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**PHYLOGENETIC ANALYSIS OF penA ALLELE DIVERSITY IN *Neisseria gonorrhoeae*
ISOLATES FROM GLOBAL SOURCES**

Marissa A. Konieczko

Abstract

Antibiotic resistant *Neisseria gonorrhoeae* represents a serious threat to human health. As the second most frequently acquired sexually transmitted infection in the world, gonorrhea has incidence rates as high as 24/1000 people. Thirty percent of all gonococcal infections in the US during 2017 were resistant to at least one antibiotic and resistance to the last available monotherapy, ceftriaxone, is on the rise. The research herein aims to examine the evolution and divergence of penA, the most important genetic locus associated with gonococcal resistance.

Ninety sequences from 14 countries spanning three continents (North America, Asia, and Europe) and the period from 1950 to 2018 were acquired from GenBank. Based on sequence alignments of the penA coding region, maximum clade credibility and maximum likelihood trees were constructed. Two main clades were identified: A and B. Clade A is primarily Asian, male, and antibiotic resistant. Clade B mainly represents North American female isolates with susceptible phenotypes. The tMRCA of the MCC tree was 2238 BCE.

These results support the tree structure observed in other studies that focused on the evolution of the entire gonococcal genome. They also suggest an older date for the emergence of the penA gene than that previously found for the gonococcus, one which supports the date found in the historical record (i.e., 2600 BCE). No inferences about transmission routes can be made, but it appears that AMR strains evolved in Asia, while the majority of susceptible strains derive from North America.