

## Introduction

In 2020, the WHO estimated 82.4 million new *Neisseria gonorrhoeae* (NG) infections and recognized gonorrhea as a major public health problem. In France, surveillance of NG is based on the National Reference Center for Sexually Transmitted Infections (STI NRC) and a voluntary laboratory network. However, geographical constraints in the French overseas departments and regions complicate this survey, resulting in a lack of data [1, 2]. This study presents a phenotypic and genotypic update of NG infection data from the French Polynesia Referral Hospital (FPRH), which is located in Tahiti.

## Methods

Between May 2021 and November 2023, 48 isolates from 48 patients were sent to the STI NRC for gonococcal expertise at Saint-Louis Hospital in Paris, France. Demographic data were also collected. Antimicrobial susceptibility testing was performed using chocolate agar and E-test strips (Biomérieux), and the results were interpreted according to EUCAST guidelines. Genomic characterization, including typing, resistome analysis, and construction of a phylogenomic tree, was performed using whole genome sequencing (WGS) with Illumina technology (Illumina, <https://www.illumina.com/>) as previously described [4].

## Results

### Characteristics of patients with gonorrhea in Tahiti (n=48)

The patients were mostly male (73%) with an average age of 26.6 years (range: 0-47 years). Over 50% of patients presented to the emergency department with symptoms. Most samples were urogenital (90%).

### Antimicrobial resistance of Tahitian isolates

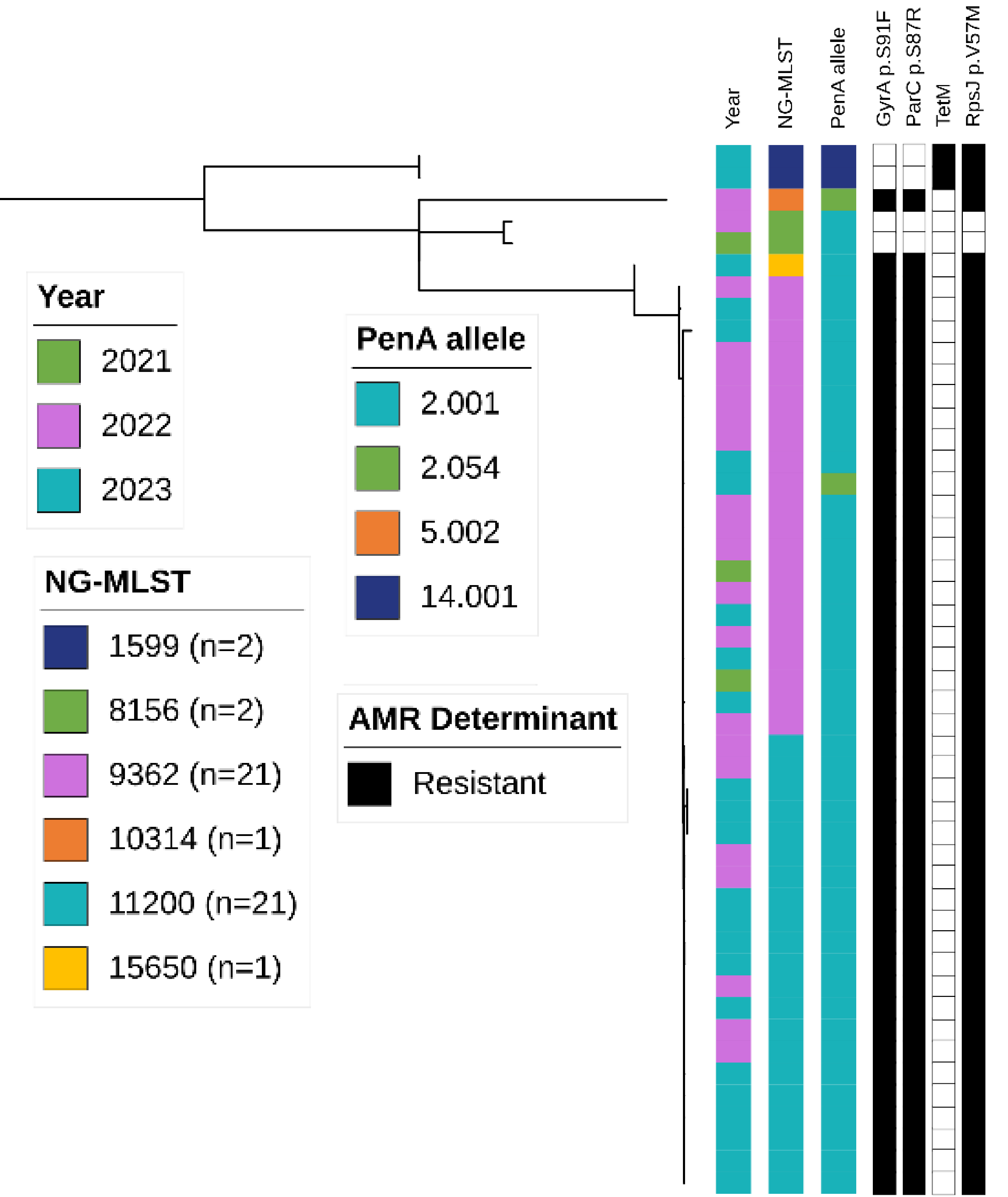
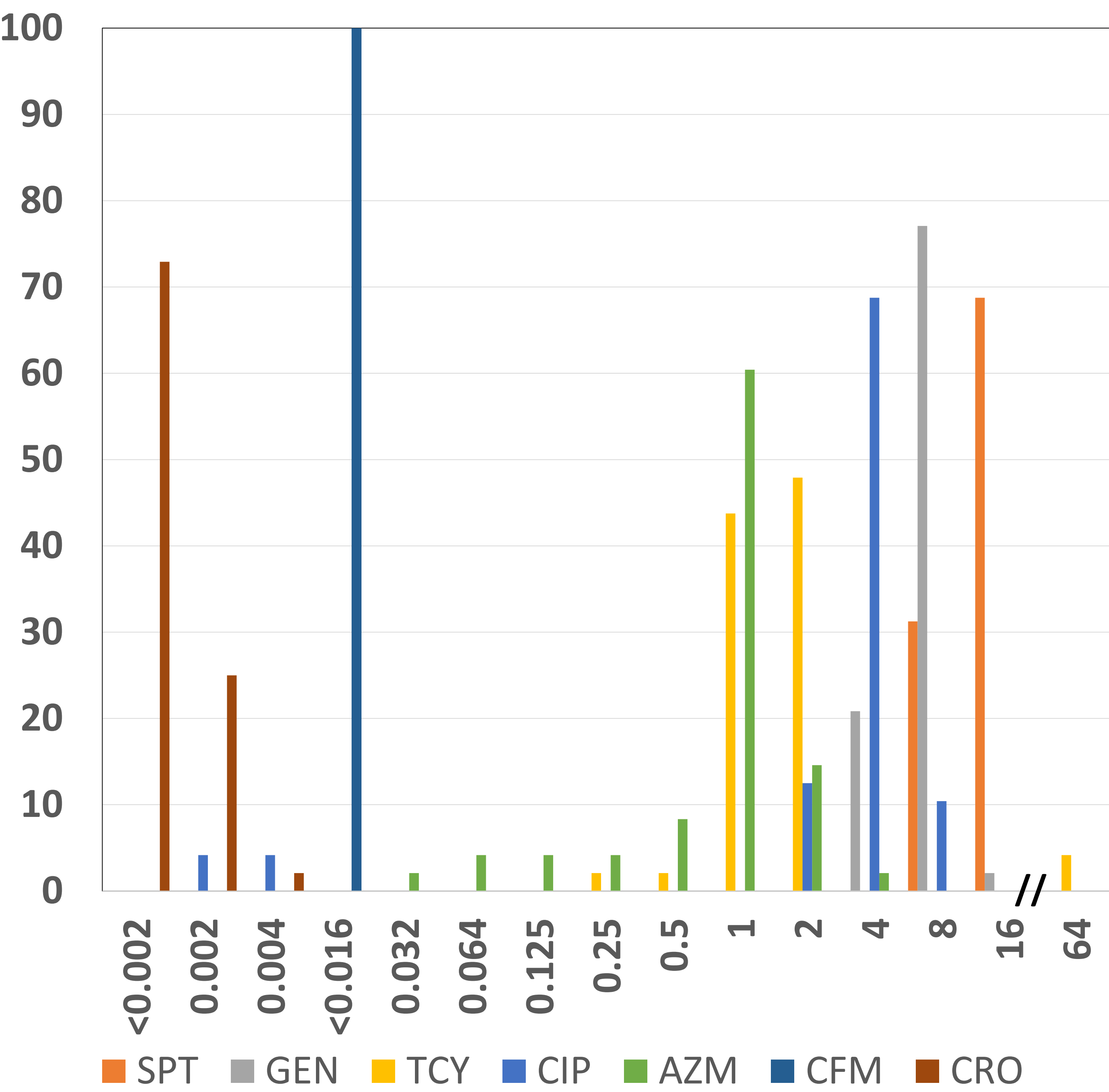
Resistance to tetracycline, ciprofloxacin, and azithromycin was observed in 96%, 92%, and 17% of isolates, respectively. Interestingly, all isolates resistant to ciprofloxacin were also resistant to tetracycline. However, two isolates with high-level tetracycline resistance were susceptible to ciprofloxacin. All isolates resistant to azithromycin were also resistant to tetracycline and fluoroquinolones. No isolates from Tahiti were resistant to cefixime or ceftriaxone. Figure 1 shows the overall distribution of MICs.

### Genotypic analysis of Tahitian strains

All isolates harbored a non-mosaic *penA*, which resulted in susceptibility to cefixime and ceftriaxone. All isolates resistant to ciprofloxacin had an S91F mutation in GyrA and an S87R mutation in ParC. All tetracycline-resistant isolates possessed the V57M mutation in RpsJ, including two isolates that produced Tet(M), resulting in high-level resistance. ST9362 and ST11200, the NG-MLST sequence types, each accounted for 44% of the isolates. The ST9362 clone is frequently detected in metropolitan France, whereas the ST11200 clone was identified in only one isolate in 2022.

### Figure 2 – Phylogenomic tree of the Tahitian isolates.

**Figure 1 – Distribution of MIC Values in Tahitian Isolates.** Spectinomycin (SPT), Gentamicin (GEN), Tetracycline (TCY), Ciprofloxacin (CIP), Azithromycin (AZM), Cefixime (CFM), Ceftriaxone (CRO). The x-axis is in mg/L and the y-axis in %



## Conclusion

NG isolates from French Polynesia were primarily found in men exhibiting genital symptoms. Nearly all of the isolates were resistant to ciprofloxacin and tetracycline, with over 90% resistant to both. Two dominant *Neisseria gonorrhoeae* clones circulating in Tahiti were identified: ST9362, which circulates in Metropolitan France, and ST11200, which seems to be specific to French Polynesia. Repeating this type of survey would improve the monitoring of and provide updated data on gonococcal infections in French Polynesia.