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# Surveillance of Invasive Meningococcal Disease in Portugal from 2020 to 2024

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# Background & Aim

In 2002, invasive meningococcal disease (IMD) became a notifiable disease in Portugal, with the National Reference Laboratory for *Neisseria meningitidis* at the National Institute of Health Doutor Ricardo Jorge (INSA) being responsible for laboratory research.

This study aims to present data on laboratory-confirmed invasive meningococcal disease, including the genetic diversity of *Neisseria meningitidis* strains identified in Portugal from 2020 to 2024.

# Material and Methods

**National Reference Laboratory for *Neisseria meningitidis*,**
**National Institute of Health Doutor Ricardo Jorge (INSA)**

Biological sterile products (blood, cerebrospinal fluids (CSF))

*Neisseria meningitidis* culture

DNA extration

Group identification (A, B, C, W and Y) real-time PCR (CDC (https://www.cdc.gov/meningitis/))

Whole Genome Sequencing
(Illumina MiSeq)

**Genomic analysis**

*in silico* characterization
(https://pubmlst.org/organisms/neisseria-spp)
- MLST
- Finetyping (*porA*, *fetA*)

Core-genome MLST(cgMLST)
(https://pubmlst.org/organisms/neisseria-spp)

Phylogenetic analysis (Graptree[1])

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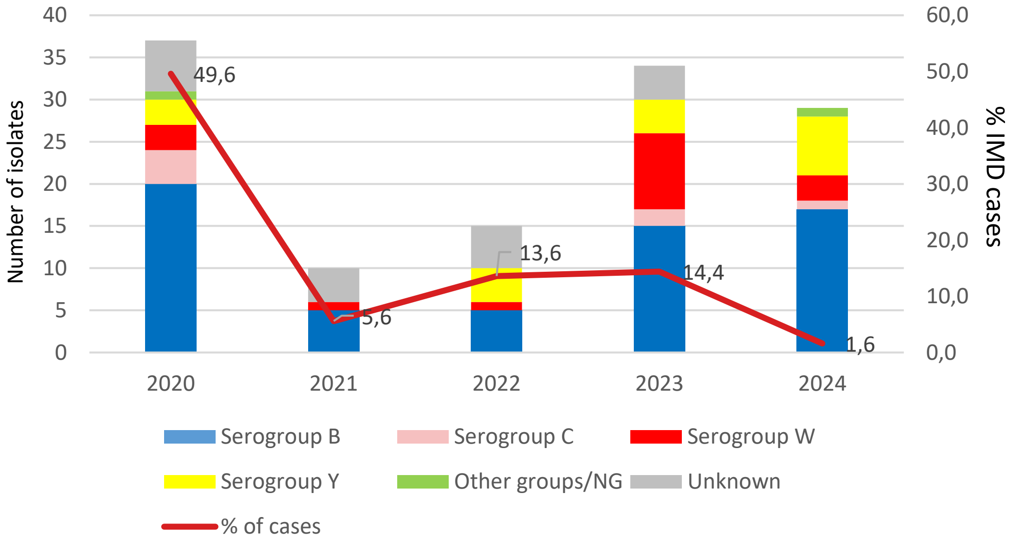
1- Z Zhou, NF Alikhan, MJ Sergeant, N Luhmann, C Vaz, AP Francisco, JA Carrico, M Achtman (2018) "GrapeTree: Visualization of core genomic relationships among 100,000 bacterial pathogens", Genome Res; doi: https://doi.org/10.1101/gr.232397.117

# Results

## Incidence of confirmed cases of IMD in Portugal by year of onset and number of cases per serogroup, 2020-2024

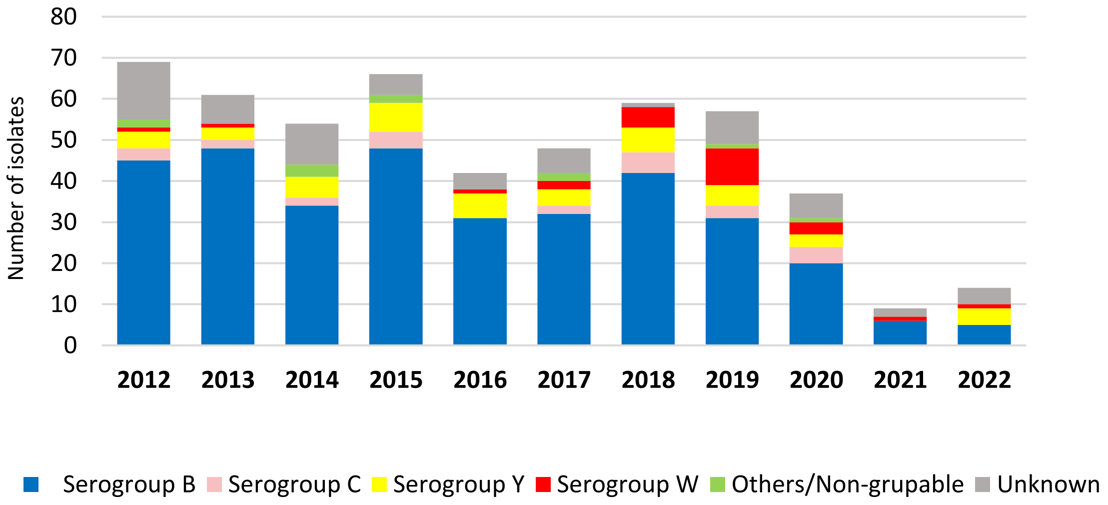
- 125 laboratory-confirmed cases of IMD
- Serogroup B was the most prevalent (49.6%), followed by serogroups Y (14.4%), W (13.6%) and C (5.6%)

### 2020-2024



Unknown are confirmed cases from other laboratories and not sent to the LNR

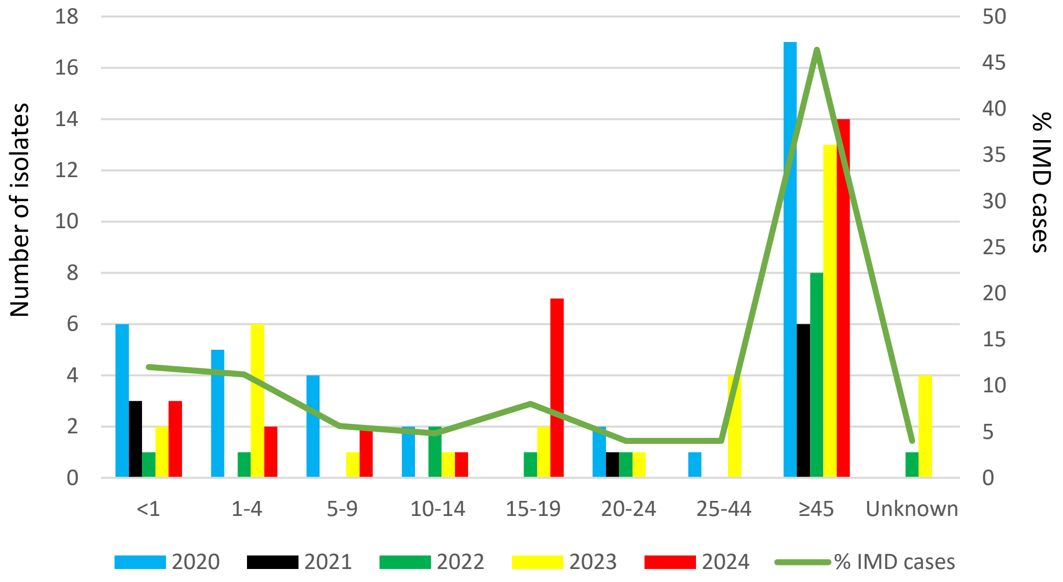
### 2012-2022



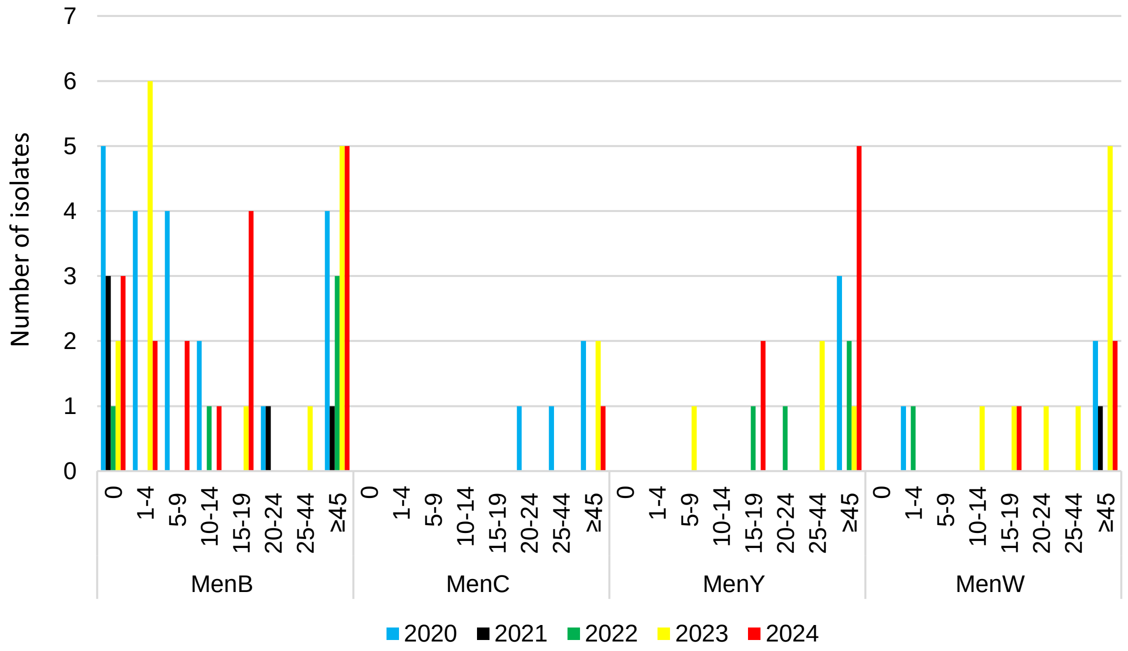
Bettencourt, C., Simões, M. J., Gonçalves, P., & Lavado, P. B. (2024). Vigilância laboratorial da doença invasiva meningocócica em Portugal, 2012-2022. Boletim Epidemiológico Observações. Volume 13 – Número Especial 16, Epidemiologia. https://www.insa.min-saude.pt/category/informacao-e-cultura-cientifica/publicacoes/boletim-epidemiologico-observacoes-suplemento-16/

# Results

**Number of IMD cases by year of onset and *per* age group, Portugal, 2020-2024**

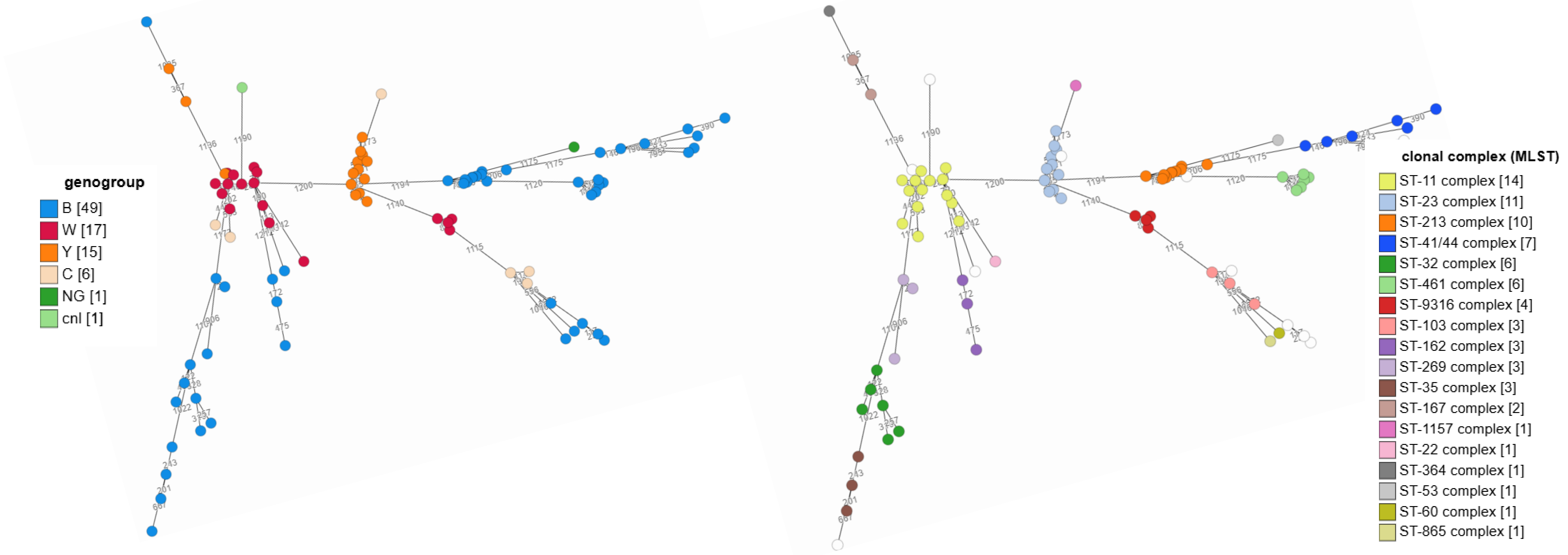


**Number of IMD cases *per* age group and serogroup Portugal, 2020-2024**



# Results

- 89 (71.2%) isolates characterized based on WGS
- Major clonal complexes (cc): B cc213 (20.4%) and cc41/44 (14.3%), Y cc23 (73.3%), W cc11 (70.6%), and C cc11/cc103 (33.3% each)



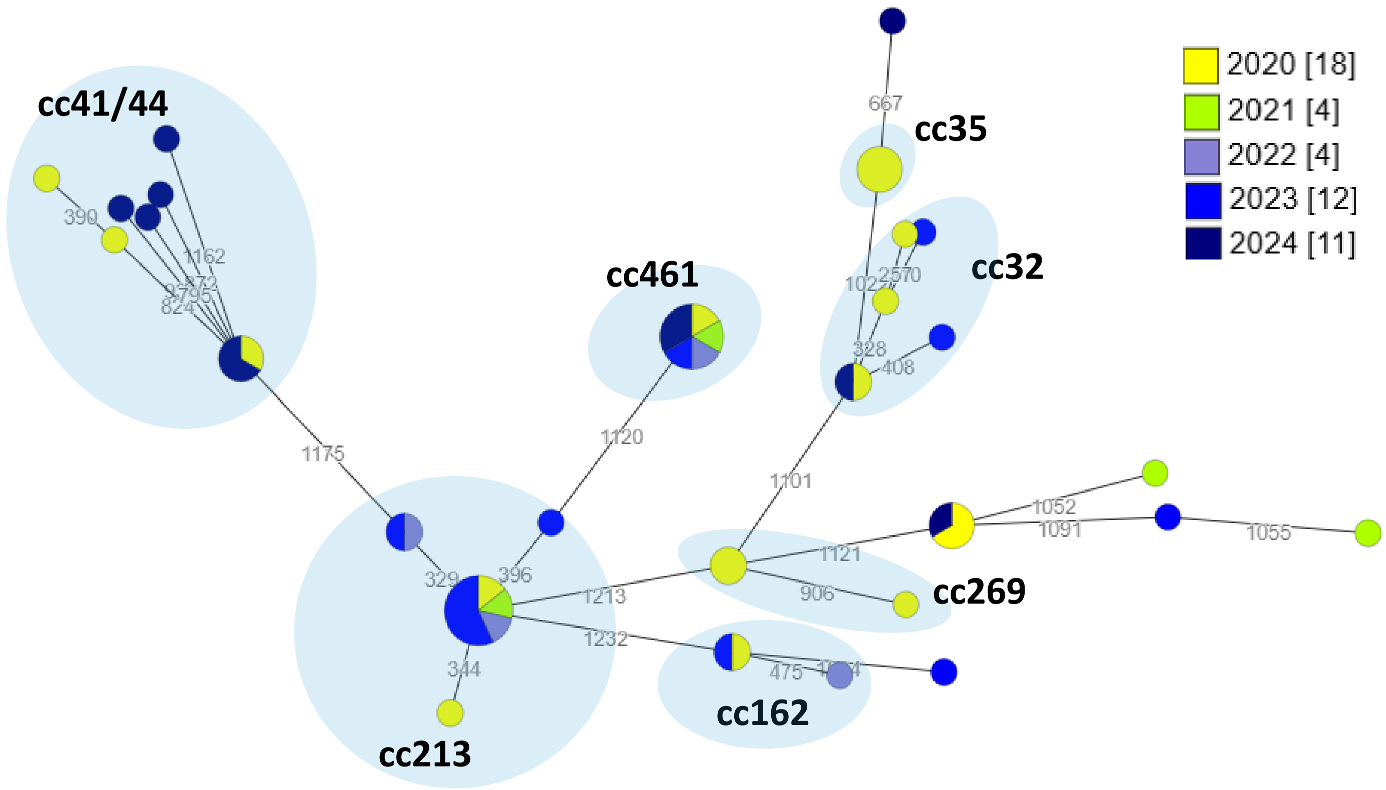
The genetic diversity among isolates was evaluated by a gene-by-gene analysis using the newly improved cgMLST schema v3, with 1329 core *loci* from pubMLST database. Minimum spanning tree was generated with the MSTreeV2 method of GrapeTree.

# Results

## Genetic clusters identified among the Portuguese invasive *Neisseria meningitidis* serogroup B isolates, 2020-2024

- 49 serogroup B isolates (55%), assigned to 11 clonal complexes

- Major clonal complexes: cc213 (20.4%), cc41/44 (14.3%), cc461, and cc32 (12.2% each)



The genetic diversity among isolates was evaluated by a gene-by-gene analysis using the newly improved cgMLST schema v3, with 1329 core loci from pubMLST database. *N. meningitidis* core-loci. Minimum spanning tree was generated with the MSTreeV2 method of GrapeTree. Filled small circles represent unique allelic profiles and are coloured by year of onset (with clonal complexes depicte by filled large circles).

# Conclusions

- Although cases of meningococcal disease have decreased in recent years in Portugal, IMD due to serogroup B and serogroup W continues to be a concern due to the number of cases and the emergence of new strains
- WGS analysis revealed high genetic diversity among *Neisseria meningitidis* isolates (especially in the MenB population) and the identification of the expansion of new genotypes (namely the MenB cc213 and MenW cc11 clusters)
- Based on the observed data, the cc213 requires special attention, as it is associated with low vaccination coverage (4CMenB) and, in recent years, an increase in the number of IMD cases in Portugal
- Overall, this study highlighted genome-based surveillance as an important tool for identifying the emergence of new virulent strains and provided important information for public health policymakers in order to control meningococcal disease more effectively

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# Our Team

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## VigLab-DIM – Network for the Laboratory Surveillance of Meningococcal Disease

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