data analysis of anonymized public-access data.

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Sexually Transmitted Diseases • Volume 50, Number 8, August 2023 V57M and tetM by genogroup. This analysis was limited to the genogroups with more than 50 isolates. Statistical analyses were conducted using Stata V16 and the  $\chi^2$  test to compare groups.

## RESULTS

Clonality by Genogroup

We found strong evidence of clonal spread of rps.J V 57M and tetM by genogroup (Fig. 1).

BREACH SYMPOSIUM genogroups with more than 50 isolates. rpsJ V57M mutation (n = 592). For th

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