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Characterization of recombination events among co-circulating populations of Neisseria gonorrhoeae and Neisseria meningitidis in the U.S

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Background

Neisseria gonorrhoeae (Ng) and Neisseria meningitidis (Nm) has high genomic similarity and undergo extensive recombination. Nm is typically found in the oropharynx and occasionally causes of urethritis, while Ng causes urogenital infection, it can also cause oropharyngeal infections. Nm strains causing urethritis cases harbor Ng genes and mosaic antimicrobial resistance (AR) genes have been described in Ng sharing similarity with Nm; both presumably acquired by recombination. In this study, we characterize the recombination hot spots within lineages of the two species and understand donor/recipient dynamics of recombination events at the genus level.

Aim/Methods

We analyzed the genomes of Ng (n=1591) and Nm (n=1553) isolates from urethral, pharyngeal, and rectal anatomic sites collected through the enhanced Gonococcal Isolate Surveillance Project (eGISP) during 2017-2020 from 12 U.S cities. Recombination events were detected using GUBBINS within each identified lineages of Ng and Nm, and the direction of recombination events were predicted using fastGEAR.

Results

Phylogenetic analysis inferred 22 and 29 major lineages within Ng and Nm, respectively. The average recombination per mutation events (ρ/θ) rates for each lineage varied among the two species (Ng: 0.00798-0.05495; Nm: 0.04189-0.2737) and were statistically significant suggesting that the lineages within Ng ($p=1.3\times10\text{-}13$) and Nm ($p=2.2\times10\text{-}16$) could have different recombination rates. ρ/θ rates within lineages for the three anatomic sites were not significantly different, but rates in Nm pharyngeal isolates were higher compared to the other sites, while it was uniform among the 3 sites for Ng. The highly recombinant lineages were genogroup (GG) 3a (MLST-9363) and Clonal Complex (CC) 41/44 for Ng and Nm, respectively. Several important genes associated with AR, virulence, or host adaptation were identified to be hotspots of recombination across multiple lineages within Ng and Nm. The direction of recombination events was not only between Ng and Nm but also from other Neisseria species.

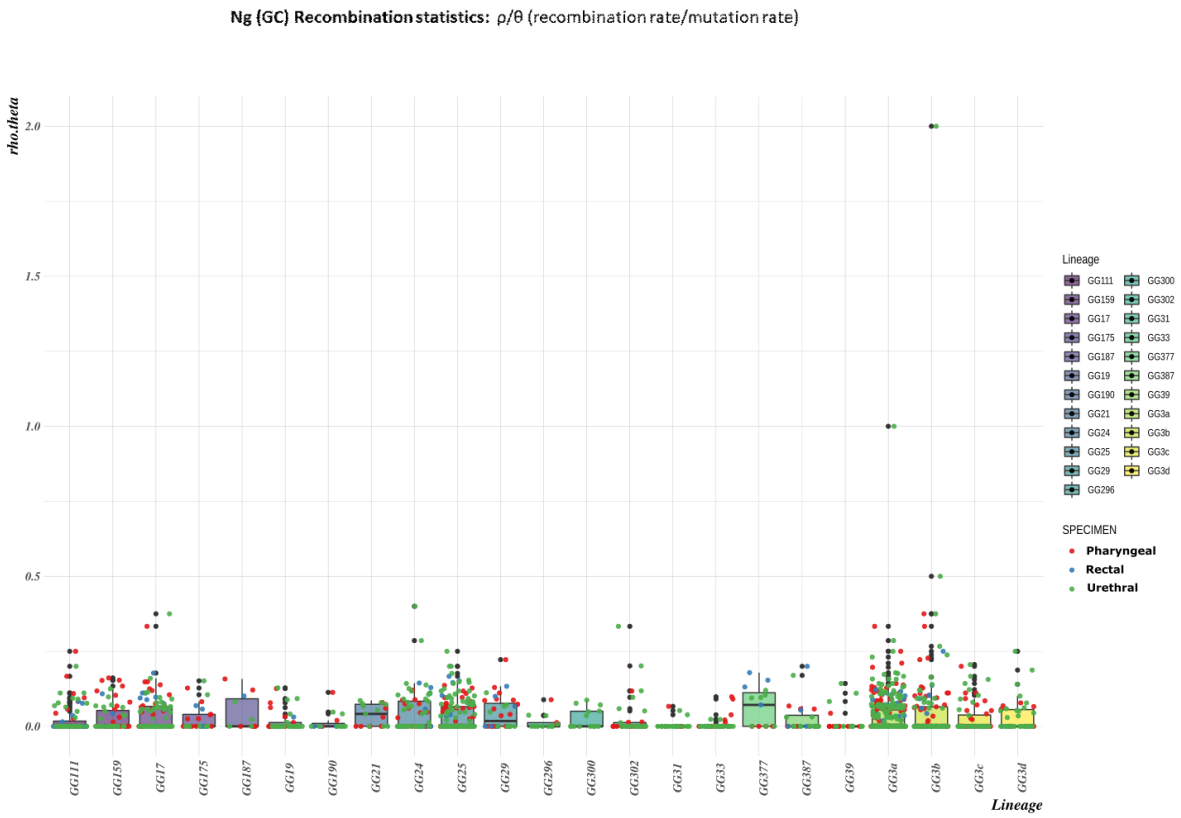
Conclusions

Our results indicate that lineages of Ng and Nm circulating in the U.S have significantly different recombination rate phenotypes, which may have differential effects on the evolution of AR lineages, emergence of new AR/pathogenic strains and serogroups, and adaptations for improved colonization and immunity evasion, thus posing a public health challenge.

Uploaded File(s)

Supplemental Document Upload

Ng (GC) recombination statistics across lineages: ρ/θ (recombination rate/mutation rate)



Nm recombination statistics across lineages: ρ/θ (recombination rate/mutation rate)