

Invasive Meningococcal Diseases in southern Vietnam in a ten year period from 2012 to 2021

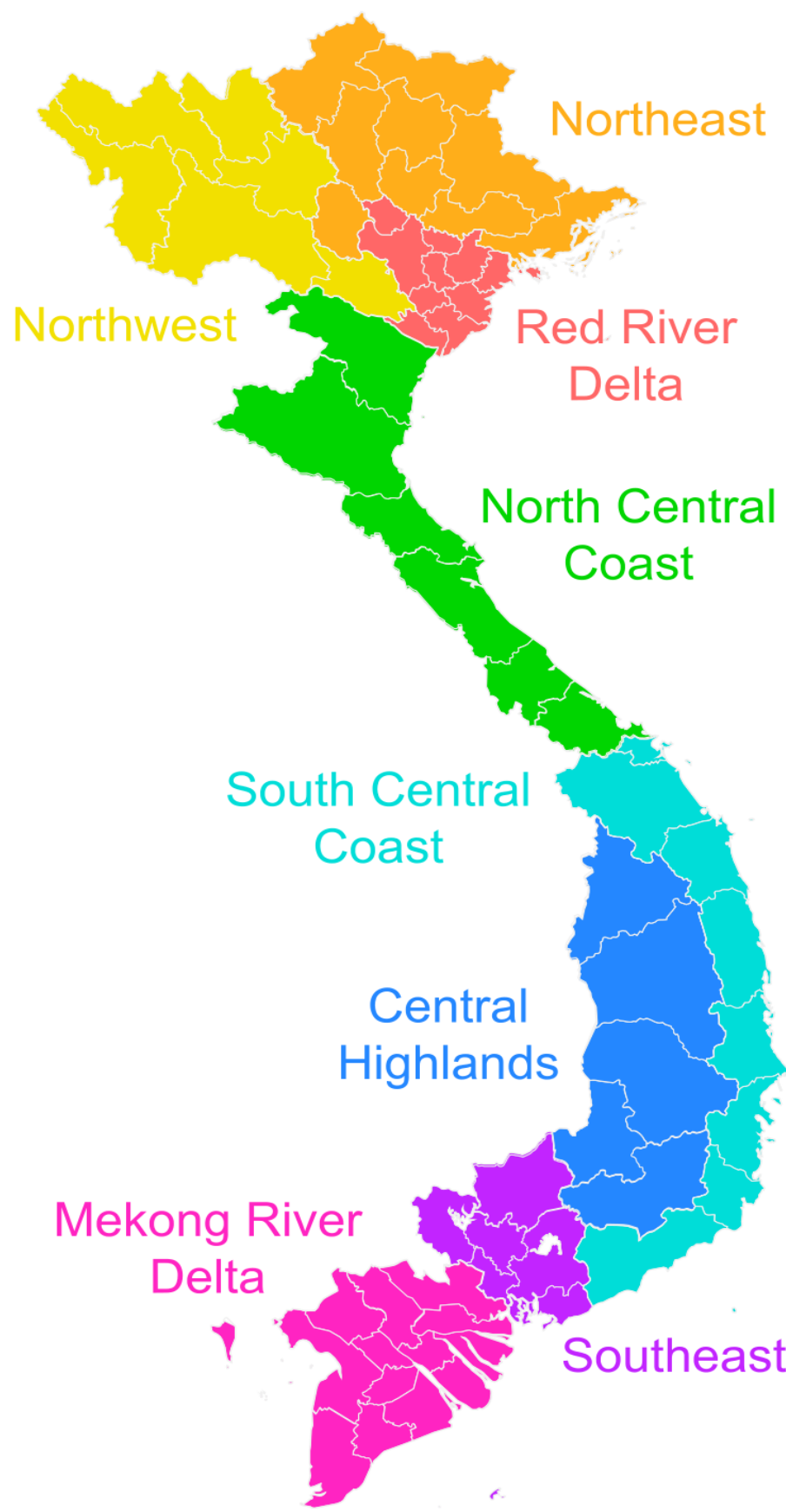
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Introduction

Neisseria meningitidis (Nm), encapsulated one of six most popular serogroup A, B, C, W, Y, and X, causes Invasive Meningococcal Disease (IMD), including meningitis and sepsis. In South Vietnam, this severe infection was first noticed in South Vietnam in the 1950s, with 12 cases, while two major outbreaks was reported in the 1970s. NmC played main role in the second epidemic, presenting 96% of the cases and a fatality rate of around 25% among roundly 7000 patient-cases (1). Since then, IMD has been poorly documented and characterize in the country.

This work aimed to describe IMD in the Southern over ten years from 2012 to 2021 as well as to characterize the strains collected from the cases.



Results (continued)

All 20 isolates determined susceptibility were resistant/reduced susceptible to at last one antibiotic. Of those, thirteen resisted chloramphenicol (MIC from 32 to 256 mg/L), eleven were intermediated penicillin (MIC at 0.19 - 0.38 mg/L), five resisted ciprofloxacin (MIC at 0.19 - 0.5 mg/L), and one was reduced susceptibility to ceftriaxone, with MIC at 0.125 mg/L. The reduced susceptibilities to penicilline and ciprofloxacin were associated with alternation of *penA* and *gyrA*, respectively, while chloramphenicol resistance was due to *catP* gene.

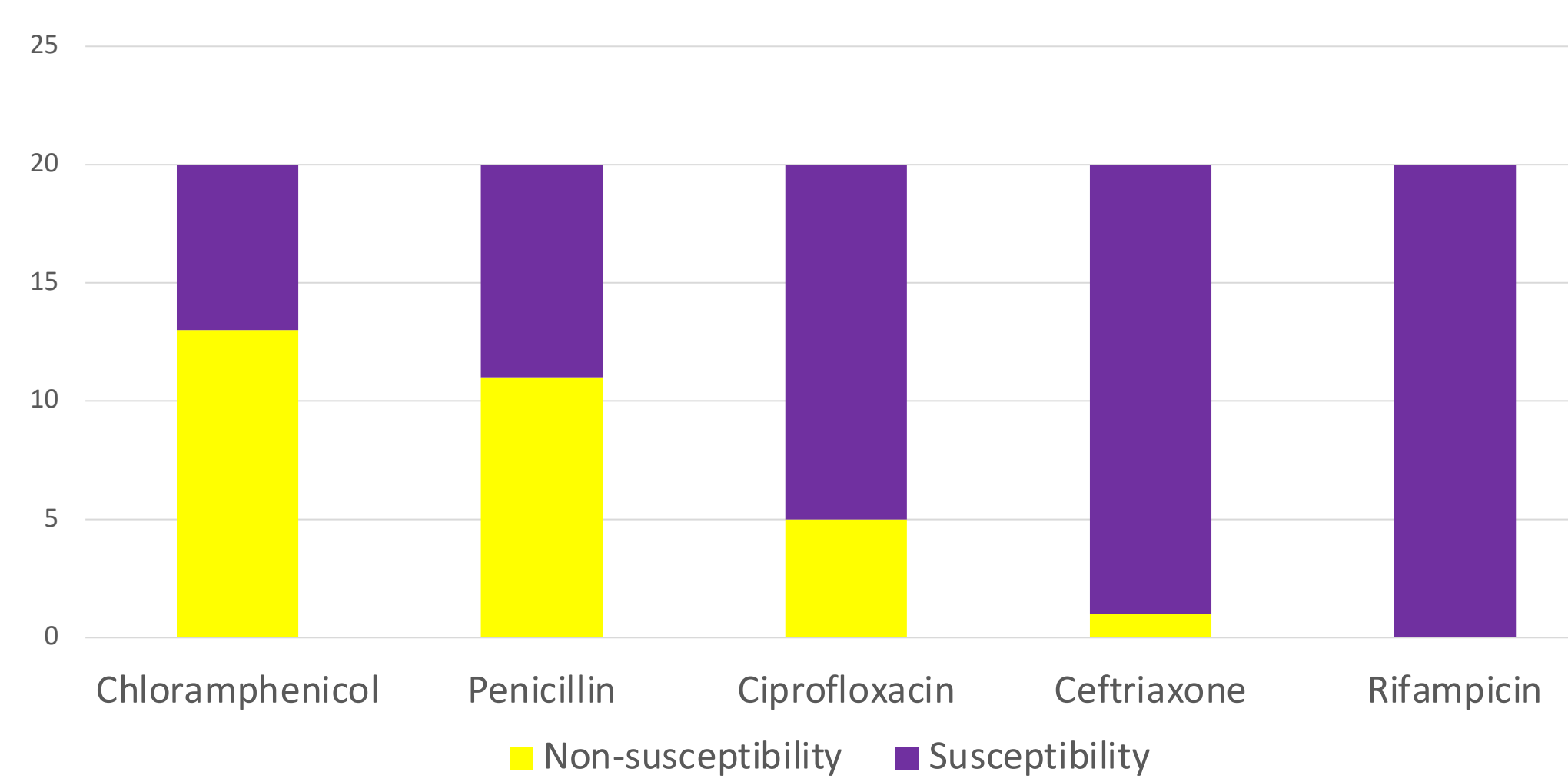
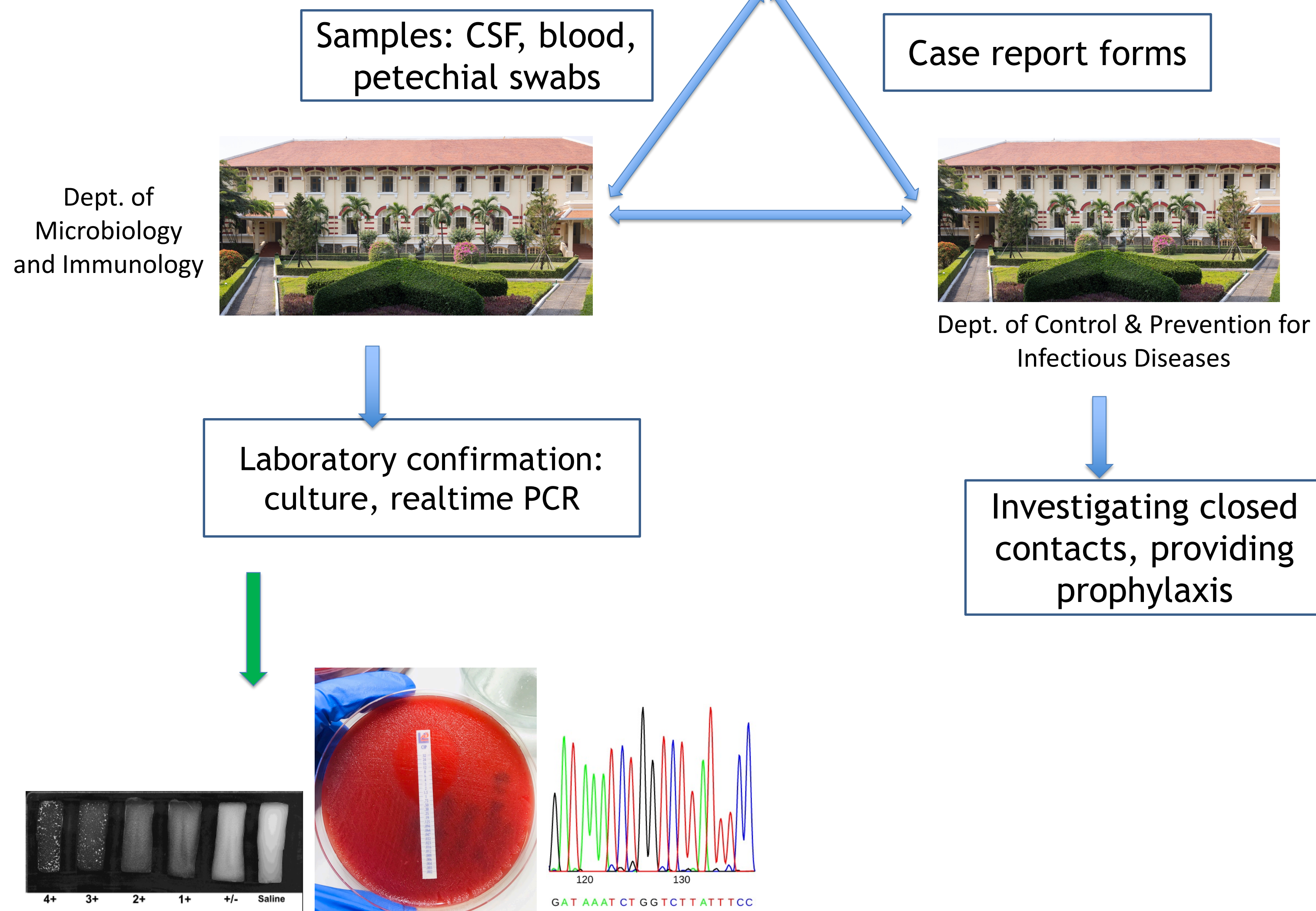


Figure 2. the susceptibility among Nm collected from IMD in southern Vietnam from 2012 to 2021. The antimicrobial susceptibility testing was determined with E-test, then being referred to CLSI 2020.

Methods

The Surveillance



Multilocus Sequence Typing and Genotyping

Analyzing 31 MLST profiles we found 16 different STs which belonged to 3 clonal complexes, including CC4821 (n=3), CC41/44 (n=1), and CC162 (n=1). Two-third (n=20) of strains belonged to a lineage of ST-1576, not assigned a CC, which included seven different ST. The most common genotype among NmB was B:P1.19,15;F4-6:ST-1576 (n=7) while 2 NmC were C:P1.5-1,2-2;F5-8:ST-4821 clonal complex.

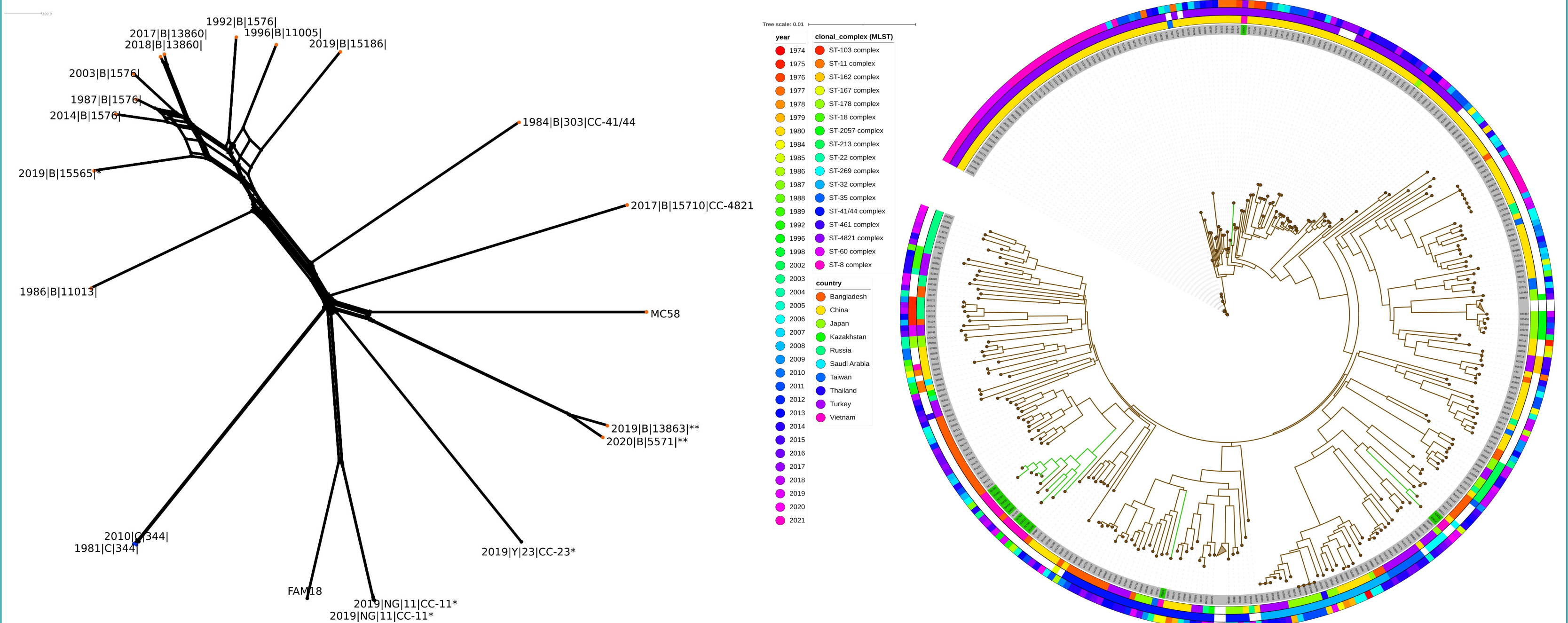


Figure 3: The relationship ST-1576 among IMD strains in Vietnam. The network was based-on gene-by-gene approach, displayed with Splitstree v4. Orange spots represent for NmB, blue for NmC and black for others; *sexually transmitted infectious Nm.

Figure 4. The relationship between 13 NmB in south Vietnam to 370 NmB in Asia. The neighbor-joining tree was generated using the Genome Comparator, being annotated and visualized by iTOL. The inner represents for country, the middle indicates clonal complex, and the outer illustrates for year.

Results

Totally, 54 cases were laboratory-confirmed over ten years, of which 34 (63%) were positive with realtime PCR only while 20 cases were confirmed by bacterial culture. Children under five and teenagers aged between 18 and 24 accounted for 78% of the cases (42/54). NmB was the most dominant, accounting for 93% of the cases (50/54).

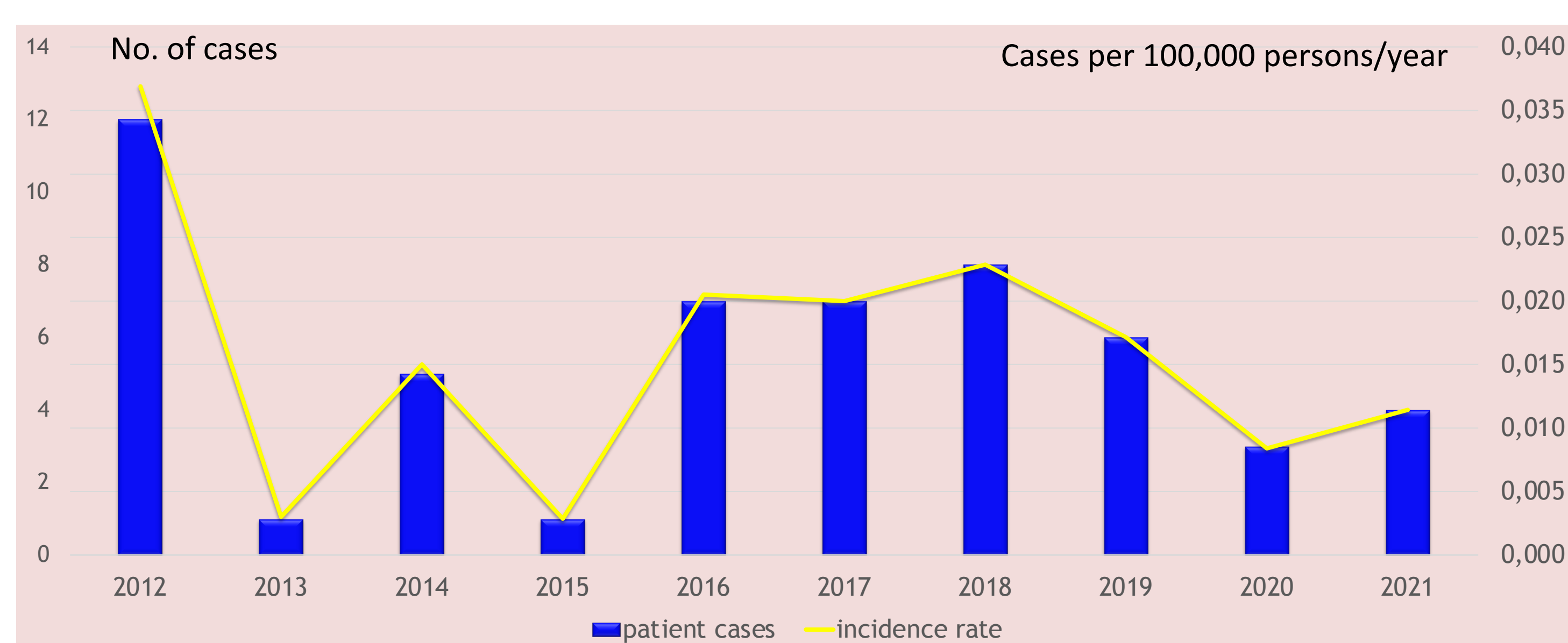


Figure 1. The incidence rate of IMD in southern Vietnam within a period of ten years, with it averaging 0.02 case per 100,000 individuals per year.

Conclusions

NmB dominated the cases of IMD in southern Vietnam during the last decade. It is noteworthy that more than half of the isolates were resistant/non-susceptible to antibiotics (penicillin, ciprofloxacin, and ceftriaxone) used for prophylaxis and treatment of IMD. Chloramphenicol-resistant ST-1576 was first detected in Vietnam in 1998 (2) and accounted in our current study for approximately two-thirds of the cases. The ST-1576 lineage differs from other genotypes in Asia. It seems now to spread across Southeast Asia after the acquisition of chloramphenicol resistance and more recently other antibiotic resistance. Our data has important implications on NmB vaccination and continued surveillance of antimicrobial resistance among meningococcal strains.

Acknowledgements

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